

PR 28-JUN-2000; 2000US-0214986P.
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PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
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PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225266P.
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PR 14-AUG-2000; 2000US-0225268P.
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PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
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PR 12-SEP-2000; 2000US-0231968P.
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PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
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PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
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PR 01-NOV-2000; 2000US-0244617P.
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PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251030P.
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PR 06-DEC-2000; 2000US-0251479P.
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PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
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PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465566/50.
XX N-PSDB; AAS40878.
XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,
XX treating neural, immune system, muscular, reproductive, pulmonary,
XX cardiovascular, renal, proliferative disorders and cancerous diseases.
XX Claim 11; SEQ ID NO 1004; 1180pp; English.
XX The present invention relates to the isolation of novel human enzyme
XX polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
XX encoding them. The enzyme polypeptides of the invention may comprise the
XX functional classes of oxidoreductases, transferases, hydrolases, lyases,
XX isomerases or ligases. The sequences of the invention are useful in the

CC diagnosis, treatment, prevention and/or prognosis of a wide range of
 CC disorders including hyperproliferative disorders (e.g. cancer),
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
 CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
 CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
 CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
 CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
 CC infectious disorders (e.g. influenza). The polynucleotides of the
 CC invention can also be used in gene therapy. AAU22915-AAU23814 represent
 CC the novel human enzyme polypeptides of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX.

SQ Sequence 628 AA;

Alignment Scores:
 Pred. No.: 2,48e-287 Length: 628
 Score: 3195.00 Matches: 628
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 70.94% Indels: 0
 DB: 4 Gaps: 0

US-09-945-326-1 (1-2452) x AAU23008 (1-628)

QY 46 GGGTGGGGAACATCGGCGAGCATGAGCGGCTCGGGCTCTTCTTCGCGCACCCAGCGCTGCG 105
 DB 1 GlyTrpGlyThrSerGlySerMetSerGlyCysGlyLeuPheLeuArgThrAlaAla 20
 QY 106 GTCCTGCTCCGCGGGTCTGGTGGTCTTACCGCGAACCGCGGGCTACTCGCGCACCGC 165
 DB 21 AlaArgAlaCysArgGlyLeuValValSerThrAlaAsnArgArgLeuLeuArgThrSer 40
 QY 166 CCGCTCTAGAGCTTTCGCGAAGAGCTTTCCTAGCGCAAAATCAAGAGAAAGAGTT 225
 DB 41 ProProValArgAlaPheAlaLysGluLeuPheLeuGlyLysIleLysLysGluVal 60
 QY 226 TTCCATTTTCAGAAATGAGCAAGATGAACTTAATGAAATCAATCAGTTCTTGGGACCC 285
 DB 61 PheProPheProGluValSerGlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyPro 80
 QY 286 GTGGAAAAATTTTCATCAAGAGGTGGACTCCCGAAAAATTTGACCAAGGAGGAAAAATC 345
 DB 81 ValGluLysPhePheThrGluGluValAspSerArgLysIleAspGlnGluGlyLysIle 100
 QY 346 CCAGATCAAACTTTGGAGAAATTCAGAGCCTAGGGCTTTTGGGCTGCGCAAGTCCCGAA 405
 DB 101 ProAspGluThrLeuGluLysLeuLysSerLeuGlyLeuPheGlyLeuGlnValProGlu 120
 QY 406 GAATATCGTGGCTGGGCTTCTCCAAACCATGTACTCAAGACTAGGGGAGATCATCAGC 465
 DB 121 GluTyrglyGlyLeuGlyPheSerAsnThrMetTyrSerArgLeuGlyGluIleSer 140
 QY 466 ATGATGGGTCCATCATGTGACCCCTGGCAGCGCACCGAGGCTATTGGCTCAAGGGATC 525
 DB 141 MetAspGlySerIleThrValThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIle 160
 QY 526 ATCTTGGCTGGCCTAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGAG 585
 DB 161 IleLeuAlaGlyThrGluGluGlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGlu 180
 QY 586 CACATTGCGGCTTCTGCCTCAGCGAGCCAGCGAGTGGGCGGATGCGAGCTCAATCCGG 645
 DB 181 HisIleAlaAlaPheCysLeuThrGluProAlaSerGlySerAspAlaAlaSerIleArg 200
 QY 646 AGCAGAGCCACACTAAGTGAAGACAGAAGACACTACATCTCAATGCTCAAGGTCTGG 705
 DB 201 SerArgAlaThrLeuSerGluAspLysLysHisTyrIleLeuAsnGlySerLysValTrp 220
 QY 706 ATTACTAATGAGAGCTGGCCAAATATTTTACTGTGTGTTGCAAGAGACTGAGGTCTGAT 765
 DB 221 IleThrAsnGlyGlyLeuAlaAsnIlePheThrValPheAlaLysThrGluValValAsp 240

QY 766 TCTGATGATCAGTGAAGACAAATACAGCATTCATTAGTAGAAAGAGACTTTGGTGA 825
 DB 241 SerAspGlySerValLysAspLysIleThrAlaPheIleValGluArgAspPheGlyGly 260
 QY 826 GTCACTAATCGGAAACCCGAGATAAATTAGGCATTCGGGGCTCCAACTTTGTAAGTC 885
 DB 261 ValThrAsnGlyLysProGluAspLysLeuGlyIleArgGlySerAsnThrCysGluVal 280
 QY 886 CATTTTGAACACCAAGATACCTGTGGAAAAATCTCTCGAGAGGTCGAGATGGGTTT 945
 DB 281 HisPheGluAsnThrLysIleProValGluAsnIleLeuGlyGluValGlyAspGlyPhe 300
 QY 946 AAGTGGCCATGAACATCTCTCAACAGCGCGGTTTCAGCATGGGCAGCGTCTGGCTGGG 1005
 DB 301 LysValAlaMetAsnIleLeuAsnSerGlyArgPheSerMetGlySerValValAlaGly 320
 QY 1006 CTGCTCAAGAGATTGATTGAAATGACTGTCTGAGTACGCTTCAGCAAGAAACAGTTTAAAC 1065
 DB 321 LeuLeuLysArgLeuIleGluMetThrAlaGluTyrAlaCysThrArgLysGlnPheAsn 340
 QY 1066 AAGAGGCTCAGTGAATTTGGATTGATTTCAGGAGAAATTTTCACCTGATGGCTCAGAAGCT 1125
 DB 341 LysArgLeuSerGluPheGlyLeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAla 360
 QY 1126 TAGCTCATGGAGATGATGACTTACCTCACAGCAGGAGTGTGTGACCAACCTGGCTTCCC 1185
 DB 361 TyrValMetGluSerMetThrTyrLeuThrAlaGlyMetLeuAspGlnProGlyPhePro 380
 QY 1186 GACTGTCTCCATCGAGCGCATGGTGAAGTGTTCAGCTCCGAGGCGCTGSCAGTGT 1245
 DB 381 AspCysSerIleGluAlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCys 400
 QY 1246 GTGAGTGAAGCGCTGCAGATCCTCGGGGCTTGGGCTACACAGGGAGTATCCGTACGAG 1305
 DB 401 ValSerGluAlaLeuGlnIleLeuGlyLeuGlyTyrThrArgAspTyrProTyrGlu 420
 QY 1306 CGCATCTGGTGACACCCGCATCTCTCATCTTCGAGGGAAACCAATGAGATTCCTCGG 1365
 DB 421 ArgIleLeuArgAspThrArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArg 440
 QY 1366 ATGTACATCCCTCGAGCGTCTGAGCATGCGCGCGCATCTCTGACTACCAGGATCCAT 1425
 DB 441 MetTyrIleAlaLeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrArgIleHis 460
 QY 1426 GAGCTTAAAAGCGCCAAAGTGAGCACAGTATCATGATACCGTTGGCCCGAGGCTTCGGGAC 1485
 DB 461 GluLeuLysGlnAlaLysValSerThrValMetAspThrValGlyArgLeuArgAsp 480
 QY 1486 TCCTTGGGCGGAATGTGTGACCTTGGGCTGACAGGCAACCATGGAGTTGTCCACCCAGT 1545
 DB 481 SerLeuGlyArgThrValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSer 500
 QY 1546 CTTTGGCAGCATGCCAACAGTTTGAGGAACACCTACTGCTTCGGCCGCGACCGTGGAG 1605
 DB 501 LeuAlaAspSerAlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGlu 520
 QY 1606 ACATGTCTGTCTCGCTTTGGCAAGACCATCATGAGGAGCAGCTGGTACTGAAGCGGTG 1665
 DB 521 ThrLeuLeuLeuArgPheGlyLysThrIleMetGluGluGlnLeuValLeuLysArgVal 540
 QY 1666 GCCAACATCTCATCAACCTGTATGGCATGACGGCCGTGTGTCTCGGGCCAGCGCTCC 1725
 DB 541 AlaAsnIleLeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSer 560
 QY 1726 ATCGGCTTGGGCTCCGCAACCGACGAGGTTCTCTTGGCCAACTCTTGGCTTCTGGGTG 1785
 DB 561 IleArgIleGlyLeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysVal 580
 QY 1786 GAAGCTTACTTGCAAGATCTTTCAGGCTCTCTCAGCTGACAGAGTATGTCTCCAGAAAC 1845
 DB 581 GluAlaTyrLeuGlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsn 600

QY 1846 CTAGATGACAGATTAGAAAGTGTCCAGCAGATCCTTGAGAGCGAGCCATATCTGT 1905
Db LeuAepGluGlnIleLysValSerGlnGlnIleLeuGluLysArgAlaTyrIleCys 620
QY 1906 GCCACCTCTGTGACAGACATGC 1929
Db 621 AlaHisProLeuAepArgThrCys 628
RESULT 2
ADM87776
ID ADM87776 standard; protein; 628 AA.
XX AC
XX AC
XX ADM87776;
XX 03-JUN-2004 (first entry)
XX Human EST derived amino acid sequence SEQ ID NO:869.
XX
XX respiratory; cytostatic; antiarthritic; antiinflammatory;
KW gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KW inflammatory condition; arthritis; inflammatory bowel disease;
KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW graft versus host disease; human; expressed sequence tag; EST.
XX OS
XX Homo sapiens.
XX
XX WO2004009834-A2.
XX
XX 29-JAN-2004.
XX
XX 19-JUL-2002; 2002WO-US022858.
XX
XX 21-JUL-2001; 2001US-0306971P.
XX 28-MAR-2002; 2002US-00112944.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Yang Y, Wang G, Zhang J, Ren F, Xue A, Wang J;
PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX
XX N-PSDB; ADM87558.
XX
XX WPI; 2004-143291/14.
XX
XX New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease, graft
PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT versus host disease.
XX
XX Example 2; SEQ ID NO 869; 591pp; English.
XX
XX The present invention describes an isolated polynucleotide (I): (a)
XX comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
XX which encodes a polypeptide with biological activity, where the
XX polynucleotide hybridizes to (I) under stringent hybridisation conditions
XX or has greater than 99% sequence identity with (I). (I) has respiratory,
XX cytostatic, antiarthritic, antiinflammatory, gastrointestinal,
XX antibacterial, immunosuppressive, antidiabetic and antirheumatic
XX activities, and can be used in gene therapy. (I) can be used for
XX generating polynucleotides encoding chimeric or fusion proteins and
XX heterologous protein sequences. The polynucleotides can be used to
XX express recombinant protein for analysis, characterisation or therapeutic
XX use; as markers for tissues in which the corresponding protein is
XX preferentially expressed; as molecular weight markers on gels; as
XX chromosome markers or tags to identify chromosomes or to map related gene
XX positions; to compare with endogenous DNA sequences in patients to
XX identify potential genetic disorders; as probes to hybridise and discover
XX genes, related DNA sequences; as a source of information to derive PCR
XX primers for genetic fingerprinting; as a probe to subtract-out known
XX sequences in the process of discovering other novel polynucleotides; for
XX selecting and making oligomers for attachment to a gene chip or other
XX support, including for examination of expression patterns; to raise anti-

CC protein antibodies using DNA immunisation techniques; and as an antigen
CC to raise anti-DNA antibodies or elicit another immune response. The
CC polynucleotides and polypeptides can also be used as nutritional carbon
CC or supplements, e.g. as a protein or amino acid supplement, as a carbon
CC source, as a nitrogen source or as a source of carbohydrates. The
CC polynucleotides and polypeptides can also be used to treat cancer. The
CC compositions are useful for promoting better or faster closure of non-
CC healing wounds, for the generation and regeneration of tissues, for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, and conditions resulting from
CC systemic cytokine damage. The compositions can also be used to treat
CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
CC or graft versus host disease. The present sequence represents an
CC expressed sequence tag (EST) derived amino acid sequence from the present
CC invention. N.B. The sequences for this patent were obtained from the
CC USPTO web site from an equivalent US patent US20040048249A1.
XX
SQ Sequence 628 AA;
Alignment Scores:
Pred. No.: 4,23e-285 Length: 628
Score: 3171.00 Matches: 623
Percent Similarity: 99.52% Conservative: 2
Best Local Similarity: 99.20% Mismatches: 3
Query Match: 70.40% Indels: 0
DB: 8 Gaps: 0
US-09-945-326-1 (1-2452) x ADM87776 (1-628)
QY 46 GGCTGGGGAACATCGGGCAGCATGAGCGGTGGCGCTCTTCTGGCCACCGGTGCG 105
Db 1 GlyTyrGlyThrSerGlySerMetSerGlyCysGlyLeuPheLeuArgThrAlaAala 20
QY 106 GCTCGTGCCTCGCGGGTCTGTGGTCTCTTACCGCGAACCGCGGCTACTGCGCACCAGC 165
Db 21 AlaArgAlaCysArgGlyLeuValValSerThrAlaAsnArgArgLeuLeuArgThrSer 40
QY 166 CGCCCTGTAGAGCTTTTCGCAAGAGCTTTCTAGGCAAAATCAAGAGAGAGAGTT 225
Db 41 ProProValArgAlaPheAlaLysGluLeuPheLeuGlyLysLysLysLysGluVal 60
QY 226 TTCCCATTTCCAGAGTTAGCCAAAGATGAACCTTAATGAATCAATCATGTTCTTTGGGACCC 285
Db 61 PheProPheProGluValSerGlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyPro 80
QY 286 GTGGAATAATTTCTACTGAAGAGGTGGACTCCCGAAAAATTCACCGAGAGAGGAAAAATC 345
Db 81 ValGluLysPhePheThrGluGluValAspSerArgLysIleAspGlnGluGlyLysIle 100
QY 346 CCAGATGAAACTTTGGAGAAATTTGAAGAGCTTAGGGCTTTTTCGGCTGCAAGTCCCGAGAA 405
Db 101 ProAspGluThrLeuGluLysLeuLysSerLeuGlyLeuPheGlyLeuGlnValProGlu 120
QY 406 GAATATGTGGCTGGCTTCTCCAAACACATGTACTCAAGACTAGGGGAGATCATCAGC 465
Db 121 GluTyrGlyGlyLeuGlyPheSerAsnThrMetTyrSerArgLeuGlyGluThrIleSer 140
QY 466 ATGGATGGTCCATCATCTGTACCTCGACCTGGCAGCGCAGCAGCTATTGGCTCAGGGGATC 525
Db 141 MetAspGlySerIleThrValThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIle 160
QY 526 ATCTTGGCTGGCACTGAGGAGAGAAAGCAAAATCTTGCCTAAACTGGCGTCCGGGGAG 585
Db 161 IleLeuAlaGlyThrGluGluGlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGlu 180
QY 586 CACATTGCGACCTTCTGCTCAGCGAGCCAGCCAGTGGGAGCGATCGACCTCAATCCGG 645
Db 181 AlaLeuAlaAlaPheCysLeuThrGluProAlaAsnGlySerAspAlaAala***IleArg 200
QY 646 AGCAGAGCCACACTAGTGAAGACAGAGAGAGACTACATCTCAATGGCTCCAGAGGTCTGG 705
Db 201 SerArgAlaThrIleuSerGluAspLysLysHisTyrIleLeuAsnGlySerLysValTyr 220

QY 706 ATTTACTAATGAGAGCTGGCCAAATATTTTACTGTGTGTTGCAAAAGACTGAGGTGCTTGAT 765
Db ILeThrAsnGlyGlyLeuAlaAsnIlePheThrValPheAlaIleThrGluValValAsp 240
QY 766 TCTGATCGATCAGTGAAGCAAAATCACAGCATTCATAGTAAAGAGCTTTGGTGA 825
Db SerAspGlySerValIleAspLysIleThrAlaPheIleValGluArgAspPheGlyGly 260
QY 826 GTCACTAATGGGAACCCGAAGATAAATATAGGCATTCGGGGCTCCAACTTTGTAAGTC 885
Db ValThrAsnGlyLysProGluAspLysLeuGlyIleArgGlySerAsnThrCysGluVal 280
QY 886 CATTTTGAACACCAAGATACCTGTGGAAACATCTTGGAGAGTTCGGAGATGGGTTT 945
Db HisPheGluAsnThrLysIleProValGluAsnIleLeuGlyGluValGlyAspGlyPhe 300
QY 946 AAGTGGCCATGACATCTCTCAACNGCGCGGTTCAGCATGGCGCAGCTCGTGGCTGG 1005
Db LysValAlaMetAsnIleLeuAsnSerGlyArgPheSerMetGlySerValValAlaGly 320
QY 1006 CTGCTCAAGAGATTGATTGAATGACTGCTGAGTACGCTGCACAAAGCAACAGTTTAAC 1065
Db LeuLeuLysArgLeuIleGluMetThrAlaGluTyraCysThrArgLysGlnPheAsn 340
QY 1066 AAGAGGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCACATGATGGCTCAGAAGCT 1125
Db LysArgLeuSerGluPheGlyLeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAla 360
QY 1126 TAGCTCATGAGAGATGACTACTACCTACACAGCGGATGCTGCACCACTGCTTCCC 1185
Db TyrValMetGluSerMetThrTyraLeuThrAlaGlyMetLeuAspGlnProGlyPhePro 380
QY 1186 GACTGCTCCATCAGGCGAGCATGCTCAAGTGTTTCAGCTCCGAGGCGCTGTCAGTGT 1245
Db AspCysSerIleGluAlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCys 400
QY 1246 GTGAGTGAGCGCTGCAGATCCTCGGGGCTTGGGCTTACAAAGGGACTATCCGTACGAG 1305
Db ValSerGluAlaLeuGlnIleLeuGlyLeuGlyTyraThrArgAspTyraProTyraGlu 420
QY 1306 CGATACCTGGTGNACCCGCTCTCTCTATCTTCGAGGGAACCATGATGATCTCCGG 1365
Db ArgIleLeuArgAspThrArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArg 440
QY 1366 ATGTACATCCCTCGAGGCTGTCAGCATGCGGCGCATCTGACTACCAAGATCCAT 1425
Db MetTyraIleAlaLeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHis 460
QY 1426 GAGCTTAAACAGGCGCAAGTGAGCACAGTCACTGATACCGTTGGCCGGAGGCTTCGGGAC 1485
Db GluLeuLysGlnAlaLysValSerThrValMetAspThrValGlyArgArgLeuArgAsp 480
QY 1486 TCCCTGGCCGAACTGTGGACCTGGGCTGACAGGCAACCATGAGTTGTGCCCCCACT 1545
Db SerLeuGlyArgThrValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSer 500
QY 1546 CTTGCGGACAGTGCACAAAGTTTGAGGAGAACACCTACTGCTTCGCGCGGACCGGTGGAG 1605
Db LeuAlaAspSerAlaAsnLysPheGluGluAsnThrTyraCysPheGlyArgThrValGlu 520
QY 1606 ACATGCTGCTCGCTTTGGCAGACACCATCATGAGGAGCAGCTGTGTACTGAAGCGGGTG 1665
Db ThrLeuLeuLeuArgPheGlyLysThrIleMetGluGluGlnLeuValLeuLysArgVal 540
QY 1666 GCCACATCTCATCAACCTGTATGGATGACGCGCTGTCTGCGGGGCGACCGCTCC 1725
Db AlaAsnIleLeuIleAsnLeuTyraGlyMetThrAlaValLeuSerArgAlaSerArgSer 560
QY 1726 ATCGCATTCGGCTCCGCAACACGACGACGAGTCTCTTGGCCACACCTTCTGGGTG 1785
Db IleArgIleGlyLeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysVal 580

QY 1786 GAGCTTACTTGCAGAAATCTCTTCAGCCTCTCTCAGCTGCAGCAAGTATGCTCCAGAAAC 1845
Db GluAlaTyraLeuGlnAsnLeuPheSerLeuSerGlnLeuAspLysTyraAlaProGluAsn 600
QY 1846 CTAGATGAGCAGATTAAAGAAAGTGTCCTCCAGCAGATCTCTGAGAGCGAGCCTATATCTGT 1905
Db LeuAspGluGlnIleLysLysValSerGlnGlnIleLeuGluLysArgAlaTyraIleCys 620
QY 1906 GCCCACCCTCTGCAGCAGGACATGC 1929
Db 621 AlaHisProLeuAspArgThrCys 628
RESULT 3
AAB73691
ID AAB73691 standard; protein; 621 AA.
XX AAB73691;
XX 11-SEP-2001 (first entry)
XX Human oxidoreductase protein ORP-24.
XX Human oxidoreductase protein; ORP; cell proliferative disorder;
KW arteriosclerosis; cirrhosis; psoriasis; cancer; endocrine disorder;
KW diabetes mellitus; diabetes insipidus; dwarfism; hirsutism; amenorrhea;
KW osteoporosis; metabolic disorder; obesity; phenylketonuria;
KW hypercholesterolemia; reproductive disorder; infertility;
KW ovulatory defect; menstrual cycle defect; endometriosis;
KW polycystic ovary disease; spermatogenesis disruption; impotence;
KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; Creutzfeldt-Jakob disease;
KW meningitis; cerebral palsy; muscular dystrophy; mood disorder; anxiety;
KW schizophrenic disorder; infection; autoimmune disorder;
KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS; asthma;
KW allergy; Crohn's disease; atopic dermatitis; gout; multiple sclerosis;
KW rheumatoid arthritis; ulcerative colitis; drug screening; gene therapy.
XX Homo sapiens.
XX WO200144448-A2.
XX 21-JUN-2001.
XX 07-DEC-2000; 2000WO-US033158.
XX 16-DEC-1999; 99US-0172367P.
XX (INCY-) INCYTE GENOMICS INC.
XX Yue H, Lal P, Tang YT, Hillman JL, Baughn MR, Azimzai Y, Lu DAM;
WPI; 2001-390245/41.
XX N-PSDB; AAH24246.
XX Novel human oxidoreductase protein (ORP) useful for diagnosing, treating
PT and preventing cell proliferative, neurological, viral, reproductive and
PT autoimmune/inflammatory disorders associated with abnormal expression of
PT ORP.
XX Claim 1; Page 117-119; 136pp; English.
XX Sequences AAB73668-AAB73694 represent 27 novel human oxidoreductase
CC proteins, designated ORP-1 to ORP-27 respectively, and sequences AAH24223
CC -AAH24249 represent cDNAs encoding ORP-1 to ORP-27. Human ORP proteins
CC and nucleic acids are useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. arteriosclerosis, cirrhosis, psoriasis,
CC cancers); endocrine disorders (e.g. type I or II diabetes mellitus,
CC diabetes insipidus, dwarfism, hirsutism, amenorrhea, osteoporosis);
CC metabolic disorders (e.g., obesity, phenylketonuria,
CC hypercholesterolemia); reproductive disorders (e.g., infertility,
CC ovulatory and menstrual cycle defects, endometriosis, polycystic ovary
CC disease, disruption of spermatogenesis, impotence); neurological

CC disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's
CC disease, Parkinson's disease, meningitis, Creutzfeldt-Jakob disease,
CC cerebral palsy, muscular dystrophy, mood, anxiety and schizophrenic
CC disorders); viral, bacterial, fungal and parasitic infections; and
CC autoimmune/inflammatory disorders such as acquired immunodeficiency
CC syndrome (AIDS), allergies, asthma, Crohn's disease, atopic dermatitis,
CC gout, multiple sclerosis, rheumatoid arthritis or ulcerative colitis.
CC Human ORP proteins and nucleotides can be used to identify compounds
CC which modulate their activity or expression. ORP nucleic acid sequences
CC may also be used for assessing the toxicity of a test compound, to detect
CC upstream sequences such as promoters and regulatory elements, and to
CC create knock out or knock in animals or transgenic animals to model human
CC disease. Oligonucleotide primers derived from ORP gene sequences may be
CC used to detect single nucleotide polymorphisms (SNPs) and for mapping the
CC naturally occurring genomic sequences. Antibodies specific for ORP
CC proteins may be used in the diagnosis of disorders associated with
CC aberrant ORP expression, in assays to monitor patients being treated with
CC ORP or modulators thereof, and for assessing toxicity of potential drugs
XX
SQ Sequence 621 AA;

Alignment Scores:
Pred. No.: 1.99e-283 Length: 621
Score: 3153.00 Matches: 621
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.00% Indels: 0
DB: 4 Gaps: 0

US-09-945-326-1 (1-2452) x AAB73691 (1-621)

QY 67 ATGAGCGCTGCGGCTCTTCTCCGACACACGCGCTCGGCTCGCTCCCGGGCTG 126
DB 1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu 20
QY 127 GTGGTCTCTACCGGAACCGCGGCTACTGGCCACCGCGCTGACGAGCTTTGCC 186
DB 21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProValArgAlaPheAla 40
QY 187 AAAGAGCTTTCTAGGCAAAATCAAGAGAAAGAGTTTCCCATTTCCAGAGTTAGC 246
DB 41 LysGluLeuPheLeuGlyLysIleLysLysGluValPheProPheProGluValSer 60
QY 247 CAAGATGAACCTAATGAATCAATCAGTTCTTGGGACCGCTGGAAAAATCTTCACCTGAA 305
DB 61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80
QY 307 GAGTGGACTCCGAAAAATTTGACAGAGGAAATCCAGATGAAACTTTGGAGAAA 366
DB 81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100
QY 367 TTGAAGAGCTAGGCTTTTGGCTGCACTCCAGAGAAATATGTTGGCTCGGCTTC 426
DB 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluLysGlyGlyLeuGlyPhe 120
QY 427 TCCAAACACATGTTACTCAAGACTAGGGAGATCATCAGCATGGATGGTCCATCAGCTGTG 486
DB 121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
QY 487 ACCCTGGCAGCGCACCGGCTATTGGCTCAAGGGATCATCTTGGCTGGCAGCTGAGGAG 546
DB 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleLeuAlaGlyThrGluGlu 160
QY 547 CAGAAAGCCAAATATTGCTCCCTAACTGGCGTCCGGGAGACATTTGCAGCCCTCTGCTC 606
DB 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180
QY 607 ACGGAGCCAGCAGTGGAGCGATGACGCTCAATCCGGACGACGACCACTAAGTGAA 666
DB 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
QY 667 GACAAGAGCACTACCTCTCAATGGCTCCAGGCTCGGATTTACTAATGGAGGCTGCC 726

DB 201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
QY 727 AATATTTTACTGTGTTTCCAAAGACTGAGGTCTGTTGATTCTGATGATCAGTGAAGAC 786
DB 221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
QY 787 AAAATCACAGCATTCATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAA 846
DB 241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260
QY 847 GATAAATAGGATTCGGGGCTCCACACCTTGTGAAGTCCATTTGAAAACACCAAGATA 906
DB 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
QY 907 CTGTGTAAGAACATCTTCGAGAGTCCGAGATGGGTTTAAAGTGGCCATGAACATCCTC 966
DB 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMethAsnIleLeu 300
QY 967 AACAGCGCGGTTACGATGGCAGCGTGGTGGCTGCTCAAGAGATTGATTGAA 1026
DB 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
QY 1027 ATGACTGCTGAGTACGCTGCACAGGAAACAGTTTAAACAAGAGGCTCAGTGAATTGGA 1086
DB 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
QY 1087 TTGATTTCAGGAGAAATTTGCACCTGATGGCTCAGAAGCTTTACGTATGGAGAGTATGACC 1146
DB 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
QY 1147 TACCTCACAGCGGATGCTGGACCAACCTGGCTTTCCGACTGCTCCATCGAGGCGACC 1206
DB 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
QY 1207 ATGGTCAAGGTGTTACGCTCCGAGCGCGCTGTCAGTGTGTGAGTCAGGCGCTGCAGATC 1266
DB 381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400
QY 1267 CTCGGGCGCTTGGGCTACACAAGGGACTATCCGTACGAGCGCATATCGGTGACACCCGC 1326
DB 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
QY 1327 ATCTCTCTCATCTTCAGGGAACCAATGAGATTCTCGGATGTACATCGCCCTGACGGGT 1386
DB 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY 1387 CTCAGCATCCCGCGCATCTCTGACTACAGGATCCATGAGCTTAAACAAGGCCAAAGTG 1446
DB 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY 1447 AGCACAGTCATGATACCGTTGGCCGAGGCTTTCGGGACTCCCTGGGCCCGAACTGGGAC 1506
DB 461 SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480
QY 1507 CTGGGCTGACAGGCAACCATGAGTTGTGCACCCAGTCTCGGACAGTCCGACAGCCACAAG 1566
DB 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY 1567 TTTGAGGAGAACCTACTCTCTTCGGCCGACCGTGGAGACACTGTCTGCTCCGCTTTGGC 1626
DB 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuArgPheGly 520
QY 1627 AAGACCATCATGAGGAGCAGCTGTACTGAAGGGTGGCCACATCTCTCATCAACCTG 1686
DB 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
QY 1687 TATGGCATGACGCGCGTGTCCGGCCAGCGCTCCCATCCGATTCGGCTGGCTCCCGAAC 1746
DB 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY 1747 CAGCACCAAGAGGTTCTCTTTGGCCAAACACCTTCTCGTGGAGGCTTACTTGCAGAACTC 1806
DB 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Db 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
Qy 967 AACAGCGCGGTTACACATGGGAGCGTGTGGCTGGCTGCTCAAGAGATTGATTGAA 1026
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Qy 1027 ATGACTCTCAGTACGCTGCACAGGAACACAGTTTAAACAGAGGCTCAGTGAATTGGGA 1086
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Qy 1087 TTGATTACAGAGAAATTTGCACCTGATGGCTCAGAGGCTTACGTCTGAGAGATGATGACC 1146
Db 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
Qy 1147 TACCTACAGCAGGATCTGGACCACTGGCTTTCCCGACTGCTCCATCGAGGCGACC 1206
Db 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
Qy 1207 ATGGTGAAGTGTTCAGCTCCGAGCGCGCTGGCAGTGTGTGAGTAGGCGCTGCAGATC 1266
Db 381 MetValLysValPheSerSerGluAlaAlaTyrGlnCysValSerGluAlaLeuGlnIle 400
Qy 1267 CTCGGGGCTTGGCTACACAGGAGCTATCCGTACGAGCGCATACTGCGTGACACCCGC 1326
Db 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
Qy 1327 ATCTCTCTCATCTCGAGGACCAATGAGATTCCTCGGATGTACATCGCCCTGACGGGT 1386
Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
Qy 1387 CTGCAGCATCGCGCCGCTCCTGACTACAGGATCCATGAGCTTAAACAGGCCAAAGTG 1446
Db 441 LeuGlnHisAlaGlyArgIleLeuThrArgIleHisGluLeuLysGlnAlaLysVal 460
Qy 1447 AGCACACTCATGATACCTGTGGCCGAGGCTTGGGACTCCCTGGGCCCAACTGTGGAC 1506
Db 461 SerThrValMetAspThrValGlyArgLeuArgAspSerLeuGlyArgThrValAsp 480
Qy 1507 CTGGGGCTGACGACACCATGAGTGTGCACCCAGCTTCGGGACAGTGCACACAAAG 1566
Db 481 LeuGlyLeuThrGlyAsnHisGlyValAlaHisProSerLeuAlaAspSerAlaAsnLys 500
Qy 1567 TTTGAGGAGAACCTACTCTCGGCGGACCGTGGAGACACTGCTGCTCCGCTTTGGC 1626
Db 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuArgPheGly 520
Qy 1627 AAGACCATCATGAGGAGCAGCTGGTACTGAAGCGGTGGCCCAACATCTCATCAACCTG 1686
Db 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
Qy 1687 TATGGCATGACGCGCTGCTCGCGGCGCAGCGCTCCATCCGATTTGGCTCCGCAAC 1746
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Qy 1747 CACGACCACAGGTTCTCTTGGCCCAACACCTCTCTGCGTGAAGCTTACTTGCAGAAATCTC 1806
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
Qy 1807 TTCAGCTCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGACGAGATTAGAAA 1866
Db 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
Qy 1867 GTCTCCACAGATCTCTGAGAGCGGCTATATCTGTCCACCCCTCTGGCAGGACA 1926
Db 601 ValSerGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
Qy 1927 TGC 1929
Db 621 Cys 621

RESULT 5
AAE21680
.ID AAE21680 standard; protein; 621 AA.

XX AAE21680;
XX AC
XX DT 16-JUL-2002 (first entry)
XX DE Human acyl dehydrogenase DHDR-7 (62112 protein).
XX KW Human; dehydrogenase-7; DHDR-7; 62112 protein; CNS disorder; epilepsy;
KW Alzheimer's disease; AS; Pick's disease; differentiation disorder;
KW Huntington's disease; autonomic function disorder; hyperthyroidism;
KW depression; schizophrenia; panic migraine; cardiac related disorder;
KW anxiety; obesity; arteriosclerosis; restenosis; Parkinson's disease;
KW angina; hypertension; cardiomyopathy; arrhythmia; muscle weakness;
KW arterial inflammation; cell proliferation disorder; growth disorder;
KW diabetes mellitus; hypertension; migration disorder; gene therapy;
KW fertility disorder; autoimmune disorder; metabolic disorder; ataxia;
KW cancer; hepatic disease; acyl-CoA dehydrogenase; beta-oxidation; enzyme.
XX OS Homo sapiens.
XX PH
XX Key Location/Qualifiers
XX Domain 1..36
FT /note= "Dehydrogenase domain"
FT Domain 23..123
FT /note= "Dehydrogenase precursor domain"
FT Domain 37..426
FT /note= "Acyl-CoA very long chain dehydrogenase domain"
FT Domain 70..432
FT /note= "Dehydrogenase-related long acyl-CoA chain
FT oxidoreductase domain"
FT Domain 74..448
FT /note= "Short chain related acyl-CoA dehydrogenase
FT specific domain"
FT Domain 85..438
FT /note= "Acyl CoA dehydrogenase domain"
FT Domain 85..177
FT /note= "Acyl CoA dehydrogenase middle domain"
FT Domain 147..431
FT /note= "ACD-3 acyl-CoA dehydrogenase domain"
FT Domain 172..549
FT /note= "Oxidoreductase acyl-CoA dehydrogenase family
FT domain"
FT Domain 179..286
FT /note= "Acyl CoA dehydrogenase C-terminal domain"
FT Region 179..191
FT /note= "Acyl CoA dehydrogenase signature 1"
FT Domain 207..604
FT /note= "Acyl-CoA oxidase dehydrogenase oxidoreductase
FT flavoprotein domain"
FT Domain 290..441
FT /note= "Acyl CoA dehydrogenase N-terminal domain"
FT Region 399..418
FT /note= "Acyl CoA dehydrogenase signature 2"
FT Domain 408..611
FT /note= "Dehydrogenase butyryl domain"
FT Domain 432..580
FT /note= "Polysaccharide deacetylase domain"
FT Domain 439..621
FT /note= "Very long chain dehydrogenase domain"
FT Region 460..476
FT /note= "Sugar transport protein signature"
XX WO200218582-A2.
XX PN
XX 07-MAR-2002.
XX PF 31-AUG-2001; 2001WO-US027186.
XX PR 31-AUG-2000; 2000US-0229831P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Meyers R, Hunter JJ;

Db	121	Ser	Asn	Thr	Met	Tyr	Ser	Arg	Leu	Gly	Glu	Leu	Leu	Leu	Leu	Ser	Met	Asp	Gly	Ser	Ile	Thr	Val	140		
Qy	487	ACC	CTG	CAG	CGC	CAC	CA	GGC	TAT	TGG	CCT	CA	AGG	GGG	ATC	AT	T	TGG	CT	TGG	C	TG	C	AGG	AG	546
Db	141	Thr	Leu	Ala	Ala	His	Gln	Ala	Ile	Gly	Leu	Leu	Ser	Gly	Ile	Ile	Leu	Ala	Gly	Thr	Glu	Glu	160			
Qy	547	CAG	AA	GCC	AAA	TAC	TTC	GC	TAA	AC	TGG	CGT	CGG	GAG	CAC	AT	TG	CAG	GC	TTC	TG	CCT	606			
Db	161	Gln	lys	Ala	lys	tyr	Leu	Pro	lys	Leu	Ser	Gly	Leu	His	Ile	Ala	Ala	Phe	Cys	Leu	180					
Qy	607	ACG	GAG	CC	AGC	CAG	TGG	GAG	CGAT	G	CAG	CCT	CA	AT	CCG	GAG	CAG	AC	CAC	TA	AGT	GAA	666			
Db	181	Thr	Glu	Pro	Ala	Ser	Gly	Ser	Asp	Ala	Ala	Ser	Ile	arg	Ser	Arg	Ala	Thr	Leu	Ser	Glu	200				
Qy	667	GAC	AA	GAG	CAC	TAC	AT	CCT	CA	AT	TGG	CT	CA	AGG	TCT	TG	GA	T	T	AA	T	TG	GAG	CA	726	
Db	201	Asp	lys	lys	His	tyr	Ile	Leu	Asn	Gly	Ser	lys	Val	Trp	Ile	Thr	Asn	Gly	Gly	Leu	Ala	220				
Qy	727	AAT	AT	TTTT	TAC	TGT	TTT	GTT	G	CAA	AGA	CTG	AGG	T	CGT	TGA	T	T	GA	T	T	GA	T	GA	786	
Db	221	Asn	Ile	Phe	Thr	Val	Phe	Ala	lys	Thr	Glu	Val	Val	Asp	Ser	Asp	Gly	Ser	Val	lys	Asp	240				
Qy	787	AAA	AT	CAC	AG	CAT	TCA	TAG	TAG	AAA	GAG	ACT	T	TGG	TG	GAG	T	CA	CTA	AT	T	G	GA	846		
Db	241	Lys	Ile	Thr	Ala	Phe	Ile	Val	Glu	Arg	Asp	Phe	Gly	Gly	Val	Thr	Asn	Gly	lys	Pro	Glu	260				
Qy	847	GAT	AAA	T	TAG	CCAT	T	CGG	GCT	CA	AC	T	TG	TGA	GT	C	CA	T	T	T	T	T	T	906		
Db	261	Asp	lys	Leu	Gly	Ile	arg	Gly	Ser	Asn	Thr	Cys	Glu	Val	His	Phe	Glu	Asn	Thr	Lys	Ile	280				
Qy	907	CCT	GT	G	AAA	AAC	AT	C	T	T	G	G	AGG	T	CGG	AT	T	AA	G	T	T	T	T	966		
Db	281	Pro	Val	Glu	Asn	Ile	Leu	Gly	Glu	Val	Gly	Asp	Gly	Phe	lys	Val	Ala	Met	Asn	Ile	Leu	300				
Qy	967	AAC	AG	CGG	CG	TT	CAG	CAT	TGG	CAG	CGT	CGT	TGG	TGG	CT	GCT	C	A	G	A	G	A	T	1026		
Db	301	Asn	Ser	Gly	arg	Phe	Ser	Met	Gly	Ser	Val	Val	Ala	Gly	Leu	Leu	lys	Arg	Leu	Ile	Glu	320				
Qy	1027	ATG	ACT	C	T	CAG	TAC	GGC	T	C	CA	AGG	AAA	CAG	TTT	AA	CA	AGG	CGC	T	CAG	T	T	1086		
Db	321	Met	Thr	Ala	Glu	tyr	Ala	Cys	Thr	Arg	lys	Gln	Phe	Asn	lys	arg	Leu	Ser	Glu	Phe	Gly	340				
Qy	1087	TTG	AT	T	CAG	GAA	AAT	T	TG	CAT	CGC	T	CAG	AGC	TTT	ACG	T	C	T	G	G	AG	A	G	1146	
Db	341	Leu	Ile	Gln	Gly	lys	Phe	Ala	Leu	Met	Ala	Gln	Lys	Ala	tyr	Val	Met	Glu	Ser	Met	Thr	360				
Qy	1147	TAC	CT	C	A	CAG	AGG	AT	G	CT	G	G	CA	AC	T	G	G	T	T	T	T	T	T	1206		
Db	361	Tyr	Leu	Thr	Ala	Gly	Met	Leu	Asp	Gln	Pro	Gly	Phe	Pro	Asp	Cys	Ser	Ile	Glu	Ala	Ala	380				
Qy	1207	ATG	GT	GAAG	TGT	T	CAG	CT	CCG	AGG	CGC	CT	G	G	CAG	TGT	G	T	G	A	G	T	T	1266		
Db	381	Met	Val	lys	Val	Phe	Ser	Ser																		

Alignment Scores:

QY	1027	ATGACTGCTCAGTACGCCCTGCACAAGGAACAGTTTAAACAAGAGGCTCAGTGAATTTGGGA	1086
Db	321	MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly	340
QY	1087	TTGATTCCAGGAGAAATTTGCACACTCATGGCTTCAGAAAGGCTTACGCTCATGGAGAGTATGACC	1146
Db	341	LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr	360
QY	1147	TACCTCTACACAGAGGATGCTGGACCAACTTGGCTTTCCGACTGCTCCATCTCAGGAGCAGCC	1206
Db	361	TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla	380
QY	1207	ATGGTGAAGCTGTTCAGCTCCGAGGCGCCTGCACAGTGTCTGAGTAGGCGCTGCACATC	1266
Db	381	MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle	400
QY	1267	CTCGGGGGCTTGGCTACACAAGGGACTATCCGTACAGCGCATCTACTGCTGCACCCCGC	1326
Db	401	LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg	420
QY	1327	ATCCTCCTCATCTTCGAGGGAAACAATGAGATTCCTCGGATGTATCATCGCCCTGCACGGGT	1386
Db	421	IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly	440
QY	1387	CTGCAGCATCCGGCGCGCATCTCTGACTACACAGATCCATCAGCTTAAACAGGCCAAAGTG	1446
Db	441	LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal	460
QY	1447	AGACAGCTCATGATACCGTTTGGCCGGAGGCTTCGGGACTCCCTGGGCGCGAAGCTGTGGAC	1506
Db	461	SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp	480
QY	1507	CTGGGGCTGACAGGCACCAATGGAGTTGTGCACCCCAAGTCTTCGCGACAGTGCACCAAG	1566

67	QY	ATGAGCGGCTCGGGGCTCTTCTGCGCACCA	CGGCTGCGGCTGTCGCTGCGCGGGTCTG	126
1	Db	MetSerGlyCyseGlyLeuPheLeuArgThrThrAlaAlaA	ArgAlaCyseArgGlyLeu	20
127	QY	GTGGTCTCTACCGGAA	CGGGCGGTACTGCGCACCGCCGCTGTACGAGCTTCGCC	186
21	Db	ValValSerThrAlaAsnArgLeuLeuArgThrSerPro	ProValArgAlaPheAla	40
187	QY	AAAGAGCTTTTCTAGGCAAAATCAAGAAAGAAG	ATTTTCCCATTTCCAGAAAGTTAGC	246
41	Db	LysGluLeuPheLeuGlyLysIleLysLysGluValPhe	ProPheProGluValSer	60
247	QY	CAAGATGAACCTTAATGAAATCAATCAGTCTT	TGGGACCGTGGAAAAATTCCTCACTGAA	306
61	Db	GlnAspGluLeuAsnGluIleAsnGlnPheLeuGly	ProValGluLysPhePheThrGlu	80
307	QY	GAGTGGACTCCGAAAAAATTACACAGGAAGG	AAAAATCCAGATGAAACTTTGGAGAA	366
81	Db	GluValAspSerArgLysIleAspGlnGluGlyLys	IleProAspGluThrLeuGluLys	100
367	QY	TTGAAGACCTAGGCGCTTTTCGGCTGCAAGT	CCACGAAGAATATGGTGGCGCTCGGCGCTTC	426
101	Db	LeuIysSerLeuGlyLeuPheGlyLeuGlnValPro	GluGluLysIleGlyLeuGlyPhe	120
427	QY	TCCAAACACCATGTACTCAAGACTAGGGGAG	ATCATCAGCATGGATGGGTTCATCACTGTG	486

Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
 QY 1567 TTTGAGGAGAACACTACTGCTTCGGCCGGACCGTGGAGACACTGCTCGCTTTGGC 1626
 Db 501 PheGluGluAsnThrTyrcysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
 QY 1627 AAGACCATCATGGAGGACAGCTGGTACTGAAGCGGGTGGCCAACTCTCATCAACTG 1686
 Db 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
 QY 1687 TATGGCATGCGCGCTGCTCGGGCCGACCGCTCCATCCGATGGCTCCGCAAC 1746
 Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
 QY 1747 CACGACCACGAGGTCTCTTCGGCAACACTTCCTGCGTGAAGCTTACTTCGCAATCTC 1806
 Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
 QY 1807 TTCAGCCTCTCTCAGCTGGACACAGTATGCTCCAGAAACCTAGATGACAGATTAGAAA 1866
 Db 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
 QY 1867 GTGTCCTCCAGCAGATCTTGAGAACGAGCTATATCTGTGCCACCTCTGGACAGACA 1926
 Db 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
 QY 1927 TGC 1929
 Db 621 Cys 621
 RESULT 6
 ADJ69253
 ID ADJ69253 standard; protein; 621 AA.
 XX
 AC ADJ69253;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human heat mitochondrial protein as a therapeutic target SeqID1059.
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087768-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.
 XX
 PA (BUCK-) BUCK INST AGE RES.
 XX
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX
 DR WPI; 2003-845369/78.
 XX
 PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX

PS Claim 1; SEQ ID NO 1059; 180pp; English.
 XX
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX
 SQ Sequence 621 AA;
 Alignment Scores:
 Pred. No.: 1,98e-283 Length: 621
 Score: 3153.00 Matches: 621
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 70.00% Indels: 0
 DB: 7 Gaps: 0
 US-09-945-326-1 (1-2452) x ADJ69253 (1-621)
 QY 67 ATGAGCGCTGCGGCTCTTCTGCGCACACGCGTGGCTCGTCTCGCGGCTCTG 126
 Db 1 MetSerGlyCysGlyLeuPheLeuArgThrAlaAlaAargAlaCysArgGlyLeu 20
 QY 127 GTGGTCTCTACCGCGAAACCGCGGCTACTGCGCACCCAGCCCGCTCTACAGCTTCGCC 186
 Db 21 ValValSerThrAlaAsnArgLeuLeuArgThrSerProValArgAlaPheAla 40
 QY 187 AAAGAGCTTTTCTAGGCAAAATCAGAGAAGAAGAGTTTCCCATTTCCAGAGTTAGC 246
 Db 41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer 60
 QY 247 CAAGATGAATTAATGAAATCAATCAGTTCTTGGGACCGTGGAAAAATTTCTTCACTGAA 306
 Db 61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80
 QY 307 GAGTGGACTCCCGAAAAATTCACAGGAAGGAAAAATCCAGATGAATTTGGAGAAA 366
 Db 81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100
 QY 367 TTGAGAGCGCTAGGGCTTTTGGGCTGCAAGTCCCAGAGAATAATGCTGGCTGGGCTTC 426
 Db 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyLeuGlyPhe 120
 QY 427 TCCAACACCATGTACTCAAGACTAGGGAGATCATCAGCATGGATGGGTCCATCACTGTG 486
 Db 121 SerAsnThrMetTy-SerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
 QY 487 ACCCTGGCAGCGCACCGCTATTGGCTCAGGGGATCATCTTGGCTGGCTAGGAG 546
 Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleLeuAlaGlyThrGluGlu 160
 QY 547 CAGAAGCCAAATACTTGGCTAAACTGGGCTCGGGGAGCACATTCGACCTTCTGGCTC 606
 Db 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaPheCysLeu 180
 QY 607 ACGAGCCACCGCAGTGGAGCGCATCGAGCTCAATCCGAGCAGAGCCACACTAAGTGAA 666
 Db 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
 QY 667 GACAAGAGCACTACATCTCAATCGCTCCAGGCTCGATTACTTAATGGAGCACTGGCC 726
 Db 201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220

Qy 727 AATATTTTACTGTGTTTGCAGAAAGACTGAGTCGCTGATTCTGTGATCGATCATGATGAGTAAAGAAC 786
Db 221 AenilePheThrValPheAlaLysThrGluValValAaspSerAspGlySerValLysAasp 240
Qy 787 AAAATACACAGCATTCATAGTAGAAGAGACTTTGGTGAGTCACTTAATGGAAACCCGAA 846
Db 241 LysileThrAlaPheIleValIGluArgAaspPheGlyGlyValThrAsnGlyLysProGlu 260
Qy 847 GATAAATTTAGGCATTTCGGGGCTCCAAACACTTGTGAAGTCCATTTTGAATAACACCAAGATA 906
Db 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
Qy 907 CCTGTGAAACATCCTTTGGAGAGTCGGAGATGGGTTTAAGTGGCCATGAACATCCTC 966
Db 281 ProValGluAenileLeuGlyGluValGlyAaspGlyPheLysValAlaMetAsnIleLeu 300
Qy 967 AACAGCGCGCGTTCAGCATCGGCAGCGTCGCTGGCTGGCTGCACAGAGATTGATTGAA 1026
Db 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
Qy 1027 ATGACTGCTGAGTACGCTGCACAGAGAAACAGTTTAAACAGAGCTCAGTGAATTTGGA 1086
Db 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
Qy 1087 TTGATTTCAGGAGAAATTTGCACTGATGGCTCAGAGGCTTACGTATCGAGAGTATGACC 1146
Db 341 LeuileGlnGlyLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
Qy 1147 TACCTCACAGCAGGATGCTGGACCACTGGCTTCCGACTGCTCCATCGAGCGACCC 1206
Db 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaA 380
Qy 1207 ATGTTGAAGGTGTTTCAGTCCGAGCGCGCTGGCAGTGTGTGAGTGGAGCGCTCAGATC 1266
Db 381 MetValLysValPheSerSerGluAlaAlaIleArgLysCysValSerGluAlaLeuGluIle 400
Qy 1267 CTCGGGGCTTGGCTACACAAAGGACTATCCGTACGAGCGCATCTCGGTGACACCCGC 1326
Db 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
Qy 1327 ATCCCTCATCTTCGAGGGACCAATGAGATTCTCCGGATGTACATCGCCCTCAGCGGT 1386
Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
Qy 1387 CTGAGCATGCGCGCGCATCTCTACCTACAGGATCCATGAGCTTAAACAGCGCAAAAGTG 1446
Db 441 LeuGlnHisAlaGlyArgIleuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
Qy 1447 AGCAGTCATGATACCGTTTGGCGGAGGCTTCGGGACTCCCTGGGCGCAACTGTGGAC 1506
Db 461 SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAasp 480
Qy 1507 CTGGGGCTGACAGCAACCATGAGTGTGTGACCCCGAGTCTTGGGACAGTGGCCAAAG 1566
Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAaspSerAlaAsnLys 500
Qy 1567 TTTGAGGAGAACCTACTGCTTCGGCGGAGCGCTGGAGACACTGCTGCTCCGCTTTGGC 1626
Db 501 PheGluGluAenThrTyrCysPheLysArgThrValGluThrLeuLeuLeuArgPheGly 520
Qy 1627 AAGACCATCATGAGGAGCAGCTGCTGATGAAGCGGGTGGCCAACTCCTCATCAACCTG 1686
Db 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAenileLeuIleAsnLeu 540
Qy 1687 TATGGCATGAGCGCGTGTCTCGGGCGCAGCGCTCCATCCGATTTGGCTCCGCAAC 1746
Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
Qy 1747 CACGACACGAGGTTCTCTTCGCGCAACACCTTCTCGCTGGAGCTTACTTCGCAAGTCTC 1806
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy 1807 TTGAGCCTCTCTAGCTGGACAAGTAGTCTCCAGAAAACCTAGATGACGACATTAGAAA 1866
Db 581 PheSerLeuSerGlnLeuAaspLysTyrAlaProGluAsnLeuAaspGluGlnIleLysLys 600
Qy 1867 GTGTCCAGCAGATCCTTTGAGAGCGAGCTTATATCTGTGCCACCTCTCGACAGGACA 1926
Db 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAaspArgThr 620
Qy 1927 TGC 1929
Db 621 Cys 621
RESULT 7
ADJ70247
ID ADJ70247 standard; protein; 621 AA.
XX AC ADJ70247;
XX XX
DT 06-MAY-2004 (first entry)
XX DE Human heat mitochondrial protein as a therapeutic target SeqID2053.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis; LHON;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX OS Homo sapiens.
XX PN WO2003087768-A2.
XX PD 23-OCT-2003.
XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DB;
XX MPI; 2003-845369/78.
XX PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX PS Claim 1; SEQ ID NO 2053; 180pp; English.
XX CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytosratic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX

Db	281	ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu	300
Qy	967	AACAGCGCGGTTTCAGCATGGGAGCGTCTGGTGGCTGCTCAAGAGATTGATTGAA	1026
Db	301	AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu	320
Qy	1027	ATGACTGCTCAGTACGCTCCACAAGAAACAGTTTAAACAGAGGCTCAGTGAATTGGGA	1086
Db	321	MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly	340
Qy	1087	TTGATTTCAGGAGAAATTTGCACCTGATGGCTCAGAAGCTTACGTCATCGAGAGATTGACCC	1146
Db	341	LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr	360
Qy	1147	TACCTACAGCAGGATGCTGGACCACTGGCTTCCGACTGCTCCATCGAGGACGCC	1206
Db	361	TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla	380
Qy	1207	ATGCTGAAGTGTTCAGCTCCGAGCGCGCTGGCAGTGTGTGAGTAGAGGCGCTGCAGATC	1266
Db	381	MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle	400
Qy	1267	CTCGGGGCTTGGGCTACACAAGGGACTATCCGTACGAGCGCATCTGCGTGACACCCGC	1326
Db	401	LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg	420
Qy	1327	ATCTCTCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT	1386
Db	421	IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly	440
Qy	1387	CTCAGCATCCGCGCGCATCTCGTACACAGATCCATGAGCTTAAACAGGCCAAAGTG	1446
Db	441	LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal	460
Qy	1447	AGCACAGTCAATGATACCTGTGGCGGAGGCTTCGGGACTCCCTGGGCGCGAACTGTGGAC	1506
Db	461	SerThrValMetAspThrValGlyArgLeuArgAspSerLeuGlyArgThrValAsp	480
Qy	1507	CTGGGCTGACAGGCAACCATGAGTTGTGCACCCCGAGTCTTCGGGACAGTGCACAAG	1566
Db	481	LeuGlyLeuThrGlyAsnHisGlyValValIleProSerLeuAlaAspSerAlaAsnLys	500
Qy	1567	TTTGAGGAGAACCTACTCTTCGCGCGGACCGTGGAGACACTGCTGCTCCGCTTTGGC	1626
Db	501	PheGluGlnAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly	520
Qy	1627	AAGACCATCATGGAGGACGAGCTGGTACTGAAGCGGGTGGCCCAACATCTCATCAACCTG	1686
Db	521	LysThrIleMetGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu	540
Qy	1687	TATGGCATGACGGCGTGTGTCGGGGCAGCGGCTCCATCGCATTTGGGCTCCGGCAAC	1746
Db	541	TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn	560
Qy	1747	CAGCACACAGGTCTCTTGGCCCAACACCTCTCGGTGGAAGCTTACTTGCAGAACTCTC	1806
Db	561	HisPheHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu	580
Qy	1807	TTCAGCCCTCTCTCAGCTGGCAAGTAGTCTCCAGAAACCTAGATGACGAGATTAAAGAA	1866
Db	581	PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys	600
Qy	1867	GTGTCCAGCAGATCTCTTGAGAGCGGAGCGCTATCTGTGCCACCTCTGGACAGGACA	1926
Db	601	ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr	620
Qy	1927	TGC	1929
Db	621	Cys	621

RESULT 9
,AAB41800

ID	AAB41800 standard; protein; 565 AA.
XX	AAB41800;
AC	
XX	08-FEB-2001 (first entry)
DT	
XX	Human ORFX ORF1564 polypeptide sequence SEQ ID NO:3128.
DE	
XX	Human; open reading frame; ORFX; detection; cytotstatic; hepatotropic;
KW	vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW	anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW	immunosilant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW	antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW	cholesterol ester storage; systemic lupus erythematosus; infection;
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW	thrombosis; contraceptive.
XX	
OS	Homo sapiens.
XX	
PN	WC2000058473-A2.
XX	
PD	05-OCT-2000.
XX	
PF	31-MAR-2000; 2000WO-US008621.
XX	
PR	31-MAR-1999; 99US-0127607P.
PR	02-APR-1999; 99US-0127636P.
PR	05-APR-1999; 99US-0127728P.
PR	30-MAR-2000; 2000US-00540763.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shimkets RA, Leach M;
XX	
XX	WPI; 2000-602362/57.
DR	N-PSDB; AAC76009.
XX	
PT	Novel nucleic acids and peptides derived from open reading frame X,
PT	useful for treating e.g. cancers, proliferative disorders,
PT	neurodegenerative disorders and cardiovascular disease.
XX	
PS	Claim 11; Page 2345-2346; 5507pp; English.
XX	
CC	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC	which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC	sequences have activities such as: cytotstatic; hepatotropic; vulnary;
CC	antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC	anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC	cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC	dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC	antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC	sequences can be used for determining the presence of or predisposition
CC	to, or preventing or treating pathological conditions associated with an
CC	ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC	proteins in gene therapy vectors. The proteins and nucleic acids may be
CC	used to treat cancers, proliferative disorders, neurodegenerative
CC	disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC	diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC	storage, systemic lupus erythematosus, severe combined immunodeficiency
CC	(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC	disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC	cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC	enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX	
SQ	Sequence 565 AA;

Alignment Scores:

Pred. No.: 1.42e-256 Length: 565
Score: 2864.00 Matches: 564
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 63.59% Indels: 0
DB: 3 Gaps: 0

US-09-945-326-1 (1-2452) x AAB41800 (1-565)

Qy 238 GAAGTTAGCAAGATGAACCTTAATCAATCAATCAGTCTTTGGGACCCGTCGAAATAATTC 297
Db 2 GluValSerGlnAspGluLeuAAsnGluIleAsnGlnPheLeuGlyProValGluLysPhe 21

Qy 298 TTCTACTGAAGAGTGGACTCCCGGAAAAATTCACAGGAAGGAAAAATCCAGATGAACCT 357
Db 22 PheThrGluGluValAspSerArgLysIleAspGlnGluLysIleProAspGluThr 41

Qy 358 TTGCAGAAATTAAGAGCCTAGGCTTTTGGCTGCAAGTCCAGAGATATGCTGGC 417
Db 42 LeuGluLysLeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluThrGlyGly 61

Qy 418 CTGGGCTTCTCAACACCATGACTCAAGACTAGGGAGATCATCAGCATGGATGGTCC 477
Db 62 LeuGlyPheSerAsnThrMetTyrSerArgLeuGlyGluIleLysSerMetAspGlySer 81

Qy 478 ATCACTGTGACCTGGCAGCCACCGAGCTATTCGCTCAAGGGATCATCTTGGCTGGC 537
Db 82 IleThrValThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleLeuAlaGly 101

Qy 538 ACTGAGAGCAGAAAGCAATATCTCCCTAACTGGCGTCCGGGAGCAGCATTCGAGCC 597
Db 102 ThrGluGlnGlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAla 121

Qy 598 TTCTGCTCTCAGGAGCCAGCAGTGGGAGCGATCAGCTCAATCCGGAGCAGAGCCACA 657
Db 122 PheCysLeuThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThr 141

Qy 658 CTAAGTGAAGACAAGAGCACTACATCTCTCAATGGCTCCAAGGCTCTGGATTAATGGA 717
Db 142 LeuSerGluAspLysLysHisTyrIleLeuAsnGlySerLysValTyrPheThrAsnGly 161

Qy 718 GGACTGCCCAATATTTTACTGTGTTTGCAGAACTGAGTCTGTTGATCTGATGATCA 777
Db 162 GlyLeuAlaAsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySer 181

Qy 778 GTGAAGACAAAAATCACAGCATTCATAGTAGAAGAGACTTTGTGGAGTCACTAATGGG 837
Db 182 ValLysAspLysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGly 201

Qy 838 AAACCCGGAAGATAAATTAGGCATTCGGGGCTCCAAACACTTGTGAAGTCCATTTTGAAG 897
Db 202 LysProGluAspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsn 221

Qy 898 ACCAGATACCTGTGGAAGAACATCTTGGAGAGTCCGAGATGGGTTAAGTGGCCCATG 957
Db 222 ThrLysIleProValGluAAsnIleLeuGlyValGluValAspGlyPheLysValAlaMet 241

Qy 958 AACATCTCAACAGCGCCGCTTCAGCATGGCAGCTGCTGGCTGGCTGCTCAAGAGA 1017
Db 242 AsnIleLeuAsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLysArg 261

Qy 1018 TTGATTGAATGACTGTGAGTACGCTCGCAAGGAAACAGTTTAAACAAGAGCTCAGT 1077
Db 262 LeuIleGluMetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSer 281

Qy 1078 GAATTTGGATTGATCAGGAAATTTGCACTGATGGCTCAGAGGCTTACGTCATGGAG 1137
Db 282 GluPheGlyLeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGlu 301

Qy 1138 AGTATGACCTACCTCACAGAGGAGTCTGGACCAACCTGGCTTCCGAGCTGCTCCATC 1197
Db 302 SerMetThrTyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIle 321

Qy 1198 GAGCGACCCATGGTGAAGGTGTTTCAGCTCCGAGGCGCCCTGGCAGTGTGTGAGTGGCG 1257
Db 322 GluAlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAla 341

Qy 1258 CTCGAGATCTCCGGGGCTTGGGCTACACAAGGAGCTATCCGTACGAGCGCATACTCGT 1317
Db 342 LeuGlnIleLeuGlyLeuGlyTyrThrArgAspLysPheProLysGluArgIleLeuArg 361

Qy 1318 GACACCCGATCTCTCATCTTCGAGGGAACCAATGAGATTTCTCCGGATGTACATGCC 1377
Db 362 AspThrArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAla 381

Qy 1378 CTGACGGCTCTGACGATGCCGCGCATCTGACTACCGAGATCCATGAGCTTAAACAG 1437
Db 382 LeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGln 401

Qy 1438 GCCAAAGTGAAGCAGTCATGATACCGTGGCGGAGGCTTCGGGACTCCCTCGGCCGA 1497
Db 402 AlaLysValSerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArg 421

Qy 1498 ACTGTGACCTGGGCTGACAGGCAACCATGAGTGTGTGCACCCAGCTTCTTGGCAGCAGT 1557
Db 422 ThrValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSer 441

Qy 1558 GCCAACAGTTTGAAGGAAACACTACTCTGCTGGCGCGGACCGTGGAGAGACTGCTGCTC 1617
Db 442 AlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeu 461

Qy 1618 CGTTTTGGCAAGACCATCATGAGGAGCAGCTGTACTGAAGCGGTGGCCCAACATCCTC 1677
Db 462 ArgPheGlyLysThrIleMetGluGluGlnLeuValLysArgValAlaAsnIleLeu 481

Qy 1678 ATCAACCTGTATGGCATGACGGCGCTGCTGCGGGCCGACCGCTCCATCCGATTTGGG 1737
Db 482 IleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGly 501

Qy 1738 CTCGCAACCAACGACGACGAGGTCTCTTGGCCAAACACCTTCTGCGTGGAGGCTTACTTG 1797
Db 502 LeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeu 521

Qy 1798 CAGAACTCTTTCAGCTCTCTCAGCTGGCAAGTATGCTCCAGAAAACCTAGATGAGCAG 1857
Db 522 GlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGln 541

Qy 1858 ATTAAGAAAGTCCCGACGATCTTGAAGAGCGAGCTATATCTGTGCCCACTCTG 1917
Db 542 IleLysLysValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeu 561

Qy 1918 GACAGGACATGC 1929
Db 562 AspArgThrCys 565

RESULT 10
AAB94077
ID AAB94077 standard; protein; 498 AA.
XX
AC AAB94077;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:14271.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000BP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX (HELI-) HELIX RES INST.
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 DR
 XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 XX
 PS Claim 8; SEQ ID NO 14271; 2537pp + Sequence Listing; English.
 CC The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 498 AA;
 Alignment Scores:
 Pred. No.: 3,62e-225 Length: 498
 Score: 2526.00 Matches: 498
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 56.08% Indels: 0
 DB: 4 Gaps: 0
 US-09-945-326-1 (1-2452) x AAB94077 (1-498)

QY 736 ACTGTGTTTGCAGAGCTGAGGTGCTTGTGATTCGATCGATGAGTCAAGATGACCTGCT 1035
 DB ThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAspLysIleThr 120
 QY 796 GCATTTCATAGTAAAGAGAGACTTTGGTGGAGTCACTAATCGGAAACCCGAGAGTAATTA 855
 DB 121 AlaPheIleValGluArgAspPheGlyValThrAsnGlyLysProGluAspLysLeu 140
 QY 856 GGCATTGCGGGCTCCAACTTGTGAAGTCCATTTTGAATAACCAAGATACCTCTGGAA 915
 DB 141 GlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIleProValGlu 160
 QY 916 AACATCTTGGAGAGTGGAGATGGTTTAAAGTGGCCATGAACATCTCCAACAGCGGC 975
 DB 161 AsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeuAsnSerGly 180
 QY 976 CGGTTTCAGCATGGCGAGCGTGGCTGCTCAAGAGATTTGATGAAATGACCTGCT 1035
 DB 181 ArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGluMetThrAla 200
 QY 1036 GAGTACGCTGCAAGGAAACAGTTTAAACAAGAGCTCAGTGAATTTGGATTGATTTCAG 1095
 DB 201 GluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGlyLeuIleGln 220
 QY 1096 GAGAAATTTGCATGATGCTCAGAGAGCTTACGTTCATGAGAGATGATGACCTACCTCACA 1155
 DB 221 GluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThrTyrLeuThr 240
 QY 1156 GCAGGATGTCGACCAACCTGGCTTTCCGACTGCTCCATCGAGCAGCCATGGTGAAG 1215
 DB 241 AlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaMetValLys 260
 QY 1216 GGTGTCAGTCCGAGCCGCTGGCGAGTGTGTGAGTGAGGCGCTGCAGATCTCTCGGGGC 1275
 DB 261 ValPheSerSerGluAlaAlaTyrGlnCysValSerGluAlaLeuGlnIleLeuGlyGly 280
 QY 1276 TTGGGTACACAGGAGCTATCCGTACGAGCGCATCTCGGTGACACCGCATCTCTCCCTC 1335
 DB 281 LeuGlyTyrThrArgAspLysProTyrGluAlaGlyLeuArgAspThrArgIleLeuLeu 300
 QY 1336 ATCTTCAGGGAACCAATGAGATTTCTCGGATGTATCATCGCCCTGACGGGTCTGCAGCAT 1395
 DB 301 IlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGlyLeuGlnHis 320
 QY 1396 GCGGCGCGATCTGACTACAGGATTCATGAGCTTAAACAGGCCAAAGTGAGCAGTCTC 1455
 DB 321 AlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysValSerThrVal 340
 QY 1456 ATGGATACCGTTGGCGGAGGCTTCGGGACTCCCTGGGCGCAACTGTGGACCTGGGGCTG 1515
 DB 341 MetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAspLeuGlyLeu 360
 QY 1516 ACAGGCAACATGGAGTTGTGACCCCATGCTTCGGGACAGTCCGCAACAAAGTTTGGAGG 1575
 DB 361 ThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLysPheGluGlu 380
 QY 1576 AACACTACTGCTTCGGCGGACCGTGGAGACACTGCTGCTCCGCTTTCGGGAGGACCATC 1635
 DB 381 AsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGlyLysThrIle 400
 QY 1636 ATGGAGGACGAGCTGGTACTGAAGCGGTGGCAACATCTCATCACTGTATGGCATG 1695
 DB 401 MetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeuTyrGlyMet 420
 QY 1696 AGCGCGGTGCTGCTCGCGGCGCAGCGCTCCATCCGATTTGGGCTCCGCAACACCAACAC 1755
 DB 421 ThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsnHisAspHis 440
 QY 1756 GAGGTTCCTTGGGCCAACACCTTCTGCGTGAAGCTTACTTGCAGAACTCTCTTCAGCTC 1815
 DB 441 GluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeuPheSerLeu 460

Qy 1816 TCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATAGCAGATTAGAAAGTCTCCAG 1875
Db 461 SerGlnLeuAepLysTyrAlaProGluAasnLeuAaspGluGlnIleLysLysValSerGln 480
Qy 1876 CAGATCTTGGAGACGAGCCCTATATCTGTGCCACCTCTGGACAGGACATGC 1929
Db 481 GlnIleLeuGluLysA-gAlaTyrIleCysAlaHisProLeuAaspA-gThrCys 498

RESULT 11
AAU23012
ID AAU23012 standard; protein; 306 AA.
XX AC AAU23012;
XX DT 18-DEC-2001 (first entry)
XX DE Novel human enzyme polypeptide #98.
XX KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX OS Homo sapiens.
XX PN WO200155301-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001239.
XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
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PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
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PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
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PR 18-AUG-2000; 2000US-0226278P.
PR 22-AUG-2000; 2000US-0226681P.
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PR 23-AUG-2000; 2000US-0227182P.
PR 30-AUG-2000; 2000US-0227009P.
PR 01-SEP-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.

XX OS Rattus sp.
 XX PN WO200216428-A1.
 XX PD 28-FEB-2002.
 XX PF 20-AUG-2001; 2001WO-JP007117.
 XX PR 21-AUG-2000; 2000JP-00254263.
 XX PR 07-SEP-2000; 2000JP-00276633.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Tojo H, Katayama N, Kakimoto S;
 XX DR WPI; 2002-269344/31.
 XX PT Protein binding to insulin-responsive aminopeptidase and glucose
 PT transporter 4, useful for prevention and treatment of diseases associated
 PT with blood sugar level disturbance.
 XX PS Disclosure; Page 90-92; 103pp; Japanese.
 XX CC The present invention describes human MD25 (very long chain acyl-CoA
 CC dehydrogenase (VLCAD)), which binds to insulin-responsive aminopeptidase
 CC (IRAP) and to glucose transporter 4 (GLUT4). MD25 has antidiabetic
 CC activity. IRAP and GLUT4 are involved in the intracellular regulation of
 CC glucose metabolism and glucose transport across the cell membrane.
 CC Expression of MD25 (whose ligands are these proteins) is also involved in
 CC this regulatory process. MD25 can be used in the prevention, treatment
 CC and diagnosis of diseases involving disturbances of glucose metabolism,
 CC such as diabetes and other hyperglycaemic disorders. The present sequence
 CC represents rat VLCAD which is given in the exemplification of the present
 CC invention
 XX SQ Sequence 653 AA;

Alignment Scores:
 Pred. No.: 4.35e-117 Length: 653
 Score: 1365.00 Matches: 303
 Percent Similarity: 62.77% Conservative: 110
 Best Local Similarity: 46.05% Mismatches: 202
 Query Match: 30.31% Indels: 43
 DB: 5 Gaps: 13

US-09-945-326-1 (1-2452) x ABB06991 (1-653)

Qy 30 GGGAGACTGAGCTGAGCTGGGG---AACATCGGGCAGCATGAGCGGTGCGGGCTCTT 86
 Db 11 GlyArgGlnLeuLeuArgLeuGlyAlaArgSerArgSerAlaAlaLeuGlnGlyGln 30
 Qy 87 CTTGGCAGCAGCGCTGGGCTGGCTGCGGGGTCTGGTCTCTACCGGGAACCG 146
 Db 31 Pro-ArgProThrSerAlaGlnArg-----LeuTyrAlaSerGluAlaThrG1 46
 Qy 147 GCGGCTACTGCGC-----ACCAGCCCGCTGT 173
 Db 46 nAlaValLeuGluLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAl 66
 Qy 174 ACGAGCT-----TTGCCAAGAGCTTTTCTAGGCAAAATCAAGAAGAAAGA 221
 Db 66 aArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspG1 86
 Qy 222 AGTTTTCCTTCCAGAGTTACCAAGATGAATTAATGAA-----AT 266
 Db 86 nValPheProThrProSerVal-----LeuAsnGluGlyGlnThrGlnPheLe 102
 Qy 267 CAATCAGTCTTGGGACCGTGGAAATCTTCACTGAAGAGGTGGACTCCCGGAAAT 326
 Db 102 uLysGluLeuValGlyProValAlaArgPheGluGluValAsnAspProAlaLysAs 122
 Qy 327 TGACCAGAGGAGGAAATCCAGATGAACCTTTTGGAGAAATTGAAGAGCCTTAGGGCTTTT 386

122 nAspSerLeuGluLysValGluGluAspThrLeuGlnGlyLeuLysGluLeuGlyAlaPh 142
 387 TGGCTGCAAGTCCAGAGAATATGCTGGCTGGCTTCTCCCAACACCATGTACTCAAG 446
 142 eGlyLeuGlnValProSerGluLeuGlyLeuGlyLeuSerAsnThrGlnTyrAlaAr 162
 447 ACTAGGGAGATCATCAGCATG---GATGGTCCATCACTGTGACCTCGGAGCGCACCA 503
 162 gLeuAlaGluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisG1 182
 504 GGCTATTGGCTCAAGGGGATCATCTTGGCTGGCTGAGGAGCAGAGCAAGCAATACTT 563
 182 nSerIleGlyPheLysGlyIleLeuLeuTyrGlyThrLysAlaGlnLysGluLysLe 202
 564 GCCTAAACTGGCTCCGGGAGCATTTCAGCCCTTCTGCTCAGGAGCCAGCGCAGTGG 623
 202 uProArgValaSerGlyGlnAlaLeuAlaPheCysLeuThrGluProSerSerG1 222
 624 GAGCATGTCAGCTCAATCCGAGCAGAGCCACACTAAGTGAAGCAAGAACACTACAT 683
 222 ySerAspValaSerIleArgSerSerAlaValProSerProCysGlyLysTyrTrTh 242
 684 CCTCAATGGCTCCAGCTCTGGATTACTAATGGAGCTGGCCATATTTTACTGTGT 743
 242 rLeuAsnGlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAspIlePheThrValPh 262
 744 TGCAAGACTGAGTCTGCTGAT---TCTGATGATCAGTGAAGCAACAAATCACAGCAT 800
 262 eAlaLysThrProIleLysAspAlaThrGlyAlaValLysGluLysIleThrAlaPh 282
 801 CATAGTAGAAGAGACTTTTGGTGGAGTCACTAATGGGAAACCCGAAAGATAAATAGGCAT 860
 282 eValValGluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGlyI1 302
 861 TCGGGGCTCCAAACACTGTGCAAGTCCATTTTGAACACCAAGATACCTGTGGAACAT 920
 302 eLysAlaSerAsnThrSerGluValTyrPheAspGlyValLysValProAlaGluAsnVa 322
 921 CCTTGGAGAGCTCGGAGATGGGTTTAAAGTGGCCATGAACATCTCAACAGCGCCGCTT 980
 322 lLeuGlyGluValGlyAspGlyPheLysValAlaValAsnIleLeuAsnAsnGlyArgPh 342
 981 CAGCATGGGCGAGCTGCTGGCTGGCTGCTCAAGAGATGATGAATGAATAGCTGCTGAGTA 1040
 342 eGlyMetAlaAlaThrLeuAlaGlyThrMetLysAlaIleAlaLysAlaValAspHi 362
 1041 CGCTGCACAAGAAACAGTTTAAACAGAGCTCAGTGAATTTGGATTGATTCAGGAGAA 1100
 362 sAlaThrAsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLy 382
 1101 ATTTGCACTCATCGCTCAGAAAGCTTACGTTCAGTGGAGAGTATGACCTACCTCACAGCAGG 1160
 382 sLeuAlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAl 402
 1161 GATGCTGGACCAACCTGGCTTTCCGAGTCTCTCATCGAGGAGCCATGTGAAGGTGT 1220
 402 aAsnMetAspGln---GlyPheLysAspPheGlnIleGluAlaIleSerLysIlePh 421
 1221 CAGCTCGAGCGCGCTGGCAGTGTGTGAGTGGCGCTCAGATCTCTCGGGGCTTGGG 1280
 421 eGlySerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGlyGlyMetG1 441
 1281 CTACACAAGGGATATCCGTACGAGCGCATCTGCGTGACACCCCGCATCTCTCTCATCTT 1340
 441 yPheMetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePh 461
 1341 CGAGGGAACCAATCAGATCTCCGGATGTATCGCCCTGACCGGTCTGCAGCATGCCGG 1400
 461 eGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysG1 481
 1401 CCGCATCTGACTACCAAGGATCCATGAGCTTAAACAG-----GCCAAAGTGAACACAT 1454

Db 162 gLeuAlaGluLeuValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisG1 182
Qy 504 GCCTATTGGCTCAAGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCAATACCT 563
Db 182 nSerIleGlyPheLysGlyIleLeuLeuTyrGlyThrLysAlaGlnLysGlyLysTyrLe 202
Qy 564 CCCTAAACTGGCTCCGGGAGCACATCGAGCCTTCTGCTCAGGAGCAGCCAGTGG 623
Db 202 uProArgValAlaSerGlyGlnAlaLeuAlaPheCysLeuThrGluProSerSerG1 222
Qy 624 GAGCGATGACGCTCAATCCGGAGCAGACACACTAAGTGAACAGCAAGCACTACAT 683
Db 222 ySerAspValAlaSerIleArgSerSerAlaValProSerProCysGlyLysTyrTh 242
Qy 684 CCTCAATGGCTCCAAGTCTGGATTACTAATGGAGGACTGGCCCAATATTTTACTGTGT 743
Db 242 rLeuAsnGlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAspIlePheThrValPh 262
Qy 744 TGCAAAGACTGAGTCTGTGAT-----TCTGATGATCATAGTGAAGACAAAATCACAGATT 800
Db 262 eAlaLysThrProIleLysAspAlaAlaThrGlyAlaValLysGlyLysIleThrAlaPh 282
Qy 801 CATAGTAGAAGAGACTTCTGTGGAGTCACCTAATGGGAAACCCCAAGATAAATTAGGCAT 860
Db 282 eValValGluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGlyI1 302
Qy 861 TCGGGGCTCCAAACACTTGTGAAGTCCATTTTGAACACCAAGATACCTGTGAAACACAT 920
Db 302 eLysAlaSerAsnThrSerGluValTyrPheAspGlyValLysValProAlaGluAsnVa 322
Qy 921 CTTTGGAGAGTCCGAGATGGTTTAAGTGGCCCATGAACATCTCAACAGCGGCCGGTT 980
Db 322 lLeuGlyGluValGlyAspGlyPheLysValAlaValAsnIleLeuAsnAsnGlyArgPh 342
Qy 981 CAGCATGGCAGCGTCTGTGGCTGGCTCAAGAGATTGATTGAATGACTGTCTGAGTA 1040
Db 342 eGlyMetAlaAlaThrLeuAlaGlyThrMetLysAlaIleAlaLysAlaValAspHi 362
Qy 1041 CGCTCGCACAGGAAACAGTTTAAACAGAGCTCAGTGAATTTTCGATTGATTACAGAGAA 1100
Db 362 sAlaThrAsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGly 382
Qy 1101 ATTTGCTGATGCTCAGAGGCTTACGTCATGAGAGATGATGACCTACCTACAGCAGG 1160
Db 382 sLeuAlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAl 402
Qy 1161 GATGCTCGACCACTGGCTTCCGCTCCGCTGCTCCATCGAGCAGCCATGTTGAGTGT 1220
Db 402 aAsnMetAspGln---GlyPheLysAspPheGlnIleGluAlaIleSerLysIlePh 421
Qy 1221 CAGCTCGAGCGCGCTCGGAGTGTGTGAGTGAGCGCTGCAGATCCTCGGGGGCTTGGG 1280
Db 421 eGlySerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGlyMetG1 441
Qy 1281 CTACACAGGAGGATATCCGTACGAGCGCATATCGTGTGACACCCGCACTCTCTCATCTT 1340
Db 441 yPheMetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePh 461
Qy 1341 CGAGGAAACCATGAGATTCTCCGATGTATCCGCTGATCCCTGACGGTCTGCAGCATGCCG 1400
Db 461 eGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysG1 481
Qy 1401 CCGCATCTCTGACTACAGGATCCATGAGTTAAACAG-----GCCAAAGTGAGCACAGT 1454
Db 481 yLysGluLeuThrGlyLeuGlyAsnAlaLeuLysAsnProLeuGlyAsnValGlyLeuLe 501
Qy 1455 CATGGATACCTTGGCCGAGGCTTCGGGACTCCCTGGCGGCAACTGTGAGCCTGGGGCT 1514
Db 501 uIleGlyGluAlaSerLysGlnLeuArgArgThrGlyIleGlySerGlyLeuSerLe 521
Qy 1515 GACAGGCAACCATGAGTGTGTGACCCCGCTTGTGGCAGACAGTCCCAACAGATTGAGGA 1574
Db 521 uSer-----GlyIleValHisProGluLeuSerArgSerGlyLeuAlaValG1 538

Qy 1575 GAACACCTACTGCTTCGGCCGAGCCGTGGAGACACTGCTGCTCGCTTGGCAAGACCAT 1634
Db 538 nAlaLeuGluGlnPheAlaThrValValGluAlaLysLeuMetLysHisLysLysGlyI1 558
Qy 1635 CATGGAGGACAGCTGGTACTGAAGCGGGTGGCCAAACATCTCTCATCAACCTGTATGGCAT 1694
Db 558 eValAsnGluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMe 578
Qy 1695 GACGGCGCTGCTGTCGGCGGCCAGCCCTCCATCCGCTGCGCTCCGCAACCAACGACCA 1754
Db 578 tValValValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHi 598
Qy 1755 CGAGGTCTCTTGGCCCAACACTTCTGCTGGGAGCT-----TACTTGCAGATCT 1805
Db 598 sGluLysMetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMe 618
Qy 1806 CTTGAGCTCTCTGAGCTGGACAAATGCTCCAGAAACCTAGATGAGCAGATTAGAA 1865
Db 618 tAlaSerLeuGlnSerAsnProGln-----GlnGlnGluLeuPheArgAsnPheArgse 636
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Db 636 rIleSerLysAlaMetValGluAsnGlyGlyLeuValThrSerAsnProLeu 653
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ABB06992
ID ABB06992 standard; protein; 655 AA.
AC ABB06992;
XX 20-JUN-2002 (first entry)
DT Mouse very long chain acyl-CoA dehydrogenase (VLCAD) protein SEQ ID:10.
DE Human; MD25; VLCAD; very long chain acyl-CoA dehydrogenase; IRAP;
KW insulin responsive aminopeptidase; GLUT4; glucose transporter 4;
KW antidiabetic; intracellular regulation; glucose metabolism; diabetes;
KW glucose transport; hyperglycaemic disorder.
OS Mus sp.
XX
PN W0200216428-A1.
XX 28-FEB-2002.
XX 20-AUG-2001; 2001WO-JP007117.
XX 21-AUG-2000; 2000JP-00254263.
XX 07-SEP-2000; 2000JP-00276633.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Tojo H, Katayama N, Kakimoto S;
XX WPI; 2002-269344/31.
XX Protein binding to insulin-responsive aminopeptidase and glucose
XX transporter 4, useful for prevention and treatment of diseases associated
XX with blood sugar level disturbance.
XX Disclosure; Page 92-95; 103pp; Japanese.
XX The present invention describes human MD25 (very long chain acyl-CoA
XX dehydrogenase (VLCAD)), which binds to insulin-responsive aminopeptidase
XX (IRAP) and to glucose transporter 4 (GLUT4). MD25 has antidiabetic
XX activity. IRAP and GLUT4 are involved in the intracellular regulation of
XX glucose metabolism and glucose transport across the cell membrane.
XX Expression of MD25 (whose ligands are these proteins) is also involved in
XX this regulatory process. MD25 can be used in the prevention, treatment
XX and diagnosis of diseases involving disturbances of glucose metabolism,
XX such as diabetes and other hyperglycaemic disorders. The present sequence
XX represents mouse VLCAD which is given in the exemplification of the

KW antidiabetic; intracellular regulation; glucose metabolism; diabetes;
 KW glucose transport; hyperglycaemic disorder.

OS Bos taurus.

PN WO2000216428-A1.

PD 28-FEB-2002.

XX 20-AUG-2001; 2001WO-JP007117.

XX 21-AUG-2000; 2000JP-00254263.

PR 07-SEP-2000; 2000JP-00276633.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Tojo H, Katayama N, Kakimoto S;

XX WPI; 2002-269344/31.

DR Protein binding to insulin-responsive aminopeptidase and glucose
 PT transporter 4, useful for prevention and treatment of diseases associated
 PT with blood sugar level disturbance.

XX Disclosure; Page 95-97; 103pp; Japanese.

XX The present invention describes human MD25 (very long chain acyl-CoA
 CC dehydrogenase (VLCAD)), which binds to insulin-responsive aminopeptidase
 CC (IRAP) and to glucose transporter 4 (GLUT4). MD25 has antidiabetic
 CC activity. IRAP and GLUT4 are involved in the intracellular regulation of
 CC glucose metabolism and glucose transport across the cell membrane.
 CC Expression of MD25 (whose ligands are these proteins) is also involved in
 CC this regulatory process. MD25 can be used in the prevention, treatment
 CC and diagnosis of diseases involving disturbances of glucose metabolism,
 CC such as diabetes and other hyperglycaemic disorders. The present sequence
 CC represents bovine VLCAD which is given in the exemplification of the
 CC present invention

XX Sequence 655 AA;

Alignment Scores:

Pred. No.: 3,16e-115 Length: 655
 Score: 1345.00 Matches: 285
 Percent Similarity: 65.51% Conservative: 110
 Best Local Similarity: 47.26% Mismatches: 194
 Query Match: 29.86% Indels: 14
 DB: 5 Gaps: 9

US-09-945-326-1 (1-2452) x ABB06993 (1-655)

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 DB 57 SerGluAlaSerThrArgGluLysArgAlaAsnSerValSerLysSerPheAlaValGly 76
 QY 193 CTTTTCCTAGCAAAATCAAGAAAGAAAGTTTTCATTTCCAGAGTT---AGCCAA 249
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 QY 250 GATGAACCTAATGAATCAATCACTTTTGGACCCGTGGAAATTTCTCACTGAGAG 309
 DB 97 AspGlnThrGlnPheLeuLysGluLeuValGlyProValThrArgPhePheGluGluVal 116
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 QY 430 AACACCATGACTCAAGACTAGGAGGAGATCATCAGCATG---GATGGTCCATCAGTGT 486
 DB 157 AsnThrGlnTyrAlaArgLeuValGluLeuValGlyMetTyrAspLeuGlyValGlyLeu 176

QY 487 ACCCTGCAGCGCACCGAGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCAGCTAGAG 546
 DB 177 ValLeuGlyAlaHisGlnSerIleGlyPheLysGlyIleLeuLeuPheGlyThrLysAla 196
 QY 547 CAGAAAGCCAAATACTTGCCTAAACTGGCTCGGGGAGACACATCTGAGCCCTTGCCTC 606
 DB 197 GlnLysGlnLysTyrLeuProLysLeuAlaSerIleGlyThrIleAlaAlaPheCysLeu 216
 QY 607 ACGGAGCCAGCCAGTGGGAGCGATGACGCTCAATCCGAGCAGCAGCACAATAAGTGA 666
 DB 217 ThrGluProSerSerGlySerAspAlaAlaSerIleArgSerSerAlaValProSerPro 236
 QY 667 GACAAGAACCATCATCTCAATGGCTCCAAGTCTGGATTCTGATTAATGAGAGCTGCC 726
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 QY 727 AATATTTTACTGTGTTTCAAGACACTGAGTCTGTTGAT---TCTGATGATCATGTA 783
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 DB 277 GluLysIleThrAlaPheValValGluArgSerPheGlyGlyValThrHisGlyProPro 296
 QY 844 GAAGATAAATTAGGCATTCGGGCTCCAAACACTTGTGAAGTCCATTTTGAACACCAAG 903
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 DB 317 ValProAlaGluAsnValLeuGlyGluValGlyGlyPheLysValAlaMetHisIle 336
 QY 964 CTCAACAGCGCGCTTTCAGCATGGGCGTCTGCTGGCTGGCTGCTCAAGAGATTGATT 1023
 DB 337 LeuAsnAsnGlyArgPheGlyMetAlaAlaAlaLeuAlaGlyThrMetLysGlyIleIle 356
 QY 1024 GAAATGACTGCTGAGTACGCTGCACAAGAAACAGTTTAAACAGAGGCTCAGTGAATT 1083
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 DB 476 GlyCysMetAspLysGlyLysGluLeuSerGlyLeuGlyAsnAlaLeuLysAsnProPhe 495
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 QY 1498 ACTGTGACCTGGGCTGACAGGCAACCATGGAGTGTGTGACACCCAGCTTTCGCGCAGT 1557
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QY 1849 GATGAGCAGATTAAAGAAAGTCTCCAGCAGATCCTTGAGAGCGAGCCTATATCTGTGCC 1908
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QY 651 AsnProLeu 653
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Search completed: May 2, 2005, 15:08:55
Job time : 385.879 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 2, 2005, 14:33:24 ; Search time 63.9282 Seconds
(without alignments)
5726.413 Million cell updates/sec

Title: US-09-945-326-1
Perfect score: 4504
Sequence: 1 cgtgtgtgtcctcctgcgc.....actgttaaaaaaaaaa 2452

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued_PatentsAA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human4.0.cdi
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Database :

- 1: /cgn2_6/ptodata/1/ias/5A.COMB.pcp.*
- 2: /cgn2_6/ptodata/1/ias/5B.COMB.pcp.*
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- 5: /cgn2_6/ptodata/1/ias/PCTUS.COMB.pcp.*
- 6: /cgn2_6/ptodata/1/ias/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	824	18.3	164	US-09-621-976-5565	Sequence 5565, Ap
2	816	18.1	601	US-09-902-540-11184	Sequence 11184, A
3	783	17.4	336	US-09-270-767-44314	Sequence 44314, A
4	691.5	15.4	390	US-09-252-991A-26058	Sequence 26058, A
5	666	14.8	389	US-09-328-352-6380	Sequence 6380, Ap
6	650	14.4	384	US-09-648-004-6	Sequence 6, Appli
7	650	14.4	384	US-10-272-419-6	Sequence 6, Appli
8	623	13.8	387	US-09-328-352-6442	Sequence 6442, Ap
9	618.5	13.7	403	US-09-252-991A-27960	Sequence 27960, A
10	608	13.5	382	US-09-328-352-4850	Sequence 4850, Ap
11	604	13.4	432	US-09-949-016-6098	Sequence 6098, Ap
12	603.5	13.4	419	US-09-252-991A-31097	Sequence 31097, A

13	596	13.2	394	4	US-09-328-352-6801	Sequence 6801, Ap
14	595.5	13.2	409	3	US-09-364-230-30	Sequence 30, Appl
15	592	13.1	459	4	US-09-949-016-10443	Sequence 10443, A
16	588.5	13.1	427	3	US-09-364-230-32	Sequence 32, Appl
17	559.5	12.4	383	4	US-09-328-352-7081	Sequence 7081, Ap
18	549.5	12.2	610	4	US-09-949-016-7708	Sequence 7708, Ap
19	546.5	12.1	421	4	US-09-949-016-5872	Sequence 5872, Ap
20	538.5	12.0	331	4	US-09-902-540-15531	Sequence 15531, A
21	514.5	11.4	402	4	US-09-328-352-4281	Sequence 4281, Ap
22	501	11.1	424	4	US-09-252-991A-24653	Sequence 24653, A
23	500	11.1	464	4	US-09-252-991A-33108	Sequence 33108, A
24	499	11.1	399	4	US-09-328-352-4360	Sequence 4360, Ap
25	481	10.7	444	4	US-09-949-016-10163	Sequence 10163, A
26	479	10.6	415	4	US-09-806-536A-13	Sequence 13, Appl
27	472	10.5	282	4	US-09-252-991A-29144	Sequence 29144, A
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30	456	10.1	270	3	US-09-364-230-28	Sequence 28, Appl
31	446.5	9.9	467	4	US-09-949-016-11236	Sequence 11236, A
32	440	9.8	279	4	US-09-902-540-10571	Sequence 10571, A
33	437.5	9.7	863	4	US-09-252-991A-19574	Sequence 19574, A
34	437	9.7	309	4	US-09-902-540-10954	Sequence 10954, A
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37	422	9.4	379	4	US-09-902-540-12816	Sequence 12816, A
38	416.5	9.2	393	4	US-09-252-991A-23105	Sequence 23105, A
39	399	8.9	683	4	US-09-252-991A-26189	Sequence 26189, A
40	399	8.9	826	4	US-09-543-681A-5053	Sequence 5053, Ap
41	392	8.7	413	4	US-09-252-991A-22542	Sequence 22542, A
42	391	8.7	227	4	US-09-270-767-32675	Sequence 32675, A
43	391	8.7	384	4	US-09-543-681A-6433	Sequence 6433, Ap
44	390.5	8.7	998	4	US-09-252-991A-21058	Sequence 21058, A
45	383.5	8.5	440	4	US-09-949-016-8372	Sequence 8372, Ap

ALIGNMENTS

RESULT 1
US-09-621-976-5565
; Sequence 5565, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5565
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16..-1
US-09-621-976-5565

Alignment Scores:			
Pred. No.:	2.95e-68	Length:	164
Score:	824.00	Matches:	164
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	18.29%	Indels:	0
DB:	4	Gaps:	0

US-09-945-326-1 (1-2452) x US-09-621-976-5565 (1-164)

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QY 127 GTGGTCTCTACCGGAACCGCGGCTACTGTGGCCACCGCCGCTGTACGAGCTTTCGCC 186
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RESULT 2

US-09-902-540-11184
; Sequence 11184, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE OF INVENTION: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11184
; LENGTH: 601
; TYPE: PR1
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(601)
; OTHER INFORMATION: unsure at all xaa locations
US-09-902-540-11184

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Percent Similarity: 51.60% Conservative: 92
Best Local Similarity: 36.09% Mismatches: 197
Query Match: 18.12% Indels: 90
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US-09-945-326-1 (1-2452) x US-09-902-540-11184 (1-601)

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271 ArgLeuLysLeuGlyAlaGlyValLeuGlyGlyMetLysLeuGlnLeuGlnAsnAlaLeu 290
QY 1036 GAGTACCGCTGCACAAGGAAACAGTTTAAACAAGAGCTCAGTGAATTTGGATTGATTCAG 1095
Db |||||
291 ArgPheThrGlnGluArgLysGlnPheAsnAlaProIleValGlnPheProLeuSerArg 310
QY 1096 GAGAAATTTGCATCGATGGCTCAGAAGGCTCATCGTCAAGAGATGATGACCTACCTCACA 1155
Db |||||
311 GluLysLeuAlaArgMetAlaAlaLeuValTyrAlaValGluSerMetThrTyrArgThr 330
QY 1156 GCAGGATGCTG-----GACCAACCTGGCTTT----- 1182
Db |||||
331 AlaGlyLeuValAspAlaArgLeuGlyGlnGlyAspLysAspAlaProAspTyrGluAla 350
QY 1183 -----CCCCGACTCTCCATCGAGGCCCATGGTGAAGGTGTTTCAGC 1224
Db |||||
351 ArgLeuLeuGluAlaValGluGluTyrAlaIleGluSerSerIleMetLysValHisGly 370
QY 1225 TCCGAGCGCGCTGGCAGTGTGTGAGTGAAGCGCTGCAGATCTCGGGGGCTTGGGCTAC 1284
Db |||||
371 SerGluSerPheGlyHisLeuValAspAlaValGlnLeuHisGlyGlyAlaGlyTyr 390
QY 1285 ACAAGGACTATCCGTACGAGCGCATACTCGGTGACACCCCGCATCTCTCTCATCTTCGAG 1344

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Db 391 IlegluGluTyrProValGluArgSerTyrArgAspAlaArgIleAsnArgIlePheGlu 410
      ::::::::::::::::::::
Qy 1345 GGAACCAATGAGATTCTCCGATGTACATCCCTGACGGGTCTGCAGCATGCGCGCGC 1404
      ::::::::::::::::::::
Db 411 GlyThrAsnGluIleAsnArgMetLeuIleThrGlyMetLeuLeuIleArgAlaValArg 430
      ::::::::::::::::::::
Qy 1405 ATCTGACTACAGGATCCATGAGCTTAACAG---GCCAAGTGGAGACAGTCAATGAT 1461
      ::::::::::::::::::::
Db 431 -----GlyAspLeuProLeuPheAlaMetAlaGlyAsnValAlaGlu 444
      ::::::::::::::::::::
Qy 1462 ACCGTTGGCGG-----AGGCTTCGGGACTCCCTGGCGGCGGACTGTG 1503
      ::::::::::::::::::::
Db 445 GluLeuSerArgGlyGluArgProArgAlaArgValGlnAspAlaLeuAlaProGlnGlu 464
      ::::::::::::::::::::
Qy 1504 GACCTGGGCTGACAGGCAACCATGAGTGTGTGACCCCGCTCTGCGGACAGTGCCAAAC 1563
      ::::::::::::::::::::
Db 465 ValAlaAlaGluAlaAlaLysHisLeuAlaLeuHis----- 476
      ::::::::::::::::::::
Qy 1564 AAGTTTGAGGAGAACACTACTGCTTCGGCGGACCGTG-----GAGACACTGCTGTC 1617
      ::::::::::::::::::::
Db 477 -----GlyLeuArgValAlaAlaGluThr----- 484
      ::::::::::::::::::::
Qy 1618 CGCTTTGGCAAGACCATCATCGAGGACGAGTGTACTGTAAGCGGTGGCGCAACATCCTC 1677
      ::::::::::::::::::::
Db 485 ---PheGlyProGluLeuGluGlnHisGlnGluValLeuAlaAlaLeuSerAspValVal 503
      ::::::::::::::::::::
Qy 1678 ATCAACCTGTATGCGCATGACGCGGTGCTGTCGGCGGCGCACCGCTCC----- 1725
      ::::::::::::::::::::
Db 504 MetAspAlaPheAlaLeuAspSerMetValThrArgThrArgGlnAlaAlaThrSerGly 523
      ::::::::::::::::::::
Qy 1726 -----ATCCGCTATGGGCTC-----CGC 1743
      ::::::::::::::::::::
Db 524 AlaLeuAspProValArgValAlaMetThrGlnLeuTyrAlaLeuAspAlaAlaProArg 543
      ::::::::::::::::::::
Qy 1744 AACACAGCAC-----GAGGTCTCTTGGCCACACCTTCTGCGTGGAGCTTACTTGCAG 1800
      ::::::::::::::::::::
Db 544 AlaTyrAspArgThrArgArgAlaLeuCysAlaThrLeuIleGlyAlaLeuAspGln 563
      ::::::::::::::::::::
Qy 1801 AATCTCTTACGCTCTCTACGCTGGACAGATGATCTCCA 1839
      ::::::::::::::::::::
Db 564 GluLeuGluArgLeuGlyThrLeuAspValPheThrPro 576
      ::::::::::::::::::::

RESULT 3
US-09-270-767-44314
; Sequence 44314, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44314
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44314

Alignment Scores:
Pred. No.: 3,25e-64 Length: 336
Score: 783.00 Matches: 169
Percent Similarity: 65.01% Conservative: 54
Best Local Similarity: 49.27% Mismatches: 104
Query Match: 17.38% Indels: 16
DB: 4 Gaps: 5

US-09-945-326-1 (1-2452) x US-09-270-767-44314 (1-336)

Qy 718 GGACTGCGCAATATTTTACTGTGTTTGCAGAAAGACTGAGTGTGTTGAT---TCTGATGGA 774
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Db 3 GlyIleAlaGluIleMetThrValPheAlaGlnThrGluGlnValAspProLysThrGly 22
Qy 775 TCAGTGAAGACAAAATCACAGCATTCATAGTAGAAAAGAGACTTTTGGTGGAGTCACTAAT 834
      ::::::::::::::::::::
Db 23 GluLysIleAspLysValThrAlaPheIleValGluArgSerPheGlyGlyValThrAsn 42
      ::::::::::::::::::::
Qy 835 GGGAAACCCCAAGATAAATTAGGCATTTCGGGGCTCCAAACACTTGTGAAGTCCATTTCGAA 894
      ::::::::::::::::::::
Db 43 GlyProGluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheGlu 62
      ::::::::::::::::::::
Qy 895 AACACCAAGATACCTGTGGAAAACATCCTTGGAGAGGTTCGAGATGGTTTTAAGGTGGCC 954
      ::::::::::::::::::::
Db 63 AspValLysIleProIleGluAsnValLeuGlyLysGluGlyAspGlyPheLysValAla 82
      ::::::::::::::::::::
Qy 955 ATGAACATCTCAACAGCGCGCTTCAGCATGCGCAGCCGCTGCGGTGGTGGCTCTCAAG 1014
      ::::::::::::::::::::
Db 83 MetAsnIleLeuAsnAsnGlyArgPheGlyMetGlyAlaThrLeuSerGlyThrMetLys 102
      ::::::::::::::::::::
Qy 1015 AGATTGATTGAATGACTGCTGAGTACGCTGCACCAAGAAACAGTTTAACAAGAGGCTC 1074
      ::::::::::::::::::::
Db 103 LysCysIleGluGlnAlaThrGluHisAlaAsnAsnArgValGlnPheGlyGlnLysLeu 122
      ::::::::::::::::::::
Qy 1075 AGTGAATTTGATTGATTTCAGGAGAAATTTGCACTGATGGCTCAGAAGGCTTACGTCATG 1134
      ::::::::::::::::::::
Db 123 LysAsnTyrGlySerIleGlnGluLysLeuAlaGlnMetAsnIleLeuGlnTyrAlaThr 142
      ::::::::::::::::::::
Qy 1135 GAGAGTATGATACCTACCTCACAGCAGGAGTGTCTGGACCAACCTGCTTCCGACATGCTCC 1194
      ::::::::::::::::::::
Db 143 GluSerMetAlaPheThrIleSerGlnAsnMetAsp---AlaGlySerLysAspTyrHis 161
      ::::::::::::::::::::
Qy 1195 ATCAGGACGACCATGTTGAAGGTTCAGCTTCGAGGCGCGCTGCGAGTGTGTGAGTGAG 1254
      ::::::::::::::::::::
Db 162 LeuGluAlaAlaIleSerLysIleTyrAlaSerGluSerAlaTyrValCysAspGlu 181
      ::::::::::::::::::::
Qy 1255 GCGCTGCAGATCTCGGGGCTTGGCTCACAAAGGACTATCGTACGACGCGATACGTG 1314
      ::::::::::::::::::::
Db 182 AlaIleGlnIleLeuGlyMetGlyTyrMetValAspThrGlyLeuGluArgValLeu 201
      ::::::::::::::::::::
Qy 1315 CGTGACACCCGCTCTCTCTCATCTTCGAGGGAAACCAATGAGATTCCTCCGATGTACATC 1374
      ::::::::::::::::::::
Db 202 ArgAspLeuArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheIle 221
      ::::::::::::::::::::
Qy 1375 GCGCTGAGCGGTCTGACGATGCGCGCGCATCTCTGACTACCGAGGATCCATGAGCTTAA 1434
      ::::::::::::::::::::
Db 222 AlaLeuThrGlyIleGlnTyrAlaGly-----SerHisLeuLysGluLeuGln 237
      ::::::::::::::::::::
Qy 1435 CAG-----GCCAAGTCAGCACAGTCATGATACCGTTGGCGCGGAGG 1476
      ::::::::::::::::::::
Db 238 ArgAlaPheLysAsnProSerAlaAsnLeuGlyLeuIlePheLysGluAlaSerArgArg 257
      ::::::::::::::::::::
Qy 1477 CTTGCGGACTCCCTGGGCGCAACTGTGGACTGTGGGCTGACAGGCAACCATGGAGTTGTG 1536
      ::::::::::::::::::::
Db 258 -----AlaAlaSerThrValGlyLeuGlyGlyThrAspLeuSerGlyHisVal 273
      ::::::::::::::::::::
Qy 1537 CACCCAGTCTTCGGGACAGTGCACCAAGTTTGAGGAGAAACACCTACTGCTTCGCGCGG 1596
      ::::::::::::::::::::
Db 274 ValGlyGluLeuLeuProTyrAlaLysLysThrAlaHisCysIleAspLeuPheGlyGln 293
      ::::::::::::::::::::
Qy 1597 ACCGTGGAGACACTGCTGCTCCGCTTTGGCAAGACCATCATGGAGGAGCAGCTGTACTG 1656
      ::::::::::::::::::::
Db 294 SerValGluGluLeuLeuArgTyrAsnLysAsnIleValAsnGluGlnIleLeuLeu 313
      ::::::::::::::::::::
Qy 1657 AAGCGGTGGCCCAACATCTCTCATCAACCTGTATGGCATGAGCGCGCTGTCTGCGGCGCC 1716
      ::::::::::::::::::::
Db 314 ThrArgLeuAlaAsnAlaAlaIleAspIleTyrAlaMetValValThrGlnSerArgSer 333
      ::::::::::::::::::::
Qy 1717 AGCGCTCTCC 1725
      ::::::::::::::::::::
Db 334 SerArgAla 336
      ::::::::::::::::::::

RESULT 4
US-09-252-991A-26058
; Sequence 26058, Application US/09252991A
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Db      191 ProGlyIleSerLeuGlyLysArgAspLysMetGlyGlnLysGlyAlaHisThrCys 210
QY      880 GAAGTCCATTTTGAACACCAAGTACCTCTGGAAACATCTTGGAGAGTC---GGA 936
Db      211 AspValIlePheGluAsnCysArgIleProAlaSerAlaLeuIleGlyValGluGly 230
QY      937 GATGGGTTTAAAGTGGCCATGAACATCTCTCAACAGCGCGGTTCAGCATGGCAGCGTC 996
Db      231 ValGlyPheLysThrAlaMetLysValLeuAspLysGlyArgIleHisIleAlaAlaLeu 250
QY      997 GTGGCTGGGCTCTCAAGAGATGATGAATGAAATGACTGTGAGTACGCTGCACAGGAAA 1056
Db      251 SerValGlyAlaAlaThrArgMetLeuGluAspSerLeuGlnTyrAlaValGluArgLys 270
QY      1057 CAGTTTAAACAGAGGCTCAGTGAATTTGGATTGATTCAG-----GAGAAA 1101
Db      271 GlnPheGlyGlnAlaIleAlaAsnPheGlnLeuIleGlnGlyMetLeuAlaAspSerLys 290
QY      1102 TTGCACTGATGGCTCAGAAGCTTACCTCATCGAGAGATGATGACTACCTCACAGCAGGG 1161
Db      291 AlaGluIleTyrAlaAlaLysCysMetValLeuAspAlaAlaArgLeuArgAspAlaGly 310
QY      1162 ATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGGCGAGCCATGGTGAAGGTGTC 1221
Db      311 Gln-----AsnValSerThrGluAlaSerCysAlaLysMetPhe 323
QY      1222 AGCTCCGAGCGCGCTGCGAGTGTGAGTGGCGCTGCAGATCCTCGGGCGCTTGGGC 1281
Db      324 AlaThrGluMetCysGlyArgValAlaAspArgGlyValGlnIleHisGlyAlaGly 343
QY      1282 TACACAGGGACTATCCGTACAGCGGCACTGCTGCAGCCCGCATCTCTCTCATCTTC 1341
Db      344 TyrIleSerGluTyrAlaIleGluArgPheTyrArgAspValArgLeuPheArgLeuTyr 363
QY      1342 GAGGAACCAATGATGATCTCCGAGTGTACATCCCTGAGCGGTCTGCAGCATGCC 1398
Db      364 GluGlyThrGlnIleGlnGlnValIleAlaArgAsnMetIleArgGluAla 382

RESULT 7
US-10-272-419-6
; Sequence 6, Application US/10272419
; Patent No. 6794165
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; APPLICANT: NAGARAJAN, VASANTHA
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; TITLE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: CL1341-A
; CURRENT APPLICATION NUMBER: US/10/272,419
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/252,553
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PR1
; ORGANISM: Acinetobacter sp.
US-10-272-419-6

Alignment Scores:
Pred. No.: 9,59e-52 Length: 384
Score: 650.00 Matches: 154
Percent Similarity: 57.89% Conservative: 77
Best Local Similarity: 38.60% Mismatches: 132
Query Match: 14.43% Indels: 36
DB: 4 Gaps: 11

US-09-945-326-1 (1-2452) x US-10-272-419-6 (1-384)
QY      247 CAAGATGAATTAATGAA-----ATCAATCAGTCTTGTGGGACCCCGTGGAAAAA 294
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Db      5 GlnAspThrLeuAsnGlnLeuValAspMetIleArgGlnPheValAspGlyVal---Leu 23
QY      295 TTCTTCACTGAAGAGGTGGACTCCCGAAAAAATTACCCAGGAAGGAAAAATCCCCAGATGAA 354
Db      24 IleProAsnGluGluIle-----ValAlaGluThrAspGluIleProAlaGlu 39
QY      355 ACTTTTGAGAAATTAAGAGACCTTAGGCTTTTGGGTGTCGAAGTCCAGAGAATATGGT 414
Db      40 IleValGlnMetLysGluLeuGlyLeuPheGlyLeuThrIleProGluGluTyrGlu 59
QY      415 GGCGTGGCGCTTCTCCAACACCATGTACTCAAGACTA-----GGGAGATCATCAGC 465
Db      60 GlyLeuGlyLeu-----ThrMetGluGluGluValTyrIleAlaPheGluLeuGlyArg 77
QY      466 ATGGATGGGTCCATCACTGTGACCCCTGGCAGCCGACCCAGCTATTGGCCCTCAAGGGGATC 525
Db      78 ThrSerProAlaPheArgSerLeuIleGlyThrAsnAsnGlyIleGlySerSerGlyLeu 97
QY      526 ATCTTGGCTGGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCGTCCGGGGAG 585
Db      98 IleIleAspGlySerGluGluGlnLysGlnTyrPheLeuProArgLeuAlaSerGlyGlu 117
QY      586 CACATTGCGACCTTCTGCTCAGGAGCCAGCCAGTGGGAGCGATCGAGCTCAATCCCG 645
Db      118 IleIleGlySerPheCysLeuThrGluProAspSerGlySerAspAlaAlaSerLeuLys 137
QY      646 AGCAGAGCCACACTAAGTGAAGAGAAGACACTACATCTCAATGGCTCCAAAGTCTGG 705
Db      138 ThrThrAlaVal-----LysAspGlyAspHisTyrIleLeuAsnGlyThrLysArgTyr 155
QY      706 ATTACTTAATGGAGGAGTGGCCCAATATTTTACTGTGTTGTTGCAAG-----ACTGAGGTC 759
Db      156 IleThrAsnAlaProHisAlaGlyValPheThrValMetAlaArgThrSerThrGluIle 175
QY      760 GTTGATCTTGATGGATCAGTGAAGAAAAAATCACAGCAATTCATAGTAGAAGAGACTTT 819
Db      176 LysGlyThrGlyGly-----IleSerAlaPheIleValAspSerLysThr 190
QY      820 GTGGAGTCACTAATGGGAAACCCGAGATAAATTAGGCATTTCCGGGCTCCACACTGT 879
Db      191 ProGlyIleSerLeuGlyLysArgAspLysLysMetGlyGlnLysGlyAlaHisThrCys 210
QY      880 GAAGTCCATTTTGAACACCAAGATACCTGTGGAAAAACATCTCTGGAGAGTC---GGA 936
Db      211 AspValIlePheGluAsnCysArgIleProAlaSerAlaLeuIleGlyValGluGly 230
QY      937 GATGGTAAAGTGGCCATGAACATCTCAACAGCGCGGTTCAGCATGGCAGCGTC 996
Db      231 ValGlyPheLysThrAlaMetLysValLeuAspLysGlyArgIleHisIleAlaAlaLeu 250
QY      997 GTGGCTGGGCTCTCAAGAGATGATGAATGACTGTGATCGCTGAGTACGCTGCACAGGAAA 1056
Db      251 SerValGlyAlaAlaThrArgMetLeuGluAspSerLeuGlnTyrAlaValGluArgLys 270
QY      1057 CAGTTTAAACAGAGGCTCAGTGAATTTGGATTGATTCAG-----GAGAAA 1101
Db      271 GlnPheGlyGlnAlaIleAlaAsnPheGlnLeuIleGlnGlyMetLeuAlaAspSerLys 290
QY      1102 TTGCACTGATGGCTCAGAAGCTTACCTCATCGAGAGATGATGACCTACTCACAGCAGG 1161
Db      291 AlaGluIleTyrAlaAlaLysCysMetValLeuAspAlaAlaArgLeuArgAspAlaGly 310
QY      1162 ATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGGCGAGCCATGGTGAAGGTGTC 1221
Db      311 Gln-----AsnValSerThrGluAlaSerCysAlaLysMetPhe 323
QY      1222 AGCTCCGAGCGCGCTGCGAGTGTGAGTGGCGGTGCGAGATCTCTCGGGGCTTGGGC 1281
Db      324 AlaThrGluMetCysGlyArgValAlaAspArgGlyValGlnIleHisGlyAlaGly 343
QY      1282 TACACAGGGACTATCCGTACAGCGGCACTGCTGCAGCCCGCATCTCTCTCATCTTC 1341
Db      344 TyrIleSerGluTyrAlaIleGluArgPheTyrArgAspValArgLeuPheArgLeuTyr 363

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Qy 1342 GAGGAACCAATGAGATTCTCCGGATGTACATCCGCTGACGGGTCTGCAGCATGCC 1398
Db 364 GluGlyThrThrGlnGlnGlnValIleIleAlaArgAsnMetIleArgGluAla 382

RESULT 8
US-09-328-352-6442
; Sequence 6442, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6442
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6442

Alignment Scores:
Pred. No.: 3,26e-49 Length: 387
Score: 623.00 Matches: 145
Percent Similarity: 56.85% Conservative: 79%
Best Local Similarity: 36.80% Mismatches: 130
Query Match: 13.83% Indels: 40
DB: 4 Gaps: 10

US-09-945-326-1 (1-2452) x US-09-328-352-6442 (1-387)
Qy 247 CAACATGAACCTAATGAATCAATCAGTCTTGGGACCCGCTGGGAAAAATCTTCACTGAA 306
Db 9 GlnGluThrLeuAsnGlnLeuValAspMetIle-----ArgGlnPheValGlu 24
Qy 307 GAGGTG-----GACTCCCGAAAAATTGACCAGGAAGGAAAAATCCCGATGAAACT 357
Db 25 GlyValLeuIleProHisGluAsnGluValAlaGluThrAspGluIleProAspIle 44
Qy 358 TTGAGAAATGAAGAGCTTAGGCTTTTGGGCTGCAAGTCCAGAGAAATATGTTGGC 417
Db 45 ValGluGlnMetLysAlaLeuGlyLeuPheGlyLeuThrIleProGluGluThrGluGly 64
Qy 418 CTGGGCTTCTCCACACCATGTACTCAAGCTAGGGGAGATCATCAGCATGGTGGTCC 477
Db 65 LeuGly-----LeuThrMetGluGluGlu 72
Qy 478 ATCACTGTGACC-----CTGGCAGCG 498
Db 73 ValTyrValAlaPheGluLeuGlyArgThrSerProAlaPheArgSerLeuIleGlyThr 92
Qy 499 CACAGGCTATGGCTCAAGGGATCATCTTGGCTGCACTGAGGAGCAGAAAGCCAAA 558
Db 93 AsnAsnGlyIleGlySerSerGlyLeuIleIleAspGlyThrGluAlaGlnLysSerPhe 112
Qy 559 TACTTGCCTAACTGGGCTCGGGGACCATTCAGCTTCTGCCTCAGGACCCAGCC 618
Db 113 PheLeuProArgLeuAlaArgGlyGluValIleSerPheCysLeuThrGluProAsp 132
Qy 619 AGTGGGAGCATGTCAGGCTCAATCCGGAGCAGCCACACTAACTGAAGACAAAGACAC 678
Db 133 AlaGlySerAspAlaAlaSerLeuLysThrSerAlaVal-----LysAspGlyAspPhe 150
Qy 679 TACATCTCAATGCTCAAGGCTCGATCTGATCTAATGAGACTGGCCCAATATTTTACT 738
Db 151 TyrValLeuAsnGlyThrLysArgPheIleThrAsnAlaProHisAlaGlyValPheThr 170
Qy 739 GTGTTTCAAGACTGAGGTGTTGATCTCATGATCAGTGAAGACAAATACACAGCA 798
Db 171 ValMetAlaArgThrAsn---PheAspIleLysGlyAla-----SerGlyIleSerAla 187
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Qy 799 TTCATAGTAGAAGAGAGACTTTGGTGGAGTCACCTAATGGGAAACCCGAAGATAAATTAGC 858
Db 188 PheIleValAspSerGlnThrProGlyIleSerLeuGlyLysArgAspLysMetGly 207
Qy 859 ATTCCGGGCTCCACACTTGTGAAGTCCATTTGAAAACCAAGATACCTGTGGAAC 918
Db 208 GlnLysGlyValHisThrCysAspValIlePheGluAsnCysArgIleProAlaSerAla 227
Qy 919 ATCTCTGGAGAGGTC---GGAGATGGGTTTAAGGTGGCCCATGAACATCTCTCAACAGCGGC 975
Db 228 LeuIleGlyValGluGlyValGlyPheLysThrAlaMetLysValLeuAspLysGly 247
Qy 976 CGGTTACAGATGGGACGCTGCTGGCTGCTGCTCAAGAGATTGATTGAATCACTGCT 1035
Db 248 ArgLeuHisIleAlaAlaLeuSerValGlyAlaAlaThrArgMetLeuAspSerLeu 267
Qy 1036 GAGTACGCTGCACAGGAACAGTTTAAACAAGAGGCTCAGTGAATTTGGATTCTATTCA 1095
Db 268 AsnTyrAlaIleGluArgLysGlnPheGlyGlnProIleAlaGluPheGlnLeuIleGln 287
Qy 1096 GAGAAATTTGCACCTGATGGCTCAGAGGCTTACGTCATGGAGATGATGACCTTCTCACA 1155
Db 288 AlaMetLeuAlaAspSerLysAlaGluIleTyrAlaAlaLysCysMetVal---LeuAsp 306
Qy 1156 GCAGGATGCTGGACCAACCTGCTTCCGACTGCTCCATCGAGGAGCCATCGTGAAG 1215
Db 307 AlaAlaArgLeuArgAspAlaGly---GlnAsnValSerThrGluAlaSerCysAlaLys 325
Qy 1216 GTGTTACGCTCCGAGCGCGCTGCGACTGTGAGTGAGGCGCTGCAGATCCTCGGGGGC 1275
Db 326 MetPheAlaThrGluMetCysGlyArgValAlaAspArgCysValGlnIleHisGlyGly 345
Qy 1276 TTGGGCTACACAGGAGACTATCCGTACGAGCGCATCTGGTGCACCCCGCATCTCTCCTC 1335
Db 346 AlaGlyTyrIleSerGluTyrAlaIleGluArgPheTyrArgAspValArgLeuPheArg 365
Qy 1336 ATCTTCAGGAGAACCAATGAGATTCTCCGGATGTACATCGCC 1377
Db 366 LeuTyrGluGlyThrThrGlnIleGlnValIleIleAla 379

RESULT 9
US-09-252-991A-27960
; Sequence 27960, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27960
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27960

Alignment Scores:
Pred. No.: 8,83e-49 Length: 403
Score: 618.50 Matches: 149
Percent Similarity: 55.42% Conservative: 71
Best Local Similarity: 37.53% Mismatches: 148
Query Match: 13.73% Indels: 29
DB: 4 Gaps: 8

US-09-945-326-1 (1-2452) x US-09-252-991A-27960 (1-403)
Qy 220 GAAGTTTTCCTCCATTTCCAGAAAGTTAGCCAAAGATGAACCTTAATGAATCAATCAGTTCTTG 279
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15	GluserMetThrTyrProSerLeuAsnPheAlaLeuGlyGluThrIleAspMetLeuArg	34
280	GGACCCGTGGAAAAATCTTCACTCAAGAGGTGGACTCCCGA-----AAAATTGACACAG	333
35	AspGlnValArgGlyPheValAlaAlaGluLeuGlnProArgAlaAlaGlnIleAspGln	54
334	GAAGGGAANAATCCAGATGAACATTTGGAGAAATTTGAAGAGCTAGGCTTTTGGGTG	393
55	AspAsnGlnPheProMetAspMetTrpArgLysPheGlyGluMetGlyLeuLeuGlyIle	74
394	CAAGTCCAGAGAATAATGGTGGCTGGCTTCTCCAACACCATCTACTCAAGACTAGG	453
75	ThrValAspGluGluTyrGlySerAlaLeuGlyTyrLeuAlaHisAlaValValMet	94
454	GAGATCATCACG--ATGGATGGGTCCATCACTGTGACCCCTGGCAGCCACACAGGCTAT	510
95	GluGluIleSerArgAlaSerAlaSerValAlaLeuSerTyrGlyAlaHisSerAsnLeu	114
511	GGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAGCCAAATACTTGCCTAA	570
115	CysValAsnGlnIleLysArgAsnGlyAsnAlaGluGlnLysAlaArgTyrLeuProAla	134
571	CTGCGCTCGGGAGACACATTGCGACCTTCTGCGCTCAAGGAGCCAGCAGTGGAGCAT	630
135	LeuValSerGlyGluHisIleGlyAlaLeuAlaMetSerGluProAsnAlaGlySerAsp	154
631	GCACCTCAATCCGAGCAGACACACTAAGTGAAGACAAGAGCACTACATCTCTCAAT	690
155	ValValSerMetLysLeuArgAlaAspArgValGlyAspArg-----PheValLeuAsn	172
691	GGCTCCAAGGTCTGGATTACTTAATGGAGCACTGGCCAAATATTTTACTGTCTTTGCAAG	750
173	GlySerLysMetTrpIleThrAsnGlyProAspAlaHisThrTyrValIleTyrAlaLys	192
751	ACTGAGTCTGTGATTCGTGATCATGATGATGAGTGAAGACAAA-----ATCACGCA	798
193	ThrAspAla-----AspLysGlyAlaHisGlyIleThrAla	204
799	TTCATAGTAGAAGAGACTTTTGTGGAGTCACTAATGGAAACCGAGAGATAAATTAGGC	858
205	PheIleValGluArgAspTrpLysGlyPheSerArgGlyProLysLeuAspLysLeuGly	224
859	ATTCGGGGTCCAACTTGTGAAGTCCATTTTGAACACCAAGATACCTGTGGAACAC	918
225	MetArgGlySerAsnThrCysGluLeuIlePheGlnAspValGluValProGluGluAsn	244
919	ATCCTTGGAGAGTCCGAGATGGTTTAAGTGGCCATGAACATCTCAACAGCGCGCGG	978
245	ValLeuGlyAlaValAsnGlyValLysValLeuMetSerGlyLeuAspTyrGluArg	264
979	TTCAGCATGGCAGCGCTGCTGGCTGGCTGCTCAAGAGATTGATTGAATGACTGTCTGAG	1038
265	ValValLeuSerGlyGlyProValGlyIleMetGlnAlaCysMetAspValValValPro	284
1039	TAGCGCTGCACAGGAACAGTTTAACAGAGGCTCAGTCAATTTGATTGATTGATTCAGGAG	1098
285	TyrIleHisAspArgGlnPheGlyGlnSerIleGlyGluPheGlnLeuValGlnGly	304
1099	AAATTT-----GCACTGATGGCTCAGAAGGCTTACGTCATCGATGGAGAGTATG	1143
305	LysValAlaAspMetTyrThrAlaLeuAsnAlaSerArgAlaTyrLeu-----	320
1144	ACCTACTCACAGAGGATCTGGACCAACCTGGGCTTCCCGACTGCTCCATCGAGGCA	1203
321	---TyrAlaValAlaAlaAlaCysAspArgGly-----GluThrThrArgLysAspAla	337
1204	GCCATGGTGAAGTGTTCAGTCCGAGGCGCCTGGCAGGTGTGTGATGAGGCGCTCAG	1263
338	AlaGlyValIleLeuTyrSerAlaGluArgAlaThrGlnMetAlaLeuAspAlaIleGln	357
1264	ATCCTCGGGGCTTGGCTTACACAGGAGATATCCGTACGAGCGCATACTGCTGATGACCC	1323

[illegible]


```
QY 841 CCCGAAGATAATTAGGCAATTCGGGGCTCCACACTTGTGAAGTCCATTTTGAACACC 900
Db 203 ValGluGluLysLeuGlyLeuHisAlaSerAspThrCysGlnLeuAlaLeuThrAspVal 222
QY 901 AAGATACCTGTGGAAAAACATCTTGGAGAGGTCCGAGATGGTTTAAAGTGGCCATGAAC 960
Db 223 ArgIleHisLysSerLeuMetLeuGlyLysGluGlyLeuLysIleAlaLeuAla 242
QY 961 ATCCTCAACAGCGCGGTTCAGCATGGCGACGCTGCTGGTGGCTCTCAAGAGATTG 1020
Db 243 AsnLeuGluGlyArgIleGlyLeuAlaGlnAlaValGlyLeuAlaArgAlaAla 262
QY 1021 ATTGAATGACTGTGAGTACCTGCGACAGAGAAACAGTTTAAACAGAGGCTCAGTGA 1080
Db 263 LeuGluGluAlaThrArgTyrAlaLysGluArgIleThrPheGlyLysProIlePheGlu 282
QY 1081 TTGGATTGATTCAGGAAATTTGCTGATGCTGCTCAGAGGCTTACGTCTGAGAGT 1140
Db 283 HisGlnThrIleAlaPheArgLeuAlaSerMetAlaThrGluIleGluAlaArgGln 302
QY 1141 ATGACCTACCTCACAGCAGGAGTGTGACCAACCTGGCTTCCGAGCTGCCATCGAG 1200
Db 303 LeuValHisTyr--AlaAlaArgLeuLysGluAlaGlyGlnPro--CysLeuAsnGlu 320
QY 1201 GCAGCATGTGAAGTGTTCAGTCTCCAGCGCGCTCGCAGTGTGTGAGCGCTG 1260
Db 321 AlaSerMetAlaLysLeuPheAlaSerGluMetThrGluArgValCysSerSerAlaLeu 340
QY 1261 CAGATCCTCGGGGCTTGGCTACACAGGAGTATCGTACGAGCGCATCTCGCTGAC 1320
Db 341 GlnValPheGlyGlyTyrGlyTyrLeuArgAspPheProIleGluArgIleTyrArgAsp 360
QY 1321 ACCGCGATCCTCCTCATCTTCGAGGAAACCAATGAGATTCTCCGAGTGTACATCGCC 1377
Db 361 AlaArgIleCysGlnIleTyrGluGlyThrSerAspIleGlnArgLeuValIleAla 379

RESULT 11
US-09-949-016-6098
; Sequence 6098, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6098
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6098

Alignment Scores:
Pred. No.: 2,1e-47 Length: 432
Score: 604.00 Matches: 157
Percent Similarity: 54.46% Conservative: 81
Best Local Similarity: 35.93% Mismatches: 155
Query Watch: 13.41% Indels: 44
DB: 4 Gaps: 14

US-09-945-326-1 (1-2452) x US-09-949-016-6098 (1-432)
QY 121 GGTCTGGTGTCTTACCGGAAACCGGGGCTACTGCGCACCGCCGCTGTACGAGCT 180
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Db 345 AlaAlaArgLeuLeuThrTyrAenAlaAlaArgLeuLeu---GluAlaGlyLysProPhe 363

QY 1189 TGCTCATCGAGCAGCCATGTGAAGTGTTCAGCTCGAGGCCCTCGCAGTGTGTG 1248

Db 364 IleLys---GluAlaSerMetAlaLysTyrTyrAlaSerGluAlaGlyGlnThrThr 382

QY 1249 ACTGAGGGCGCTCAGATCTCTGGGGCTTGGGCTACACAAAGGACTATCCGTACGAGCGC 1308

Db 383 SerLysCysIleGluTrpMetGlyValGlyTyrThrLysAspTyrProValGluLys 402

QY 1309 ATACTGCGTGACACCGCATCTCTCTTCGAGGAAACAATGAGATT 1359

Db 403 TyrPheArgAspAlaLysIleGlyThrIleTyrGluGlyAlaSerAsnIle 419

RESULT 12

US-09-252-991A-31097

; Sequence 31097, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 31097

; LENGTH: 419

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-31097

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
2.29e-47	603.50	419	136
Percent Similarity:	57.83%	Conservative:	67
Best Local Similarity:	38.75%	Mismatches:	139
Query Match:	13.40%	Indels:	9
DB:	4	Gaps:	6

US-09-945-326-1 (1-2452) x US-09-252-991A-31097 (1-419)

QY 328 GACCAGGAAGGAAATCCAGATGAACCTTTGGAGAAATTGAAGACCTAGGCTTTT 387

Db 74 AspArgGluHisArgPheProAlaGluAlaIleArgGluMetAlaSerLeuGlyPheLeu 93

QY 388 GGGCTGCAAGTCCAGAAATATGGTGGCTGGCTTCTCCAACACCATGTACTCA--- 444

Db 94 GlyMetLeuValProGluGluTrpGlyGlyAlaGlnThrGlyHisLeuAlaTyrAlaMet 113

QY 445 AGACTAGGGAGATCATCAGCATGGATGGCTCCATCTGACCTGGCAGGCGACCCAG 504

Db 114 AlaLeuGluIleAlaAlaGlyAspGlyAlaCysSerThrIleMetSerValHisAsn 133

QY 505 GCTATTGGCTCAAGGGGATCATCTTGGCTGCACCTGAGGAGCAAGCAAACTACTTG 564

Db 134 SerValGlyCysMetProIleHisLysPheGlySerAlaGluGlnLysGluArgPheLeu 153

QY 565 CCTAACTGGCTCCGGGAGCATTGCGCTTCTGCTCAGGAGCCAGCGAGTGGG 624

Db 154 ArgProLeuAlaGlnGlySerMetLeuGlyAlaPheAlaLeuThrGluProGlnAlaGly 173

QY 625 AGCGATGACCTCAATCCGAGCAGGACACACTAAGTGAAGCAAGACGACTACATC 684

Db 174 SerAspAlaSerPheLeuLysThrArgAla-----ArgArgAspGlyAspHisTyrVal 191

QY 685 CTCAAATGGCTCCAGTCTGATTAATAATGAGGAGCTGGCCAATATTTACTGTGTTT 744

Db 192 LeuAsnGlyAlaLysGlnPheIleThrSerGlySerHisAlaGlyMetValIleValPhe 211

QY 745 GCRAAGACTGAGTGTGTTGATTCGTGATGATGAAAGACAAATTCACAGCATTCATA 804

Db 212 Ala-----ValThrAspProAspAlaGly---LysArgGlyIleSerAlaPheIle 227

QY 805 GTAGAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAAAGATAAATTAGCATTCGG 864

Db 228 ValProThrAspThrProGlyTyrGluValValArgIleGluAspLysLeuGlyGlnHis 247

QY 865 GGCTCCAACACTTGTGAAGTCCATTTTGAACACCAAGATACCTCTGGAAAAACATCCTT 924

Db 248 AlaSerAspThrCysGlnLeuAlaPheAsnAspLeuArgIleProAlaThrLeuArgLeu 267

QY 925 GGAGAGTGGCAGATCGGTTTAAGTGGCCATCAACATCTCTCAACAGCGCCGGTTCAGC 984

Db 268 GlyGluGluGlyGlyTyrArgIleAlaLeuAlaAsnLeuGluGlyGlyArgIleGly 287

QY 985 ATGGGACGCTCGTGGCTGCTCAAGAGATTGATTGAATGATCTGTGAGTACGCC 1044

Db 288 IleAlaAlaGlnAlaValGlyMetAlaArgAlaAlaPheGluAlaAlaArgAspTyrAla 307

QY 1045 TGCACAAGGAAACAGTTTAAACAGAGCTCAGTGAATTTGGATTGATTTCAGGAGAAATTT 1104

Db 308 HisGluArgGluThrPheGlyLysProIleIleGluHisGlnAlaValAlaPheArgLeu 327

QY 1105 GCATCTGATGCTCAGAAAGCTTACGTCATGGAGAGTATGACCTACCTCAGCAGGATG 1164

Db 328 AlaAspMetAlaThrArgIleAlaValAlaArgGlnMetValHis---HisAlaAlaSer 346

QY 1165 CTGGACCAACCTGGCTTTCCCGACTGCTCCAGCAGCAGCATGGTGAAGTGTTCAGC 1224

Db 347 LeuArgGluAlaGlyLeuPro---CysLeuThrGluAlaSerMetAlaLysLeuPheAla 365

QY 1225 TCGAGGCGCCTGGCAGTGTGTGAGTGAGGCTGCAGATCCTCGGGGCTTGGGCTAC 1284

Db 366 SerGluMetAlaGluGluValCysSerAlaAlaIleGlnThrLeuGlyGlyTyrGlyTyr 385

QY 1285 ACAAGGAGCTATCCGTACGAGCGCATCTCGCTGACACCCGATCCTCTCTCATCTTCGAG 1344

Db 386 LeuLysAspPheProValGluArgIleTyrArgAspValArgValCysGlnIleTyrGlu 405

QY 1345 GGAACCAATGAGATTCTCCGATGTACATCGCC 1377

Db 406 GlyThrSerAspValGlnArgLeuValIleAla 416

RESULT 13

US-09-328-352-6801

; Sequence 6801, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE REFERENCE: GT99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 6801

; LENGTH: 394

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-6801

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
1.1e-46	596.00	394	140
Percent Similarity:	57.10%	Conservative:	73
Best Local Similarity:	37.53%	Mismatches:	138
Query Match:	13.23%	Indels:	22
DB:	4	Gaps:	9

US-09-945-326-1 (1-2452) x US-09-328-352-6801 (1-394)

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QY 286 GTGGAAATTTCTTCACTGAAGAGGTGGAC-----TCCCGAAAAATGTACCAGGAAGGG 339
Db      |||
QY 25 ValAlaAlaPheCysAlaLeuGluLeuAlaProIleAlaGlnValAspGlnAspAsn 44
Db      |||
QY 340 AAAATCCAGATGAACCTTTGGAGAAATGAAGAGCCTAGGCTTTTGGCTCGCAAGTC 399
Db      |||
QY 45 LysPheProAlaHisLeuTrpLysPheGlyAspMetGlyLeuLeuGlyMetThrVal 64
Db      |||
QY 400 CCAGAAGAATATGGTGGCTGGCTTCTCCAACACCATGTACTCAAGACTAGGGGAGATC 459
Db      |||
QY 65 SerGluGluTrpGlyGly-----AlaAsnMetGlyTyr-----LeuAlaHisIle 79
Db      |||
QY 460 ATCAGCATG-----GATGGTCCATCACTGTGACCTGGAGCGGCAC 501
Db      |||
QY 80 IleAlaMetGlnGluIleSerArgAlaSerAlaAlaIleGlyLeuSerTyrGlyAlaHis 99
Db      |||
QY 502 CAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCCAAATAC 561
Db      |||
QY 100 SerAsnLeuCysValAsnGlnIleAsnArgAsnGlyAsnGluGlnGlnLysGlnLysTyr 119
Db      |||
QY 562 TTGCCTAAACTGGCTCCGGGAGCACATTTGACAGCTTCTGCTCCACGGAGCCAGCCAGT 621
Db      |||
QY 120 LeuProLysLeuIleSerGlyGluTyr-ValGlyAlaLeuAlaMetSerGluProAsnAla 139
Db      |||
QY 622 GGGAGCCATGAGCCTCAATCCGAGGAGAGCCACACTAAGTGAAGACAAAGACACTAC 681
Db      |||
QY 140 GlySerAspValValSerMetLysLeuArgAlaGluGlnLysGlyAsp-----HisPhe 157
Db      |||
QY 682 ATCTCTCAATGGCTCAAGGCTGATTAATGAGGAGCTGGCCATATTTTACTGTG 741
Db      |||
QY 158 ValLeuAsnGlySerLysMetTrpIleThrAsnGlyGlyAspAlaAspValLeuVal 177
Db      |||
QY 742 TTTGCAAAAGACTGAGGTCGTGTGATCTCTGATGATCAGTGAAGACAAACAAATCAACGATTC 801
Db      |||
QY 178 TyrAlaLysThr-----AspProGlnAlaGlyProLysGly---MetThrAlaPhe 193
Db      |||
QY 802 ATAGTAAAGAGAGACTTTGTGGAGTCACATAATGGGAAACCCGAGATAAATAGGCATT 861
Db      |||
QY 194 LeuIleGluLysGlyMetLysGlyPheSerHisGlyAsnHisLeuAspLysLeuGlyMet 213
Db      |||
QY 862 CGGGCTCCACACTTGTGAAGTCCATTTGAAACACCAAGATACCTGTGGGAAACATC 921
Db      |||
QY 214 ArgGlySerAsnThrTyrProLeuPhePheAspAsnValGluValProAlaGluAsnVal 233
Db      |||
QY 922 CTTGGAGAGCTCGAGATGGGTTTAAAGTGCCATGAACATCTCTCAACAGCGCGCGCTTC 981
Db      |||
QY 234 LeuGlyGlyValGlyAsnGlyValLysValLeuMetSerGlyLeuAspTyrGluArgAla 253
Db      |||
QY 982 AGCATGGGCGCTGTGGCTGCTCAAGAGATTTGATTAATGATGATGCTGTGAGTAC 1041
Db      |||
QY 254 ValLeuSerAlaGlyProLeuGlyIleMetAspAlaCysLeuAspValValIleProTyr 273
Db      |||
QY 1042 GCCTGCACAGGAACAGTTTAAACAGGCTCAGTGAATTTGATTGATTCAGGAGAAA 1101
Db      |||
QY 274 LeuHisGlnArgGluGlnPheGlyGlnAlaLeuGlyGluPheGlnLeuMetGlnGlyLys 293
Db      |||
QY 1102 TTTGCTAGTGGCTCAGAAGGCTTACGTGATGAGAGATGACTACCTACCTCACAGCAGG 1161
Db      |||
QY 294 LeuAlaAspMetTyrSerThrTrpLeuAlaCysLysAlaLeuValTyrAlaValGlyAla 313
Db      |||
QY 1162 ATGCTGACCAACCTGGCTTTCCCGACTGTCTCCATC-----GAGGAGCCATGGTGAAG 1215
Db      |||
QY 314 AlaCysAspLysAlaAspHis---AspArgSerLeuArgLysAspAlaAlaSerAlaIle 332
Db      |||
QY 1216 GTGTTAGCTCCGAGCGCGCTGGCAGCTGTGTAGTGAGGCGCTGCAGATCCTCGGGGGC 1275
Db      |||
QY 333 LeuTyrAlaAlaGluLysAlaThrTrpMetAlaGlyGluAlaIleGlnThrLeuGlyGly 352
Db      |||
QY 1276 TTGGGCTACCAAGGGACTTCCGTACGAGCGCATCTGCTGCTGACCCCGCATCCTCCTC 1335
Db      |||
QY 353 AsnGlyTyrIleAsnGluPheProAlaGlyArgLeuTrpArgAspAlaLysLeuTyrGlu 372
Db      |||
QY 1336 ATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATC 1374
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Db 373 IleGlyAlaGlyThrSerGluIleArgArgMetLeuIle 385
RESULT 14
US-09-364-230-30
; Sequence 30, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09/364,230
; CURRENT FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,990
; EARLIER FILING DATE: July 31, 1998
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-364-230-30
Alignment Scores:
Pred. No.: 1,26e-46 Length: 409
Score: 595.50 Matches: 150
Percent Similarity: 54.87% Conservative: 64
Best Local Similarity: 38.46% Mismatches: 143
Query Match: 13.22% Indels: 33
DB: 3 Gaps: 13
US-09-945-326-1 (1-2452) x US-09-364-230-30 (1-409)
QY 250 GATGAACCTTAATGAATCAATCAATGTTCTTGGGACCCGTGGAATAAATTTCTTCACTGAAGAG 309
Db      |||
QY 32 AspAspThrGlnGlu-----GlnPheLysGluSerValHisLysPheAlaGlnGluThr 49
Db      |||
QY 310 GTG-----GACTCCCGGAAATTTGACCAAGGAGGAGGAAATCCCA---GATGAACTTTG 360
Db      |||
QY 50 IleAlaProHisAlaAlaIleAspAlaSerAsnHisPheProLysAspValAsnLeu 69
Db      |||
QY 361 GAGAAATTGAAG---AGCCTTAGGGCTTTTGGGCTGCAAGTCCAGAGAAATATGTTGGC 417
Db      |||
QY 70 TrpLysLeuMetGlyAspPheAsnLeuHisGlyLeuThrAlaProGluGluTyrGlyGly 89
Db      |||
QY 418 CTGGGCTTCTCCAACACCATGTACTCA-----AGACTAGGGAGATCATCAGCATGGAT 471
Db      |||
QY 90 MetGlyLeu---GlyTyrMetTyrHisCysIleAlaMetGluGluIleAsnArgAlaSer 108
Db      |||
QY 472 GGGTCCATCACTGTGACCTTGGCAGCGCAGCAGGCTATTGCGCTCAAGGGGATCATCTTG 531
Db      |||
QY 109 GlySerValGlyLeuSerTyrSerAlaHisSerAsnLeuCysIleAsnGlnLeuValArg 128
Db      |||
QY 532 GCTGGCAGCTGAGGAGCAGAAAGCCAAATCTTGCCTAAACTGGCGTCCGGGAGCACAT 591
Db      |||
QY 129 HisGlySerProAlaGlnLysLeuLysTyrLeuProLysLeuIleThrGlyGluHisVal 148
Db      |||
QY 592 GCAGCCTTCTGCTCAGGAGCCAGCAGCTGGGAGGATCGAGCCTCAATCCGAGCAGA 651
Db      |||
QY 149 GlyAlaLeuAlaMetSerGluProAsnSerGlySerAspValValSerMetLysCysLys 168
Db      |||
QY 652 GCCACACTAAGTGAAGCAGAGAGCAC-----TAGATCCTCAATGCTCCAAGGCTCGG 705
Db      |||
QY 169 Ala-----GluLysValTyrGlyGlyTyrValIleAsnGlyAsnLysMetTrp 184
Db      |||
QY 706 ATTACTAATGGAGGACTGGCCAAATATTTTACTGTGTTTGGCAAGAGACTGAGGTC--GTT 762
Db      |||
QY 185 CysThrAsnGlyProSerAlaGlnThrLeuGlyValTyrAlaLysThrAspIleThrAla 204
Db      |||
QY 763 GATTCTGTGATGATCAGTGAAGAACAAATACAGCATTCATAGTAGAAAGAGACTTTGGT 822
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Db      205 GlySerLysGly-----|||ThraAlaPheIleGluLysGlyMetAla 219
QY      823 GGAGTCACCTAATGGGAACCCAGAAATATAGGATTCGGGGCTCCAACTTGTCAA 882
Db      220 GlyPheSerThraAlaGlnLysLeuAspLysLeuGlyMetArgLysSerAspThrCysGlu 239
QY      883 GTCCATTTTGAACACACCAAGACTCTGTGGAACATCCTTGGAGAGGTGGAGATGGG 942
Db      240 LeuValPheGluAsnCysPheValProHisGluAsnValLeuGlyGluGlyLysGly 259
QY      943 TTTAAGGTGGCCATCAACATCTCAACAGCGCCGGTTCAGCATGGGCGGCTCGTGCT 1002
Db      260 ValTyrValMetMetSerGlyLeuAsnLeuGluArgPheValLeuAlaAlaGlyProSer 279
QY      1003 GGGCTGCTCAAGAGATTGATTCAAATGACTGCTGAGTACGGCTGCACAGGAACAGTTT 1062
Db      280 AlaLeuMetGlnAlaCysLeuAspValAlaValLeuTyrValArgGlnArgGluGlnPhe 299
QY      1063 AACAGAGGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCACTGATGGCTCAGAAG 1122
Db      300 GlyArgProIleGlyGluPheGlnPheIleArgGlyLysLeuAlaAspMetTyrThrSer 319
QY      1123 GCTTACGTATGAGAGATGATGACTTACCTCAGCA-----GGGATGCTG 1167
Db      320 LeuGlnSerSerArgSerPheValTyrSerValAlaArgAspCysAspAsnGlyLysVal 339
QY      1168 GACCACCTGCTTCCCGACTGCTCCATCAGGAGCCAGTGGTGAAGGTGTTCAAGTCC 1227
Db      340 AspArg-----LysAspCys-----AlaGlyValIleLeuPheAlaAla 352
QY      1228 GAGCGCCGCTGGAGTGTGTGAGTGAGCGCTGAGATCTCCGGGGCTTGGGCTACACA 1287
Db      353 GluArgAlaThrGlnValAlaLeuGlnAlaIleGlnCysLeuGlyGlyAsnGlyTyrIle 372
QY      1288 AGGACTATCCGTACGAGCGCATACTGGTGCACCCGCATCTCTCTCATCTTCGAGGGA 1347
Db      373 AsnGluTyrProThrAlaArgLeuLeuArgAspAlaLysLeuPheGluIleGlyProGly 392
QY      1348 ACCAATGAGATTCTCCGGATGTACATCGCC 1377
Db      393 ThrSerGluIleArgArgMetIleAla 402

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RESULT 15

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US-09-949-016-10443
; Sequence 10443, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10443
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10443

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Alignment Scores:
Pred. No.: 2,89e-46 Length: 459
Score: 592.00 Matches: 161
Percent Similarity: 51.61% Conservative: 79
Best Local Similarity: 34.62% Mismatches: 179

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Query Match: 13..14% Indels: 46
DB: 4 Gaps: 13
US-09-945-326-1 (1-2452) x US-09-949-016-10443 (1-459)
QY 74 GCTGCGGGCTCTTCCTCGCGCACCGCTCGCTCGCTCGCGGGTCTGTGTGTCT 133
Db 28 SerAlaGlySerCysMetAlaGluMet--AlaThrAlaThrArgLeuLeuGlyTrpA 47
QY 134 CTACCGCGAACCCCGCGCTACTCGCGCACCGCTGTACGAGCTTTCGCCCAAGAGC 193
Db 47 rgValAlaSerTrpArgLeu-----ArgProLeuAlaGlyPheValSerGln- 63
QY 194 TTTTCTAGCAAAATCAAGAAGAAAGATTTCCTATTTCCAGAGTTTAGCAAGATG 253
Db 64 -----ArgAlaHisSerLeuLeuProValAspAspAlaIleAsnGlyL 78
QY 254 AACTTAATGAATCAATCAGTTCTTGGGACCCCTGGAAAATTTCTTCTACTGAAGAGTG- 312
Db 78 euSerGluGluGlnArgGlnLeuArgGlnThrMetAlaLysPheLeuGlnGluHisLeuA 98
QY 313 -----GACTCCCGAAAAATTTGACAGGAAGGGAAAAATCCAGAT-----GAACTTTGG 361
Db 98 laProLysAlaGlnGluIleAspArgSerAsnGluPheLysAsnLeuArgGluPheTrpL 118
QY 362 AGAAATTTGAAGACCTTAGGCTTTTGGCTGCAAGTCCCAAGAAATATGTGTGGCTGG 421
Db 118 ysGlnLeuGlyAsnLeuGlyValLeuGlyIleThrAlaProValGlnTyrGlyGlySerG 138
QY 422 GCTTCTCCCAACACCATGTACTCAAGACTAGGGAGATCATCAGC---ATGGATGGGTCCA 478
Db 138 lYLeuGlyTyrLeuGluHisValLeuValMetGluGluIleSerArgAlaSerGlyAlaV 158
QY 479 TCATCTGTGACCTTGGCGAGCGCACCGAGCTATTGGCTCAAGGGGATCATCTTGGCTGGA 538
Db 158 aGlyLeuSerTyrGlyAlaHisSerAsnLeuCysIleAsnGlnLeuValArgAsnGlyA 178
QY 539 CTGAGGAGCAGAAACCAATACTTGCCTAACTGGCTCCGGGAGACATTTGAGCCT 598
Db 178 snGluAlaGlnLysGluLysTyrLeuProLysLeuIleSerGlyGlyIleGlyAlaL 198
QY 599 TCTGCTCTACCGAGCGCAGCTAGTGGGAGCGATGAGCTCAATCCGAGCAGAGCCACAC 658
Db 198 euAlaMetSerGluProAsnAlaGlySerAspValValSerMetLysLeuLysAla--- 216
QY 659 TAACTGAGACACAAGAG-----CACTACATCTCAATGGCTCCAGGTCTGGATTACTA 712
Db 217 -----GluLysLysGlyAsnHisTyrIleLeuAsnGlyAsnLysPheTrpIleThra 234
QY 713 ATGAGGAGTGGCCCAATATTTTACTGTGTTTGCAGAGACTGAGCTCGTTGATTCTGTATG 772
Db 234 snGlyProAspAlaAspValLeuIleValTyrAlaLysThrAspLeuAlaAlaValProA 254
QY 773 GATCAGTGAAGACAAAATCAAGCATTCATAGTAGAAGAGACTTTGGTGGAGTCACTA 832
Db 254 laSer-----ArgGlyIleThrAlaPheIleValGluLysLysMetProGlyPheSer 272
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QY 1013 AGAATTGATTGAATGACTCTGAGTACGCTGCACAGGAGAAACAGTTTAAACAGAGGC 1072
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

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(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query
Result

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1	3171	70.4	628	15	US-10-112-944-869	Sequence 869, App
2	3153	70.0	621	9	US-09-945-326-2	Sequence 2, Appli
3	3153	70.0	621	14	US-10-168-274-24	Sequence 24, Appl
4	3153	70.0	621	15	US-10-112-944-420	Sequence 420, App
5	3153	70.0	621	16	US-10-408-765A-1059	Sequence 1059, Ap
6	3153	70.0	621	16	US-10-408-765A-2053	Sequence 2053, Ap
7	1365	30.3	653	15	US-10-362-537-9	Sequence 9, Appli
8	1360	30.2	655	15	US-10-362-537-10	Sequence 10, Appli
9	1345	29.9	655	15	US-10-362-537-11	Sequence 11, Appli
10	1321	29.3	655	15	US-10-362-537-1	Sequence 1, Appli
11	1321	29.3	655	16	US-10-408-765A-534	Sequence 534, App
12	1312	29.1	655	16	US-10-408-765A-320	Sequence 320, App
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15	954	21.2	188	16	US-10-408-765A-2052	Sequence 2052, Ap
16	844.5	18.8	594	15	US-10-369-493-16704	Sequence 16704, A
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19	815.5	18.1	594	15	US-10-369-493-23285	Sequence 23285, A
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22	765	17.0	583	15	US-10-369-493-10383	Sequence 10383, A
23	704	15.6	373	15	US-10-369-493-16614	Sequence 16614, A
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34	650	14.4	384	14	US-10-272-413-6	Sequence 6, Appli
35	644.5	14.3	370	15	US-10-369-493-14087	Sequence 14087, A
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ALIGNMENTS

RESULT 1
US-10-112-944-869
; Sequence 869, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; SECRETED Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28

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; Sequence 2, Application US/09945326
; Patent No. US20020127680A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Hunter, John Joseph
; TITLE OF INVENTION: 62112, A NOVEL HUMAN DEHYDROGENASE AND
; FILE REFERENCE: MNI-187
; CURRENT APPLICATION NUMBER: US/09/945,326
; PRIOR FILING DATE: 2001-08-31
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-326-2

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; Sequence 24, Application US/10168274
; Publication No. US20030124106A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: HILLMAN, Jennifer
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yaida
; APPLICANT: LU, Dying Aina M.
; TITLE OF INVENTION: HUMAN OXIDOREDUCTASE PROTEINS
; FILE REFERENCE: PF-0754 PCT
; CURRENT APPLICATION NUMBER: US/10/168,274
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/172,367
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PERL Program
; SEQ ID NO 24
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030124106A1 5540437CD1
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Db 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
Qy 967 AACAGCGCGGCTTCAGCATGGCGAGCGTGGCTGGGCTGCTCAAGAGATTGATTGAA 1026
Db 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLysArgLeuIleGlu 320
Qy 1027 ATGACTGCTGACTACCCCTGCAAGGAAACAGTTTAAACAAGAGCTCAGTGAATTTGA 1086
Db 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
Qy 1087 TTGATTCCAGGAGAAATTTGCATGTGCTCAGAGGCTTACGTATGGAGAGTATGACC 1146
Db 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
```

```
QY 1147 TACCTCAGCAGGAGTGTGGACCAACCTGGCTTCCGACTCTCCATCGAGCGACCC 1206
D 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaA 380
QY 1207 ATGCTGAAGGTTCACGCTCGAGCGCCCTGGCAGTGTGTGAGTGGCGCTCAGATC 1266
D 381 MetValIysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnI 400
QY 1267 CTCGGGGCTTGGGCTACACAAAGGAGTATCCGTACGAGCGCATCTGCGTACACCGC 1326
D 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
QY 1327 ATCTCTCTCATCTTCGAGGGAACCAATGAGATTCCTCGGATGTATCATCGCCCTGACGG 1386
D 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY 1387 CTCGAGCATCGCGCCGCTACCTGCTACCGAGGATCCATGAGTTCATGAGTTCACAGGCG 1446
D 441 LeuGlnHisAlaGlyArgIleLeuThrArgIleHisGluLeuIysGlnAlaLysVal 460
QY 1447 AGCAGCTCATGATACGTTGGCGGAGGCTTCGGGACTCCCTGGCGCGAACTGTGGAC 1506
D 461 SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480
QY 1507 CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCAGTCTTCGGGACAGTGCACCAAG 1566
D 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerSerLeuAlaAspSerAlaAsnLys 500
QY 1567 TTTGAGGAGAACACTACTGCTTCGGCGGACCGTGGAGACACTGCTGCTCCGCTTTGGC 1626
D 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
QY 1627 AAGACCATCATGGAGGAGCAGCTGTGTAAGGGGTGGCCAACTCCTCATCAACCTG 1686
D 521 LysThrIleMetGluGluGlnLeuValLeuIysArgValAlaAlaIleLeuIleAsnLeu 540
QY 1687 TATGGCATGACGGCGTGTCTCGCGGCGCAGCGCTCCATCGCATTTGGGCTCCGCAAC 1746
D 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY 1747 CAGCACCAGAGTTCTCTTGGCCCAACACTTCTGCTGGAGCTTACTTGCAGATCTC 1806
D 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
QY 1807 TTCAGCTCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAAGAA 1866
D 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
QY 1867 GTGTCCAGCAGATCCTTTGAGAGCGAGCCCTATATCTGTGCCCACTCTTGGACAGGACA 1926
D 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
QY 1927 TGC 1929
D 621 Cys 621
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RESULT 4

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US-10-112-944-420
; Sequence 420, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrul
; APPLICANT: Zhao, Qing A.
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; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: Pf-Fl_genes Version 5.0
; SEQ ID NO 420
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-112-944-420

Alignment Scores:
Pred. No.: 2,43e-249 Length: 621
Score: 3153.00 Matches: 621
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.00% Indels: 0
DB: 15 Gaps: 0

US-09-945-326-1 (1-2452) x US-10-112-944-420 (1-621)

QY 67 ATCAGCGGCTGCGGGCTCTTCCTCGCCACCCAGCGCTGCGCTCGCGGGTCTG 126
D 1 MetSerGlyCysGlyLeuPheLeuArgThrAlaAlaAlaArgAlaCysArgGlyLeu 20
QY 127 GTGGTCTCTACCCGCAACCGCGGCTACTCGCCACCCAGCGCGCTGTACGAGCTTTCCGCC 186
D 21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProValArgAlaPheAla 40
QY 187 AAGAGCTTTTCTAGCGAAAATCAAGAGAAAGAGTTTTTCCCATTTCCAGAAAGTTAGC 246
D 41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer 60
QY 247 CAAGATCAACTTAATCAATCAATCAGTCTTCGGACCCCGTGGAAAATTTCTTCACTGAA 306
D 61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80
QY 307 GAGGTGGACTCCCGAAAAAATTGACAGGAGGAAAAATCCAGATGAAACTTTTGGAGAAA 366
D 81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100
QY 367 TTGAAGAGCTAGGGCTTTTGGCTGCAAGTCCCAAGAAATATGTGTGGCTGGCTTC 426
D 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe 120
QY 427 TCCAAACACCATGTACTCAGACTAGGGAGATCATCAGCATGGTGGTCCATCAGCTGTG 486
D 121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
QY 487 ACCCTGGCAGCGCACCGAGGCTATTGGCTTCAAGGGGATCATCTTGGCTGGCTAGGAG 546
D 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160
QY 547 CAGAAAGCCAAATACTTGGCTTAAACTCGGGGAGCAGATTGCGAGCTTCTGCTCCTC 606
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Db      161  GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180
QY      607  ACGAGCCAGCAGTGGAGCGATGCGACCTCAATCCGGACGACGACACACATGAAGTAA 666
Db      181  ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
QY      667  CACAAGAACACTACATCCTCAATGGCTCCAAAGTCTGGATTACTAATGAGGAGTGGCC 726
Db      201  AspLysLysHisTyrIleLeuLysGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
QY      727  AATATTTTACTGTGTTTGAAGACTGAGTGCCTGATTCTGATGATGATGATGATGATG 786
Db      221  AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
QY      787  AARATCACAGCATTCAATAGTAGAAGAGACTTGGTGGAGTCACTAATGGGAACCCGAA 846
Db      241  LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260
QY      847  GATAAATTAGGCATTCGGGGCTCCAAACACTGTGAACTCCATTTTGAAACACCAAGATA 906
Db      261  AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
QY      907  CCTGTGAAACATCCTTGGAGAGGTGGAGATGGGTTTAAGTGGCCATGAACATCCTC 966
Db      281  ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
QY      967  AACAGCGCGGTTTCACATGGGCGAGCTCGTGGCTGGCTGCTCAAGAGATTGATTGAA 1026
Db      301  AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
QY      1027  ATGACTCTCAGTACGCGCTGCACAAGGAAACAGTTTAAACAGAGGCTCAGTGAATTGGA 1086
Db      321  MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
QY      1087  TTGATTGAGAGAAATTTGCACTGATCGCTCAGAGGCTTACGTATGAGAGATGATGACC 1146
Db      341  LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
QY      1147  TACCTCACAGCAGGATGCTGGACCACTGGCTTTCCCGACTGCTCCATCGAGGAGGCC 1206
Db      361  TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
QY      1207  ATGTGTAAGTGTTCAGCTCCGAGGCGCTCGGCAGTGTGTGAGTGAAGGCGCTGCAGATC 1266
Db      381  MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400
QY      1267  CTCGGGGCTTGGGTACACAGGGACTATCCGTACGAGCGCATCTGCGTGACACCCGC 1326
Db      401  LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
QY      1327  ATCTCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1386
Db      421  IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY      1387  CTCAGCATCCCGCCGCATCCTGACTACAGGATCCATGAGCTTAAACAGGCCAACATG 1446
Db      441  LeuGlnHisAlaGlyArgIleLeuThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY      1447  AGCACATCATGATACCGTTGSCCGGAGCTTCGGGACTCCCTGGGCGGAATGTGGAC 1506
Db      461  SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480
QY      1507  CTCGGGCTGACAGCAACCATGAGTTGTGCACCCAGTCTTCGGGACAGTGGCAACAAG 1566
Db      481  LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY      1567  TTTGAGAGAACACTACTCTCTCGCCGACCGTGGAGACACTGTGCTCCGCTTTGGC 1626
Db      501  PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
QY      1627  AAGACCATCATGAGGAGCAGCTGTTACTGAAGGGGTGGCCAACTCTCATCAACCTG 1686
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Db      521  LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
QY      1687  TATGGCATGACGGCGTGTCTGTCGGGGCCAGCGCTCCATCCGCATTGGGCTCCGCAAC 1746
Db      541  TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY      1747  CACGACCACGAGGTTCTCTTGGGCCAACACCTTCTCGTGGTGAAGCTTACTTGCAGAAATCTC 1806
Db      561  HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
QY      1807  TTCAGCTCTCTCAGCTGGACAAAGTATGTCTCCAGAAAACTTAGATGACGACAGATTAAAGAA 1866
Db      581  PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
QY      1867  GTCTCCACGAGATCCTTGGAAGCCAGGCTATATCTGTGCCACCCCTCTGGACAGGACA 1926
Db      601  ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
QY      1927  TGC 1929
Db      621  Cys 621
```

RESULT 5

US-10-408-765A-1059
; Sequence 1059, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: PASTSEQ for Windows Version 4.0
; SEQ ID NO 1059
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1059

Alignment Scores:
Pred. No.: 2.43e-249 Length: 621
Score: 3153.00 Matches: 621
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.00% Indels: 0
DB: 16 Gaps: 0

US-09-945-326-1 (1-2452) x US-10-408-765A-1059 (1-621)

QY 67 ATGAGCGGCTCGGGGCTCTTCTCGCGCACCGGCTCGGCTCGTCCGCGGGGTCTG 126
Db 1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAargAlaCysArgGlyLeu 20
QY 127 GTGGTCTCTTACCGCAACCGCGGCTACTGCGCACCGCCCTGTAGAGCTTTTCGCC 186
Db 21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProValArgAlaPheAla 40
QY 187 AAGAGCTTTTCTAGGCAAAATCAAGAGAAAGAGTTTCCCATTTCCAGAGTTAGC 246
Db 41 LysGluLeuPheLeuGlyLysIleLysLysLysLysLysLysLysLysLysLysLys 60
QY 247 CAAGATGAATTAATGAATCAATCAGTTCTTGGGACCGCTGGAATAATTTCTTCACTGAA 306
Db 61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80

QY 307 GAGTGGACTCCCGAAATAATTGACAGAGAGGAAAAATCCAGATGAAACTTTTCGAGAAA 366
Db GluValAspSerArgLysIleAeApGlnGluGlyIleProAspGluThrLeuGluLys 100
QY 367 TTGAAGAGCCTAGAGCTTTTGGGCTCAAGTCCCAAGAAATATGGTGGCTCGGCTTC 426
Db LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluThrGlyGlyLeuGlyPhe 120
QY 427 TCCAACACCATGTACTCAAGACTAGGGAGATCATCAGCATGGATGGTCCATCAGCTGTG 486
Db SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
QY 487 ACCCTGGAGCGACACAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACTGAGAG 546
Db ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160
QY 547 CAGAAAGCCAAATCTTCCCTAAACTGGCGTCCGGGAGCACATTGAGCCCTTCGCTC 606
Db GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaIlePheCysLeu 180
QY 607 ACGGAGCGCAGCTGGGAGCGATGCGACCTCAATCCGGAGCAGAGCCACACTAAGTGAA 666
Db ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
QY 667 GACAAGACACTACATCCTCAATGGCTCAAGTCTGGATTAATAATGAGAGCTGGCC 726
Db AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
QY 727 AATATTTTACTGTGTGCAAGACACTGAGTCCGCTGATCTGATCTGATGATCAGTCAAGAC 786
Db AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
QY 787 AAAATCACAGCATTCATAGTAGAAGAGACTTTGGTGGAGTCATTAATGGGAAACCCGAA 846
Db LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260
QY 847 GATAAATTAGCATTCGGGGCTCCAAACACTTGTGAAGTCCATTTTGAACACCAAGATA 906
Db AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
QY 907 CCTGTGAAACATCCTTGGAGAGTCCGAGATGGGTTAAGGTGGCCATCAACATCCTC 966
Db ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
QY 967 AACAGCGCGGCTTTCAGCATGGCGAGCTGCTGGCTGGCTGCTCAAGAGATTCATTGAA 1026
Db AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
QY 1027 ATGACTCTGAGTACGCTGCACAAAGAAACAGTTTAAAGAGGCTCAGTGAATTTGGA 1086
Db MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
QY 1087 TTGATTCAGGAGAAATTTGCACTGATGGCTCAGAGGCTTACGTCATGGAGATGATGACC 1146
Db LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
QY 1147 TACCTCACAGCAGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGCGAGCC 1206
Db TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
QY 1207 ATGCTGAAGGTGTTCACTCCGAGCGCCCTGGCAGTGTGTGATGAGGCGCTCAGATC 1266
Db MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400
QY 1267 CTCGGGGCTTGGCTACACAGGAGTATCCGTACGAGCGCATCTGCGTGCACACCGC 1326
Db LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
QY 1327 ATCTCTCTCATCTTCGAGGGAACCAATGAGATTCCTCCGGATGTATCATCGCCCTCAGCGGT 1386
Db IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY 1387 CTGAGCATGCGGCGCGCATCTCTGACTACCAAGGATCCATGAGCTTAAACAGGCCAAAGTG 1446

Db 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY 1447 AGCAGCTCATGGATACCGTTGGCCGAGGCTTCCGGACTCCCTGGGCGCAACTGTGTGAC 1506
Db SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480
QY 1507 CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCAGTCTTGGGACAGTGCACCAACAG 1566
Db LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY 1567 TTTGAGGAGAACACCTACTCTTGGCCGAGCCGCTGGAGACACTGCTCCGCTTTGGC 1626
Db PheGlnGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
QY 1627 AAGACCATCATGAGGAGCAGCTGCTACTGAAGCGGTGGCCCAACATCTCTCATCAACCTG 1686
Db LysThrIleMetGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
QY 1687 TATGGCATGACGGCGCTGTGTCCGGCGCAGCGCTCCATCCGATGGGCTCCGCAAC 1746
Db TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY 1747 CAGCACCAAGCTTCTTTGGCCCAACACCTTCTGCGTGGAGCTTACTTGCAGAACTC 1806
Db HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
QY 1807 TTCAGCCTCTCTCAGCTGGACAAAGTAGTGTCCAGAAAACCTTAGATGACGAGATTAAAGAA 1866
Db PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
QY 1867 GTGTCCAGCAGATCCTTGAAGACGAGCTATATCTGTGCCACCTCTTGGACAGGACA 1926
Db ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
QY 1927 TGC 1929
Db 621 Cys 621
RESULT 6
US-10-408-765A-2053
; Sequence 2053, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2053
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2053
Alignment Scores:
Pred. No.: 2,436-249 Length: 621
Score: 3153.00 Matches: 621
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.00% Indels: 0
DB: 16 Gaps: 0
US-09-945-326-1 (1-2452) x US-10-408-765A-2053 (1-621)

! TYPE: PRT
! ORGANISM: Rat
! US-10-362-537-9

Alignment Scores:

Pred. No.: 1.16e-102 Length: 653
Score: 1365.00 Matches: 303
Percent Similarity: 62.77% Conservative: 110
Best Local Similarity: 46.05% Mismatch: 202
Query Match: 30.31% Indels: 43
DB: 15 Gaps: 13

US-09-945-326-1 (1-2452) x US-10-362-537-9 (1-653)

Qy 30 GGGAGACTGAGCTGAGCTGGGG---AACATCGGGCAGCATGAGCGCTCGGGGCTCTT 86
Db 11 GlyArgGlnLeuLeuArgLeuGlyAlaArgSerArgSerAlaAlaLeuGlnGlyGln 30
Qy 87 CTCTGGCAGCAGCGCTCGGCTCTGCTGCTGGCGGGCTCTGCTGCTCTCTACCGGAACCG 146
Db 31 Pro-ArgProThrSerAlaGlnArg-----LeuTyrAlaSerGluAlaThrGln 46
Qy 147 GCGGCTACTGCGC-----ACCAGCCCGCTGT 173
Db 46 nAlaValLeuGlnLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAl 66
Qy 174 ACCAGCT-----TTCCGCCAAAGAGCTTTTCTAGGCCAAATCAAGAAAGAAAGA 221
Db 66 aArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGln 86
Qy 222 AGTTTCCCATTTCCAGAGTTAGCCCAAGATGAATTAATGA-----AT 266
Db 86 nValPheProThrProSerVal-----LeuAsnGluGlyGlnThrGlnPheLe 102
Qy 267 CAATCAGTCTTGGAGCCCGTGGAAATTTCTTCACTGAAGAGTGCATCCCGAAAT 326
Db 102 uLysGluLeuValGlyProValAlaArgPheGluGluValAsnAspProAlaLysAs 122
Qy 327 TGACAGAGAGGAGAAATCCAGATGAATTTGAGAAATTTGAGAGCTTAGGGCTTTT 386
Db 122 nAspSerLeuGlnLysValGluGluAspThrLeuGlnGlyLeuLysGluLeuGlyAlaPh 142
Qy 387 TGGCTGCAAGTCCAGAGAAATATGTGGCTGGCTGCTGCTTCTCCAAACACCATGACTCAAG 446
Db 142 eGlyLeuGlnValProSerGluLeuGlyGlyLeuGlyLeuSerAsnThrGlnTyrAlaAr 162
Qy 447 ACTAGGGAGATCATCAGCATG---GATGGTCCATCACTGTGACCTGGCAGCGCACCA 503
Db 162 gLeuAlaGluLeuValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGln 182
Qy 504 GGCTATTGGCTCAAGGGGATCATTTGGCTGGCAGTGAAGAGAGAGAGAGAGAGAGAGAG 563
Db 182 nSerIleGlyPheLysGlyLeuLeuLeuTyrGlyThrLysAlaGlnLysGluLysTyrLe 202
Qy 564 GCCTAAATCTGGCTCCGGGAGCAGCATTTGAGCGCTTCTGCTCTACGAGCGCAGCATGG 623
Db 202 uProArgValAlaSerGlyGlnAlaLeuAlaPheCysLeuThrGluProSerSerGln 222
Qy 624 GAGCGATGACCTCATCCGAGCAGCGCACACTAAGTCAAGACAGAGAGAGAGAGAGAGAG 683
Db 222 ySerAspValAlaSerIleArgSerSerAlaValProSerProCysGlyLysTyrThr 242
Qy 684 CCTCAATGGCTCCAAAGCTCTGGATTACTTAATGGAGGAGTGGCCCAATATTTTACTGTGT 743
Db 242 rLeuAsnGlySerLysIleThrPheSerAsnGlyGlyLeuAlaAspIlePheThrValPh 262
Qy 744 TGCAAGACTGAGGTCTGTGAT---TCTGATGGATCATGTAAGAGAGAGAGAGAGAGAGAG 800
Db 262 eAlaLysThrProIleLysAspAlaAlaThrGlyAlaValLysGluLysIleThrAlaPh 282
Qy 801 CATAGTAGAAGAGACTTTGGTGGAGTCACTTAATGGGAACCCCGAAGATAAATTAGGCAT 860
Db 282 eValValGluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGlyI 302

Qy 861 TCGGGGCTCCAAACACTTGTGAAGTCCATTTTGAACACCAAGATACCTGTGGAAACAT 920
Db 302 eLysAlaSerAsnThrSerGluValTyrPheAspGlyValLysValProAlaGluAsnVa 322
Qy 921 CCTTGGAGAGGTGGAGATGGGTTTAAAGTGGCCATGAACATCTCCACAGCGCGCGTT 980
Db 322 lLeuGlyGluValGlyAspGlyPheLysValAlaValAsnIleLeuAsnGlnGlyArgPh 342
Qy 981 CAGCATGGGAGCGCTCGTGGCTGGCTCAAGAGATGATTGAAATGACTGCTGAGTA 1040
Db 342 eGlyMetAlaAlaThrLeuAlaGlyThrMetLysAlaIleAlaLysAlaValAspHi 362
Qy 1041 CGCTGTCACAAGAAACAGTTTAAACAGAGCTCAGTGAATTTGGATTGATTTCAGAGAA 1100
Db 362 sAlaThrAsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGly 382
Qy 1101 ATTTGGCACTAGTGGCTCAGAAGGCTTACGTCATGAGAGATGATACCTACCTCACAGCAG 1160
Db 382 sLeuAlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAl 402
Qy 1161 GATGCTCGACCAACCTGGCTTCCGAGCTGCTCCATCGAGCAGCAGCATGGTGAAGGTGT 1220
Db 402 aAsnMetAspGln---GlyPheLysAspPheGlnIleGluAlaIleSerLysIlePh 421
Qy 1221 CAGCTCCGAGCGCCCTGGCAGTGTGTGAGTGGCGCTCAGATCTCGGGGCTTGGG 1280
Db 421 eGlySerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGlyGlyMetGln 441
Qy 1281 CTACACAGGGAGTATCCGTACGAGCGCATCTGCGTGACACCGCATCTCTCTCATCTT 1340
Db 441 yPheMetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePh 461
Qy 1341 CGAGGGAACCAATGAGATTCTCCGGATGTATCGCTCAGCGGTCTGCAGCATGCCG 1400
Db 461 eGluGlyThrAsnAspIleLeuArgPheValAlaLeuGlnGlyCysMetAspLysGln 481
Qy 1401 CCGCATCTCTCACTACCAAGGATCCATGAGCTTAAACAG-----GCCAAAGTGCACAG 1454
Db 481 yLysGluLeuThrGlyLeuGlyAsnAlaLeuLysAsnProLeuGlyAsnValGlyLeuLe 501
Qy 1455 CATGGATACCTTGGCGGAGGCTTCCGGACTCCCTGGCGGCACTGTGGACCTGGGGCT 1514
Db 501 uIleGlyGluAlaSerLysGlnLeuArgArg-gThrGlyIleGlySerGlyLeuSerLe 521
Qy 1515 GACAGGCAACCATGGAGTGTGCACCCCACTTTCGCGACAGTGCACCAAGTTTGAGGA 1574
Db 521 uSer-----GlyIleValHisProGluLeuSerArgSerGlyGluLeuAlaValGln 538
Qy 1575 GAACACCTACTGCTTCGCGCGGACCGTGGAGACACTGCTGCTCGCTTTGGCAAAGACAT 1634
Db 538 nAlaLeuGluGlnPheAlaThrValValGluAlaLysLeuMetLysHisLysLysGlyI 558
Qy 1635 CATGGAGGAGCAGCTGGTACTGAAGCGGTGGCCACATCTCATCACTGATGGCAT 1694
Db 558 eValAsnGluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMe 578
Qy 1695 GACGGCGTCTCTCGCGGCGCAGCGCTCCATCCGATTTGGGCTCCGCAACACAGACA 1754
Db 578 tValValValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHi 598
Qy 1755 CGAGGTTCCTTGGCCCAACACTTCTCGTGGAGACT-----TACTTGCAGATCT 1805
Db 598 sGluLysMetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMe 618
Qy 1806 CTTTCAGCTCTCTCAGCTGGACAGATATGCTCCAGAAACCTAGATGAGCAGATTAGAA 1865
Db 618 tAlaSerLeuGlnSerAsnProGln-----GlnGlnGluLeuPheArgAsnPheArgSe 636
Qy 1866 AGTGTCCACAGATCTCTCGAAGAGCGAGCGCTATATCTGTGCCACCTCTG 1917
Db 636 rIleSerLysAlaMetValGluAsnGlyLeuValThrSerAsnProLeu 653

RESULT 8

US-10-362-537-10

; Sequence 10, Application US/10362537

; Publication No. US20040086510A1

; GENERAL INFORMATION:

; APPLICANT: Takeda Chemical Industries, Ltd.

; TITLE OF INVENTION: IRAP Binding Protein

; FILE REFERENCE: 2774 USOP

; CURRENT APPLICATION NUMBER: US/10/362,537

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: JP 2000-254263

; PRIOR FILING DATE: 2000-08-21

; PRIOR APPLICATION NUMBER: JP 2000-276633

; PRIOR FILING DATE: 2000-09-07

; NUMBER OF SEQ ID NOS: 11

; SEQ ID NO 10

; LENGTH: 655

; TYPE: PRT

; ORGANISM: Mouse

US-10-362-537-10

Alignment Scores:

Pred. No.:	2,99e-102	Length:	655
Score:	1360.00	Matches:	287
Percent Similarity:	66.05%	Conservative:	106
Best Local Similarity:	48.24%	Mismatches:	184
Query Match:	30.20%	Indels:	18
DB:	15	Gaps:	9

US-09-945-326-1 (1-2452) x US-10-362-537-10 (1-655)

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QY 169 CCTGTACGAGCT-----TTGCCAAAGAGCTTTCTTACGAGCAAAATCAAGAAG 216
DB 66 ProAlaArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrIle 85
QY 217 AAAGAAGTTTCCCATTTCCAGAAGTT---AGCCAAGATGAACCTTAATGAATCAATCAG 273
DB 86 AspGlnValPheProTyrProSerValLeuSerGluGlnAlaGlnPheLeuLysGlu 105
QY 274 TTTCTGGGACCCGTGGAAATTTCTTCACTGAAGAGGTGGACTCCCGAAATTTGACCAG 333
DB 106 LeuValGlyProValAlaArgPheGluGluValAsnAspProAlaLysAsnAspAla 125
QY 334 GAAGGAAATCCAGATGAATTTCCGAGAAATTTGAAGAGCCCTAGGCGCTTTTGGGCTG 393
DB 126 LeuGluLysValGluAspAspThrLeuGlnGlyLeuLysGluLeuGlyAlaPheGlyLeu 145
QY 394 CAAGTCCCAAGAATATGTTGGCTGGCTTCTCCCAACCATGTACTCAAGACTAGGG 453
DB 146 GlnValProSerGluLeuGlyGlyLeuGlyLeuSerAsnThrGlnTyrAlaArgLeuAla 165
QY 454 GAGATCATCAGCATG---GATGGGTCCATCACTGTGACCTGTGGCGGACCCAGGCTATT 510
DB 166 GluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGlnSerIle 185
QY 511 GGCCTCAAGGGATCATCTTGGCTGGCAGCTGAGAGCAGAAAGCCAAATCTTGCCTAAA 570
DB 186 GlyPheLysGlyIleLeuLeuTyrGlyThrLysAlaGlnArgGluLysTyrLeuProArg 205
QY 571 CTGGCTCCGGGAGCACATTTGAGCTTCTGCTCAGCGGACCGCCAGCTGGGAGGAT 630
DB 206 ValAlaSerGlyGlnAlaLeuAlaPheCysLeuThrGluProSerGlySerAsp 225
QY 631 GCAGCTCAATCCGGAGCAGACACACTAAGTGAAGACAAGAACGACTACATCTCAAT 690
DB 226 ValAlaSerIleArgSerSerAlaIleProSerProCysGlyLysTyrThrLeuAsn 245
QY 691 GGCTCCAGCTCGGATTACTAATGAGGACTGGCCAAATTTTACTGTGTTGCAAG 750
DB 246 GlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLys 265
QY 751 ACTGAGTCGTTGAT---TCTGATGATCAGTCAAAAGACAATATCAGCATTTATAGTA 807
DB 751 ACTGAGTCGTTGAT---TCTGATGATCAGTCAAAAGACAATATCAGCATTTATAGTA 807

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DB 266 ThrProIleLysAspAlaAlaThrGlyAlaValLysGluLysIleThrAlaPheValVal 285
QY 808 GAAAGAGACTTTGGTGGAGTCACATAATGGGAAACCCGAAAGATAAATAGGATCGCGGC 867
DB 286 GluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGlyIleLysAla 305
QY 868 TCCAACTTGTGAAGTCCATTTTGAACACCAAGATACCTGTGGAAAACATCTTTGGA 927
DB 306 SerAsnThrSerGluValTyrPheAspGlyValLysValProSerGluAsnValLeuGly 325
QY 928 GAGTCCGAGATGGTTTAAAGTGGCCATGAACATCTCAACAGCGCGGTTTCAGCATG 987
DB 326 GluValGlyAspGlyPheLysValAlaValAsnIleLeuAsnAsnGlyArgPheGlyMet 345
QY 988 GGCAGCGTCTGCTGGCTGCTCAAGAGATTGAATTAAGATGCTGCTGAGTACGCTGCTG 1047
DB 346 AlaAlaThrLeuAlaGlyThrMetLysSerLeuIleAlaLysAlaValAspHisAlaThr 365
QY 1048 ACAAGGAAACAGTTTAAACAGAGCTCAGTCAATTTGGATTGATTTCAGGAGAAATTTGCA 1107
DB 366 AsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLysLeuAla 385
QY 1108 CTGATGGCTCAGAAAGCTTACGTGATGAGAGATGATGACCTACCTCAGCAGCAGGATGCTG 1167
DB 386 ArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAlaAsnMet 405
QY 1168 GACCAACCTGGCTTCCCGACTGCTCCATCGAGCGAGCATGGTGAAGTGTTCAGCTCC 1227
DB 406 AspGln---GlyPheLysAspPheGlnIleGluAlaAlaIleSerLysIlePheCysSer 424
QY 1228 GAGCGCGCTGGCAGGTGTGAGTGAAGCGCTGCAGATCTCGGGGCTTGGGCTACACA 1287
DB 425 GluAlaAlaTrpLysValAlaAspGluCysIleGlnIleMetGlyGlyMetGlyPheMet 444
QY 1288 AGGACTATCCGTACAGCGCATCTGCTGATGACACCCGCTCCTCTCATCTTTCAGGGA 1347
DB 445 LysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePheGluGly 464
QY 1348 ACCAATGAGATTTCCGGATCTACATCGCCCTGACGGGTCTCGAGCATCGCGGCCCATC 1407
DB 465 AlaAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysGlyLysGlu 484
QY 1408 CTGACTTACCAGGATTCAGCTTAAACAG-----GCCAAAGTGAGCAGCATCATGGAT 1461
DB 485 LeuThrGlyLeuGlyAsnAlaLeuLysAsnProPheGlyAsnValGlyLeuLeuMetGly 504
QY 1462 ACGTTGGCGGAGGCTTCGGACTCCCTGGGCGGACCTGTGGACTGGGGGTGACAGGC 1521
DB 505 GluAlaGlyLysGlnLeuArgArgThrGlyIleGlySerGlyLeuSerLeuSer--- 523
QY 1522 AACCATGAGTTGTGCCCCAGTCTTGGGACAGTCCCAACAGTTTGAGGAGAACACC 1581
DB 524 -----GlyIleValHisProGluLeuSerArgSerGlyGluLeuAlaValGlnAlaLeu 541
QY 1582 TACTGCTTGGCGGACCGTGGAGACACTGTGCTCCGCTTTGGCAAGACCATCATGGAG 1641
DB 542 AspGlnPheAlaThrValValGluAlaLysLeuValLysHisLysLysGlyIleValAsn 561
QY 1642 GAGCAGCTGGTACTGAAGCGGTGCCAACATCTCTCATCACTGTATGGCATGACGGCC 1701
DB 562 GluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetValVal 581
QY 1702 GTGCTGTCCGGGCGGCGCTCCATCCGCTTGGGCTCCGCAACCCAGCAGCAGGAT 1761
DB 582 ValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHisGluLys 601
QY 1762 CTCCTTGGCAACACTTCTCGTGTGAAGCT-----TACTTGCAGATCTCTTCAGC 1812
DB 602 MetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMetAlaSer 621
QY 1813 CTCTCTCAGCTGGACAAGTATGCTCCAGAAACCTAGATGACAGATTAAGAAAGTGTC 1872
DB 622 LeuGlnSerSerProGlnHis-----GlnGluLeuPheArgAsnPheArgSerIleSer 639

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QY 1873 CAGCAGATCCTGTGAGACGAGCGCTATATCTGTCTGCCACCTCTG 1917
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Db 640 LysAlaMetValGluAsnGlyGlyLeuValThrGlyAsnProLeu 654

RESULT 9

US-10-362-537-11
; Sequence 11, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 11
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Bovine
US-10-362-537-11

Alignment Scores:

Pred. No.: 5,08e-101 Length: 655
Score: 1345.00 Matches: 285
Percent Similarity: 65.51% Conservative: 110
Best Local Similarity: 47.26% Mismatches: 194
Query Match: 29.86% Indels: 14
DB: 15 Gaps: 9

US-09-945-326-1 (1-2452) x US-10-362-537-11 (1-655)

QY 133 TCACCGCGAAGCGCGCTACTCGCAGCAGCGCGCTGTACGAGCTTCGCCAAGAG 192
Db 57 SerGluAlaSerThrArgGluLeuValArgAlaAsnSerValSerLysSerPheAlaValGly 76
QY 193 CTCTTCCTAGCAAAATCAAGAGAAAGATTTTCCCATTTCCAGAGTT--AGCAA 249
Db 77 ThrPheLysGlyGlnLeuThrAspGlnValPheProTyrProSerValLeuAsnGlu 96
QY 250 GATGAACCTTAATGAATCAATCACTTCTGGGACCCGTGGAAATCTTCACTCAAGAG 309
Db 97 AspGlnThrGlnPheLeuLysGluLeuValGlyProValThrArgPheGluGluVal 116
QY 310 GTGACTCCCGAATAATGACAGAGAGGAAATCCAGATGAACTTTGGAGAAATTG 369
Db 117 AsnAspAlaAlaLysAsnAspMetLeuGluArgValGluGluThrThrMetGlnGlyLeu 136
QY 370 AAGAGCTAGCGCTTTTGGCTGCAAGTCCAGAGAAATATGTGGCTTGGCTTCTCC 429
Db 137 LysGluLeuGlyAlaPheGlyLeuGlnValProAsnGluLeuGlyValGlyLeuCys 156
QY 430 AACACCATGTACTCAAGCATAGGGAGATCATCAGCATG--GATGGGTCCATCAGCTGT 486
Db 157 AsnThrGlnTyrAlaArgLeuValGluLeuValGlyMetTyrAspLeuGlyValGlyLeu 176
QY 487 ACCCTGCGACGCGACAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCAGGAG 546
Db 177 ValLeuGlyAlaHisGlnSerIleGlyPheLysGlyLeuLeuPheGlyThrLysAla 196
QY 547 CAGAAAGCCAAATCTTGCCTAACTGGCTCGGGGAGCAGCATTTGAGGCTTCTGCTC 606
Db 197 GlnLysGluLysTyrLeuProLysLeuAlaSerGlyGluThrIleAlaAlaPheCysLeu 216
QY 607 ACGGAGCCAGCAGTGGGAGCGATGACGCTCAATCCGGGAGCAGAGCCACACTAAGTGA 666
Db 217 ThrGluProSerSerGlySerAspAlaAlaSerIleArgSerSerAlaValProSerPro 236
QY 667 GACAAGAGCACTACATCCTCAATGGCTCCAAGGCTCTGGATTACTAATGGAGGACTGCC 726

Db 237 CysGlyLysTyrTyrThrLeuAsnGlySerLysIleTrpIleSerAsnGlyGlyLeuAla 256
QY 727 AATATTTTACTGTGTTTGCAGACACTGAGCTCGTGTGAT---TCTGATGAGTCAAGTGA 783
Db 257 AspIlePheThrValPheAlaLysThrProValThrAspThrAlaThrGlyAlaValLys 276
QY 784 GACAAATACAGCATTCATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGGAACCC 843
Db 277 GluLysIleThrAlaPheValValGluArgSerPheGlyGlyValThrHisGlyProPro 296
QY 844 GAAGATAAATAGGCATTCGGGCTCCACACITGTGAAGTCCCATTTTGAACACACCAAG 903
Db 297 GluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheAspGlyValArg 316
QY 904 ATACTCTGTGAAACATCTTTGGAGAGTCGGAGATGGGTTTAAAGTGGCCATGAACATC 963
Db 317 ValProAlaGluAsnValLeuGlyValGlyGlyPheLysValAlaMetHisIle 336
QY 964 CTCACAGCGCGGTTTCAGCATGGGCGAGCTGTGTGGCTGTCTCAAGAGATTGATT 1023
Db 337 LeuAsnAsnGlyArgPheGlyMetAlaAlaAlaLeuAlaGlyThrMetLysGlyIle 356
QY 1024 GAAATGACTCTGACTAGCTGCACAAAGGAAACAGTTTAAACAGAGCGCTCAGTGAATT 1083
Db 357 AlaLysAlaValAspHisAlaAlaAsnArgThrGlnPheGlyGluLysIleHisAsnPhe 376
QY 1084 GGATTGATTCAGGAGAAATTTGCATGCTGCTCAGAGAGGCTTACGTATCGAGAGATG 1143
Db 377 GlyLeuIleGlnGluLysLeuAlaArgMetAlaMetLeuGlnTyrValThrGluSerMet 396
QY 1144 ACCTACTCACAGCAGGATGCTGGACCAACCTGGCTTTCCGACTCTCCATCAGAGCA 1203
Db 397 AlaTyrMetValSerAlaAsnMetAspGln---GlySerThrAspPheGlnIleGluAla 415
QY 1204 GCATGTTGAGGTGTTACGCTCGAGGCGCTGCGAGTGTGTGAGTGGCGCTCGAG 1263
Db 416 AlaIleSerLysIlePheGlySerGluAlaAlaTrpLysValThrAspGluCysIleGln 435
QY 1264 ATCTCTGGGGCTTGGGCTACACAGGGACTATCCGTACGAGCGCATCTCGCGACACC 1323
Db 436 IleMetGlyGlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeu 455
QY 1324 CGCATCTCTCATCTTCAGGGAACCAATGAGATTCCTCGGATGTACATCGCCCTGAGC 1383
Db 456 ArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGln 475
QY 1384 GGTCTGAGCATCCCGCCCATCTCTGACTACAGGATCCATGAGCTTAACAG----- 1437
Db 476 GlyCysMetAspLysGlyLysGluLeuSerGlyLeuGlyAsnAlaLeuLysAsnProPhe 495
QY 1438 GCCAAAGTGAGCACAGTCATGGATACCGTTGGCGGAGGCTTCGGGACTCCCTGGGCGCA 1497
Db 496 GlyAsnAlaGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeuArgArgAlaGlyLeu 515
QY 1498 ACTGTGAGCTGGGCTGACAGCAACCATGAGTGTGTGACCCAGCTCTTGGCAGCAGT 1557
Db 516 GlySerGlyLysSerLeuSer-----GlyIleValHisGlnGluLeuSerArgSer 532
QY 1558 GCCAACAGTTTGAGGAGAACACCTACTGTTGGCGCGGACCTGCTGGGAGACACTCTGCTC 1617
Db 533 GlyGluLeuAlaValGlnAlaLeuGluGlnPheAlaThrValValGluAlaLysLeuIle 552
QY 1618 CGCTTTGGCAAGACCATCATGAGGAGCAGCTGTACTGAAGCGGGTGGCCCAACATCCTC 1677
Db 553 LysHisLysLysAspIleIleAsnGluGlnPheLeuLeuGlnArgLeuAlaAspSerAla 572
QY 1678 ATCAACCTGTATGGCATGACGGCGCTGCTCGCGGCCAGCCGCTCCATCCGCGATTGG 1737
Db 573 IleAspLeuTyrAlaMetValValLeuSerArgAlaSerArgSerLeuSerGlyGly 592
QY 1738 CTCGCAACACAGCAGAGGTTCTCTTGGCCCAACACCTTCTCGTGGGAGCT----- 1791

Db 593 HisProThraAlaGlnHisGluLysMetLeuCysAspSerTrpCysIleGluAlaAla 612
 QY 1792 ---TACTTGCAGACTCTTTCAGCTCTCTCAGCTGGACAAGTAGTCTCCAGAAACCTA 1848
 Db 613 ArgIleArgGluAsnMetThrAlaLeu---GlnSerAspProGlnGlnGlu---Leu 630
 QY 1849 GATGAGCAGATTAAAGAAAGTGTCCCGCAGAGATCCTTGAGAGAGCGAGCCTATATCTGTGCC 1908
 Db 631 PheArgAsnPheLysSerIleSerLysAlaLeuValGluArgGlyGlyValValThrSer 650
 QY 1909 CACCTCTG 1917
 Db 651 AsnProLeu 653
 RESULT 10
 US-10-362-537-1
 ; Sequence 1, Application US/10362537
 ; Publication No. US20040086510A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Takeda Chemical Industries, Ltd.
 ; TITLE OF INVENTION: IRAP Binding Protein
 ; FILE REFERENCE: 2774 USOP
 ; CURRENT APPLICATION NUMBER: US/10/362,537
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: JP 2000-254263
 ; PRIOR FILING DATE: 2000-08-21
 ; PRIOR APPLICATION NUMBER: JP 2000-276633
 ; PRIOR FILING DATE: 2000-09-07
 ; NUMBER OF SEQ ID NOS: 11
 ; SEQ ID NO 1
 ; LENGTH: 655
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-10-362-537-1
 Alignment Scores:
 Pred. No.: 4,72e-99 Length: 655
 Score: 1321.00 Matches: 297
 Percent Similarity: 61.52% Conservative: 109
 Best Local Similarity: 45.00% Mismatches: 213
 Query Match: 29.33% Indels: 41
 DB: 15 Gaps: 13
 US-09-945-326-1 (1-2452) x US-10-362-537-1 (1-655)
 QY 21 GCTAAGAGGGGAGCTGAGGCTGAGGCTGGGAAACATCGGCGAGCATGAGCGCTGCGG 80
 Db 8 AlaSerLeuGlyArgGlnLeuLeuArgLeuGly-----GlyGlySerSerArgLeuThr 25
 QY 81 GCTCTT-----CCTGCGCACACCGCTGCGGCTCGTCCCTGCGG 119
 Db 26 AlaLeuLeuGlyGlnProArgProGlyProAlaArg-----Pro 39
 QY 120 GGTCTGTGGTCTC-----TACCGCGAACCGCG 149
 Db 40 TyrAlaGlyAlaAlaGlnLeuAlaLeuAspLysSerAspSerHisProSerAspAla 59
 QY 150 GCTACTCGCCACGAGCCGCC-----TGTACGAGCTTTCGCCAAGAGCTTTTCT 200
 Db 60 LeuThrArgLysLysProAlaLysAlaGluSer-LysSerPheAlaValGlyMetPheLys 79
 QY 201 AGCGAAATCAAGAAAGAAAGTTCATTCATTCAGAAAGTTCAGAAAGTTCAGAAAGTTC 260
 Db 79 sGlyGlnLeuThrThrAspGlnValPheProTyrProSerValLeuAsnGluGlnThr 99
 QY 261 TGA---ATCAATCAGTCTTGGGACCGCTGGGAAATTCCTTCACTGAAGAGTGCAGCTC 317
 Db 99 rGlnPheLeuLysGluLeuValGluProValSerArgPhePheGluGluValAsnAspPr 119
 QY 318 CCGAAATTTGACCGAGAGGGGAAATCCAGATGAAACTTTGGAGAAATTTGAAGAGCT 377
 Db 119 oAlaLysAsnAspAlaLeuGluMetValGluGluThrThrTrpGlnGlyLeuLysGluLe 139

QY 378 AGGCTTTTGGGCTGCCAAGTCCAGAGAATATGTTGGCTGGCTTCTCCAAACACCAT 437
 Db 139 uGlyAlaPheGlyLeuGlnValProSerGluLeuGlyGlyValGlyLeuCysAsnThrGl 159
 QY 438 GTACTCAAGACTAGGGAGAGATCATCAGCATG---GATGGGTCCATCTACTGACCTGGC 494
 Db 159 nTyAlaArgLeuValGluIleValGlyMetHisAspLeuGlyValGlyIleThrLeuGl 179
 QY 495 AGCGACCAAGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACTCAGGAGCAGAAAGC 554
 Db 179 yAlaHisGlnSerIleGlyPheLysGlyIleLeuLeuPheGlyThrLysAlaGlnLysGl 199
 QY 555 CAAATACTTGCCTAAACTGGCTCCGGGAGCAGCATTCAGCCCTTTCGCTCAGGAGCC 614
 Db 199 uLysTyLeuProLysLeuAlaSerGlyGluThrValAlaAlaPheCysLeuThrGluPr 219
 QY 615 AGCCAGTGGGAGCGATGCCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAACACAAGAA 674
 Db 219 oSerSerGlySerAspAlaAlaSerIleArgThrSerAlaValProSerProCysGlyLy 239
 QY 675 GCATCATCTCTCAATGGCTCCAGGTCTGGATTACTAATGGAGGACTGGCCAAATTTT 734
 Db 239 sTyTyThrLeuAsnGlySerLysLeuTrpIleSerAsnGlyGlyLeuAlaAspIlePh 259
 QY 735 TACTGTGTTTGCACACACTGAGTCTGTTGAT---TCTGATGGATCAGTGAAGACAAAAT 791
 Db 259 eThrValPheAlaLysThrProValThrAspProAlaThrGlyAlaValLysGluLysIl 279
 QY 792 CACAGCATTCATAGTAAAGAGACTTTTGTGGAGTCACTAATGGGAAACCCCGAAGATAA 851
 Db 279 eThrAlaPheValValGluArgGlyPheGlyGlyIleThrHisGlyProProGluLysLy 299
 QY 852 ATTAGCATTCGGGCTCCAAACACTTGTGAAGTCCATTTTGAACACCAACAGATACCTGT 911
 Db 299 sMetGlyIleLysAlaSerAsnThrAlaGluValPhePheAspGlyValArgValProse 319
 QY 912 GGAACACATCTTGGAGAGTCCGAGATCGGTTTAAAGTGGGCATGAACATCTCAACAG 971
 Db 319 rGluAsnValLeuGlyGluValGlySerGlyPheLysValAlaMetHisIleLeuAsnAs 339
 QY 972 CGGCGGTTTACGATGGGCGAGCGTCTGCTGGCTGGCTGCTCAAGAGATTGATGAATGAC 1031
 Db 339 nGlyArgPheGlyMetAlaAlaLeuAlaGlyThrMetArgGlyIleIleAlaLysAl 359
 QY 1032 TCCTCAGTACGCTCCACAAAGGAAACAGTTTAAAGAGGCTCAGTGAATTTGGATTGAT 1091
 Db 359 aValAspHisAlaThrAsnArgThrGlnPheGlyGluLysIleHisAsnPheGlyLeuIl 379
 QY 1092 TCAGAGAAATTTGCACCTGATGGCTCAGAAAGCTTACGTCATGGAGAGTATGACCTACCT 1151
 Db 379 eGlnGluLysLeuAlaArgMetValMetLeuGlnTyValThrGluSerMetAlaTyrMe 399
 QY 1152 CACAGAGGATCTGGACCAACCTGGCTTCCGAGCTGCTCCATCGAGGAGCCATGCT 1211
 Db 399 tValSerAlaAsnMetAspGln---GlyAlaThrAspPheGlnIleGluAlaAlaIleSe 418
 QY 1212 GAAGTGTTCAGCTCCGAGGCGCTGCGAGTGTGTAGTAGGCGCTGCGACATCTCGG 1271
 Db 418 rLysIlePheGlySerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGl 438
 QY 1272 GGGCTTGGGCTACACAAAGGACTATCCGTACGAGCGCATCTGCGTGACACCCCGCATCT 1331
 Db 438 yGlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeuArgIlePh 458
 QY 1332 CCTCATCTTCGAGGAAACCAATGAGATTCTCGGATGTACATCGCCCTGACGGGTCTGCA 1391
 Db 458 eArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMe 478
 QY 1392 GCATCCCGCGCATCTCTGACTTACCAGGATCCATGAGCTTAAACAG-----GCCAAAGT 1445
 Db 478 tAspLysGlyLysGluLeuSerGlyLeuGlySerAlaLeuLysAsnProPheGlyAsnAl 498
 QY 1446 GAGCACATCATGGATACCGTTGGCCGAGGCTTCGGGACTCCCTTCGGCCGCACTGTGGA 1505


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QY 1152 CACAGCAGGATGTCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGCGAGCCATGGT 1211
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
399 tValSerAlaAsnMetAspGln---GlyAlaThrAspPheGlnIleGluAlaIleSe 418
QY 1212 GAAGGTGTTCACTCCGAGGCGCTGGCGAGTGTGTGAGTGGCGCTGCAGATCCTCGG 1271
Db   rlySilePheGlySerGluAlaAlaIleGlyValThrAspGluCysIleGlnIleMetGl 438
QY 1272 GGGCTTGGGCTACAAAGGAGATATCCGTACGAGCGCATCTCGCTGACACCCGACTCCT 1331
Db   yGlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeuArgIlePh 458
QY 1332 CCTCATCTTCGAGGGAACCAATGAGATTCCTCGGATGTACATGCGCTCGAGCGGTGCA 1391
Db   eArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMe 478
QY 1392 GCATCCGCGCGCATCTCTGACTACACAGGATCCATGAGCTTAAACAG-----GCCAAGT 1445
Db   tAspLysGlyLysGluLeuSerGlyLeuGlySerAlaLeuLysAsnProPheGlyAsnAl 498
QY 1446 GAGCACTCATGGATACCGTTGGCCGAGGCTTCGGGACTCCTCGTGGCGCAACTGTGGA 1505
Db   aGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeuArgArgAlaGlyLeuGlySerGl 518
QY 1506 CCTGGGCTGACAGCAACCATGAGTGTGTCACCCAGTCTTCGCGACAGTGCACAA 1565
Db   yLeuSerLeuSer-----GlyLeuValHisProGluLeuSerArgSerGlyGluLe 535
QY 1566 GTTTGAGGAGAACCTACTGCTTCGGCCGAGCGTGGAGACACTGCTGCTCGCTTTGG 1625
Db   uAlaValArgAlaLeuGluGlnPheAlaThrValValGluAlaLysLeuIleLysHisLy 555
QY 1626 CAAGACCATATGAGGAGCAGCTGGTACTGAAGCGGTGGCCCAACATCTCATCAACCT 1685
Db   sLysGlyIleValAsnGluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLe 575
QY 1686 GTATGGATGACCGCGCTGCTCGCGGCGAGCGCTCCATCGCATTCGGCTCCGCCAA 1745
Db   uTyAlaMetValValValLeuSerArgAlaSerArgSerLeuSerGluGlyHisProth 595
QY 1746 CCACGACCACGAGTCTCTTTGGCCAAACACCTCTCGCTGGAA-----GCTTACTTGA 1799
Db   rAlaGlnHisGluLysMetLeuCysAspThrTrpCysIleGluAlaAlaAlaArgIleAr 615
QY 1800 GAATCTCTTCAGCCTCTCTCAGCTGGGAAGATATGCTCCGAAACCTAGATCAGCAGAT 1859
Db   gGluGlyMetAlaAlaLeuGlnSerAspProTrpGlnGlnGlu---LeuTyArgAsnPh 634
QY 1860 TAAGAAAGTGTCCAGCAGATCTCTTGAGAGCGAGCCTATATCTGTGCCACCTCTG 1917
Db   eLysSerIleSerLysAlaLeuValGluArgGlyGlyValThrSerAsnProLeu 653
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RESULT 12

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US-10-408-765A-320
; Sequence 320, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fany, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 320
; LENGTH: 655
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-320

Alignment Scores:
Pred. No.: 2,59e-98 Length: 655
Score: 1312.00 Matches: 296
Percent Similarity: 61.36% Conservative: 109
Best Local Similarity: 44.85% Mismatches: 214
Query Match: 29.13% Indels: 41
DB: 16 Gaps: 13
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US-09-945-326-1 (1-2452) x US-10-408-765A-320 (1-655)

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QY 21 GCTAAGAGGGGAGCTGAGGCTGAGGCTGGGAAACATCGGCGAGCATGAGCGGTGCGG 80
Db 8 AlaserLeuGlyArgGlnLeuLeuArgLeuGly-----GlyGlySerSerArgLeuThr 25
QY 81 GCTCTT-----CCTGCCACACCGCTCGGCTCGGCTCGTGCCTGCGC 119
Db 26 AlaLeuLeuGlyGlnProArgProGlyProAlaArg-----Pro 39
QY 120 GGTCTGTGTGCTCTC-----TACCGCGAACCGCG 149
Db 40 TyrAlaGlyGlyAlaAlaGlnLeuAlaLeuAspLysSerAspSerHisProSerAspAla 59
QY 150 GCTACTCGCGCACCGACCGCC-----TGTCAGAGCTTTCCGCAAGAGCTTTTCT 200
Db 60 LeuThrArgLysLysProAlaLysAlaGluSer-LysSerPheAlaValGlyMetPhe 79
QY 201 AGCAAAATCAAGAAAGAAAGTTTCCCATTTCCAGAAAGTTAGCCAAGATGAACCTAA 260
Db 79 sGlyGlnLeuThrAspGlnValPheProTyProSerValLeuAsnGluGluGln 99
QY 261 TGAA---ATCAATCAGTCTTCGGACCCGTGAAAAAATCTTCTCACTGAAGAGGTGATC 317
Db 99 rGlnPheLeuLysGluLeuValGluProValSerArgPheGluGluValAsnAspPr 119
QY 318 CGAAAAATTCACAGGAGGAAATCCACATGAAACTTTGGAGAAATTCAGAGAGCCT 377
Db 119 oAlaLysAsnAspAlaLeuGluMetValGluGlnThrThrTrpGlnGlyLeuLysGlu 139
QY 378 AGGGCTTTTGGGCTGCAAGTCCCAGAAAGATATGTTGGCTTGGCTTCTCCAACACCAT 437
Db 139 uGlyAlaPheGlyLeuGlnValProSerGluLeuGlyGlyValGlyLeuCysAsnThrGl 159
QY 438 GTACTCAAGACTAGGGAGATCATCAGCATG---GATGGTCCATCATCTGTACCTGCGC 494
Db 159 nTyAlaArgLeuValGluIleValGlyMetHisAspLeuGlyValGlyIleThrLeuGl 179
QY 495 AGCGCACCGAGCTATTGGCTCAAGGGGATCATCTTTGGCTGGCACTAGGAGCAGAAAGC 554
Db 179 yAlaHisGlnSerIleGlyPheLysGlyIleLeuLeuPheCysThrLysAlaGlnLysGl 199
QY 555 CAATACTTTCCTAACTGGGCTCGGGAGGACACATTCGAGCCTTCTGCTCAGGAGCC 614
Db 199 uLysTyLeuProLysLeuAlaSerGlyGlyThrValAlaAlaPheCysLeuThrGluPr 219
QY 615 AGCCAGTGGGAGCGATGCAGCCTCAATCCGAGCAGAGCCACACTAAGTGAAGACAAGAA 674
Db 219 oSerSerGlySerAspAlaAlaSerIleArgThrSerAlaValProSerProCysGlyLy 239
QY 675 GCATACATCTCAATGCTCAAGGCTGAGTACTTAATGAGGACTGGGCAATATTTT 734
Db 239 sTyTyThrLeuAsnGlySerLysLeuTrpIleSerAsnGlyGlyLeuAlaAspIlePh 259
QY 735 TACTGTGTTTCAAGACTGAGGCTGCTTGAT---TCTGATGCATCAGTGAAGACAAAAT 791
Db 259 eThrValPheAlaLysThrProValThrAspProAlaThrGlyAlaValLysGluLysIle 279
QY 792 CACAGCATTCATAGTAAAGAGACTTTTGGTGGAGTCACTAATGGMAACCCGAGATAA 851
Db 279 eThrAlaPheValValGluArgGlyPheGlyGlyIleThrHisGlyProGluLysLy 299
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Db 101 AlaAsnIleLeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSer 120
Qy 1726 ATCCGCATTTGGCTCCGCAACACGACACAGAGTTCTTTGGCAACACACCTTCTGCGTG 1785
Db 121 IleArgIleGlyLeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysVal 140
Qy 1786 GAAGCTTACTTGCAGATCTCTTTCAGCCTCTCTCAGCTGGCAAGATGCTCCAGAAAC 1845
Db 141 GluAlaTyrLeuGlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsn 160
Qy 1846 CTAGATGAGCAGATTAAAGAAAGTCTCCAGCAGATCTTGAAGAGCGAGCCTATATCTGT 1905
Db 161 LeuAspGluGlnIleLysLysValSerGlnIleLeuGluLysArgAlaTyrIleCys 180
Qy 1906 GCCCACCCTCTGGACAGACATGC 1929
Db 181 AlaHisProLeuAspArgThrCys 188

RESULT 15

US-10-408-765A-2052
; Sequence 2052, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2052
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2052

Alignment Scores:
Pred. No.: 3,43e-69 Length: 188
Score: 954.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.18% Indels: 0
DB: 16 Gaps: 0

US-09-945-326-1 (1-2452) x US-10-408-765A-2052 (1-188)

Qy 1366 ATGTACATCGCCTGAGGGTCTCAGCATGCGCGCGCATCTGTACTACAGGATCCAT 1425
Db 1 MetTyrIleAlaLeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHis 20
Qy 1426 GAGCTTAAACAGGCAAGTGGACACAGTCATGTATACCGTTGGCGGAGCTTCGGGAC 1485
Db 21 GluLeuLysGlnAlaLysValSerThrValMetAspThrValGlyArgLeuArgAsp 40
Qy 1486 TCCCTGGGCGGAACGTGGGCTCGAGCAACCATGGAGTTGTGCACCCAGT 1545
Db 41 SerLeuGlyArgThrValAspLeuLeuThrGlyAsnHisGlyValValHisProSer 60
Qy 1546 CTTCGGGACAGTGCACAACAGTTTGGAGAGAACACCTACTGCTTCGGCGCGGACCGTGGAG 1605
Db 61 LeuAlaAspSerAlaAsnLysPheGluGlnAsnThrTyrCysPheGlyArgThrValGlu 80
Qy 1606 ACATGCTGCTCCGCTTTGGCAACACCATCATGGAGGAGGAGCTGTACTGAAGCGGGTG 1665
Db 81 ThrLeuLeuLeuArgPheGlyLysThrIleMetGluGlnLeuValLeuLysArgVal 100

Qy 1666 GCCAACATCTCTCATCAACCTGTATGGCATGACGCCGCTGTCTGCGGGGCCAGCGCTCC 1725
Db 101 AlaAsnIleLeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSer 120
Qy 1726 ATCCGCATTTGGCTCCGCAACACGACACAGAGTTCTTTGGCAACACACCTTCTGCGTG 1785
Db 121 IleArgIleGlyLeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysVal 140
Qy 1786 GAAGCTTACTTGCAGATCTCTTTCAGCCTCTCTCAGCTGGCAAGATGCTCCAGAAAC 1845
Db 141 GluAlaTyrLeuGlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsn 160
Qy 1846 CTAGATGAGCAGATTAAAGAAAGTCTCCAGCAGATCTTGAAGAGCGAGCCTATATCTGT 1905
Db 161 LeuAspGluGlnIleLysLysValSerGlnIleLeuGluLysArgAlaTyrIleCys 180
Qy 1906 GCCCACCCTCTGGACAGACATGC 1929
Db 181 AlaHisProLeuAspArgThrCys 188

Search completed: May 2, 2005, 15:56:48
Job time : 318.192 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3149	69.9	621	2	JC7892	acyl-CoA dehydroge
2	1365	30.3	655	2	A54872	acyl-CoA dehydroge
3	1321	29.3	655	2	S54183	acyl-CoA dehydroge
4	1210.5	26.9	613	2	T15905	hypothetical prote
5	821	18.2	594	2	F84085	butyryl-CoA dehydr
6	815.5	18.1	594	2	F70021	butyryl-CoA dehydr
7	711.5	15.8	650	2	A70817	probable fad10 pr
8	699	15.5	382	2	B87302	acyl-CoA dehydroge
9	691.5	15.4	384	2	B83443	probable acyl-CoA
10	690	15.3	379	2	G84124	acyl-CoA dehydroge
11	682	15.1	378	2	D69658	acyl-CoA dehydroge
12	682	15.1	381	2	AC3536	butyryl-CoA dehydr
13	678	15.1	381	2	B87472	acyl-CoA dehydroge
14	658	14.6	380	2	F84124	acyl-CoA dehydroge

Db 21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40
QY 187 AAAGAGCTTTTCCTAGGCAGAAATCAAGAGAAAGAGATTTTCCCATTTCCAGAAAGTTAGC 246
Db 41 LysGluLeuPheLeuGlyLysLeuGlyLysLysGluValPheProPheProGluValSer 60
QY 247 CAAGATGAACCTTAATGAATCAATCAGTTCTTTGGGACCCCGTGGAAAAATTTCTCACGTAA 306
Db 61 GlnAspGluLeuAsnGluLeuGlnPheLeuGlyProValGluLysPhePheThrGlu 80
QY 307 GAGGTGGACTCCGAAAAATTCACAGAGAGGAAAAATCCAGATGAAACTTTGAGAGAA 366
Db 81 GlnValAspSerArgLysLeuAspGlnGluGlyLysLeuProAspGluThrLeuGluLys 100
QY 367 TTGAAGAGCTTAGGCTTTTGGCTGCAAGTCCAGAGAAATATGCTGGCTGGCTTC 426
Db 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluThrGlyGlyLeuGlyPhe 120
QY 427 TCCAAACACCATGTACTCAAGACTAGGGAGATCATCAGCATGGATGGTCCATCAGCTGTG 486
Db 121 SerAsnThrMetTyrSerArgLeuGlyGluLeuLeuLeuSerMetAspGlySerIleThrVal 140
QY 487 ACCCTGGCAGCGCACCAGGCTATTGGCTCAAGGGATCATCTTGGCTGGCAGCTAGGAG 546
Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleLeuAlaGlyThrGluGlu 160
QY 547 CAGAAAGCCAAATACTTGCCTTAACTCGCGTCCGGGAGCACATTGCGAGCTTCTGCCTC 606
Db 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180
QY 607 ACGAGCGCAGCTAGTGGAGCGATGCGACTCAATCCGGAGCAGAGCCACACTAAGTGAA 666
Db 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
QY 667 GACAAAGACACTACATCTCAATGGCTCCAGGCTCGGATTAATGAGAGACTGGCC 726
Db 201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
QY 727 AATATTTTACTGTGTTGCAAGACTGAGGTCGTTGATTTCTGATGGATCAGTGAAAGAC 786
Db 221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
QY 787 AATATCACAGCATTCATAGTAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAA 846
Db 241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260
QY 847 GATAAATTAGGCATTCGGGCTCCACACTGTGTGAAGTCCATTTTCAAAACACCAAGATA 906
Db 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
QY 907 CCTGTGAAAAACATCTCTGGAGAGGTCGGAGATGGGTTAAGTGGCCATGAACATCCTC 966
Db 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
QY 967 AACAGCGCGGTTACGATGGCAGCGCTGGCTGGCTGCTCAAGAGATTGATTGA 1026
Db 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLysArgLeuIleGlu 320
QY 1027 ATCACTGCTGAGTACGCTGCACAGAGAAACAGTTTAAACAGAGGCTCAGTCAATTTGA 1086
Db 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
QY 1087 TTGATTCAGAGAAATTTGCACTGATGGCTCAGAAGCTTACGTCAATGGAGATGACC 1146
Db 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
QY 1147 TACCTCACAGCGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCCAGGACGCC 1206
Db 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
QY 1207 ATGGTGAAGGTGTACGCTCCGAGCGCGCTGCGAGTGTGTGAGTGAGCGCTGCAGATC 1266
Db 381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluValLeuGlnIle 400

QY 1267 CTCGGGGCTTGGGCTACACAAGGGACTATCCCTACGAGCGCATCTGCGTGACACCCGC 1326
Db 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
QY 1327 ATCCTCTCATCTTCCAGGGAACCAATGATGATCTCCGGATGTACATCGCCCTGACGGGT 1386
Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY 1387 CTCAGCATGCCCGCCGCTCTCTGACTACAGGATCCATGAGCTTAAACAGGCCAAAGTG 1446
Db 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY 1447 AGCAGAGTCATGATACCTTGGCCGGAGCTTCCGGACTCCCTGGGCGCAACTGTGGAC 1506
Db 461 SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480
QY 1507 CTGGGGCTCACAGGCAACCATGGAGTTGTGCACCCCGAGCTTTCGGACAGTCCCAACAG 1566
Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY 1567 TTTGAGGAGAACCTTACTGCTTTCGGCCGGACCGTGGAGACACTGCTGCTCCGCTTTGGC 1626
Db 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
QY 1627 AAGACCATCATCGAGGAGCAGCTGGTACTGAAGCGGGTGGCCCAACATCTCTCATCAACCTG 1686
Db 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
QY 1687 TATGGCATGACCGCGCTGCTGTCGGGGCCAGCCGCTCCATCCGATTTGGGCTCCGCAAC 1746
Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY 1747 CAGACACGAGGTTCTCTTGGCCCAACCTTCTCGCTGGAGAGCTTACTTGAGAAATCTC 1806
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
QY 1807 TTCAGCTCTCTCAGCTGGACAAAGTATGCTCCAGAAAACTTAGATGACGAGATTAGGAA 1866
Db 581 PheSerLeuSerGlnLeuAspLysIleAlaProGluAsnLeuAspGluGlnIleLysLys 600
QY 1867 GTGTCCCGACAGATCCTTTGAGAGCGAGCTATATCTGTGCCACCTCTTGACAGAGACA 1926
Db 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
QY 1927 TGC 1929
Db 621 Cys 621
RESULT 2
A: A54872
C: acyl-CoA dehydrogenase (EC 1.3.99.-) very-long-chain-specific precursor - rat
C: Species: Rattus norvegicus (Norway rat)
C: Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
C: Accession: A54872
R: Aoyama, T.; Ueno, I.; Kamijo, T.; Hashimoto, T.
J. Biol. Chem. 269, 19088-19094, 1994
A: Title: Rat very-long-chain acyl-CoA dehydrogenase, a novel mitochondrial acyl-CoA dehy-
ced amino acid sequence and distinct specificities of the cDNA-expressed protein.
A: Reference number: A54872; MUID: 94308174; PMID: 8034667
A: Accession: A54872
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-655 <AOY>
A: Cross-references: UNIPROT:P45953; GB:D30647; NID:G533356; PIDN:BA06331.1; PID:dl00689;
C: Keywords: oxidoreductase
F: 1-40/Domain: signal sequence #status predicted <SIG>
Alignment Scores:
Pred. No.: 1,2e+80 Length: 655
Score: 1365,00 Matches: 303
Percent Similarity: 62.77% Conservative: 110
Best Local Similarity: 46.05% Mismatches: 202

Query Match:	30.31%	Indels:	43
DB:	2	Gaps:	13
US-09-945-326-1 (1-2452) x A54872 (1-655)			
Qy	30	GGGAGACTGAGCTGAGGCTGGG---AACATCGGCAGCATGAGCGCTCGGGCTCTT	86
Db	11	GlyArgGlnLeuLeuArgLeuGlyAlaArgSerArgSerAlaAlaLeuGlnGlyGln	30
Qy	87	CTTCGCCACACAGCGCTGCGGCTCGCTCGCTGCGGGGTCTGTGCTCTACTACCGCAACCG	146
Db	31	Pro-ArgProThrSerAlaGlnArg-----LeuTyralaSerGluAlaThrGln	46
Qy	147	GGGGCTACTGGC-----ACGACCGCGCTGT	173
Db	46	nAlaValLeuGluLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAl	66
Qy	174	ACGAGCT-----TTCCGCAAAAGAGCTTTCTTAGCGAAATCAAGAAGAAGA	221
Db	66	aArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGln	86
Qy	222	AGTTTTCCCATTTCCAGAGTTAGCCAAGATGAACTTAATGAA-----AT	266
Db	86	nValPheProTyProSerVal-----LeuAsnGluGlyGlnThrGlnPheLe	102
Qy	267	CAATCAAGTTCTTGGGACCGGTGGAAAAATTTCTTCACTGAAGAGGTGACCTCCGAAAAAT	326
Db	102	uLysGluLeuValGlyProValAlaArgPheGluGluValAsnAspProAlaLysAs	122
Qy	327	TGACCAGGAAGGAAAAATCCCAAGATGAACTTTGGAGAAATTTGAAGAGCGCTAGGGCTTTT	386
Db	122	nAspSerLeuGluLysValGluGluAspThrLeuGlnGlyLeuLysGluLeuGlyAlaPh	142
Qy	387	TGGGCTGCAAGTCCCAGAGAATATGTGGCTCGGCTTCTCCAACACCATGTACTCAAG	446
Db	142	eGlyLeuGlnValProSerGluLeuGlyGlyLeuGlyLeuSerAsnThrGlnTyAlaAr	162
Qy	447	ACTAGGGAGATCATCAGCATG---GATGGGTCCATCACTGTGACCTCGCAGCGGACCA	503
Db	162	gLeuAlaGluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGln	182
Qy	504	GGCTATTGGCTCAAGGGGATCATCTTGGCTGGCATGAGGAGCAGCAAGCCAAATACTT	563
Db	182	nSerIleGlyPheLysGlyIleLeuLeuTyGlyThrLysAlaGlnLysGluLysTyLe	202
Qy	564	GCTAAACTGGCGTCGGGGAGACATTCGAGCTTCTGCTCAAGGAGCAGCGAGTGG	623
Db	202	uProArgValAlaSerGlyGlnAlaLeuAlaPheCysLeuThrGluProSerSerGln	222
Qy	624	GAGCATGCGACCTCAATCCGAGCAGAGCCACACTAAGTCGAAGACAGCACTACAT	683
Db	222	ySerAspValAlaSerIleArgSerSerAlaValProSerProCysGlyLysTyThr	242
Qy	684	CTTCAATGGCTCCAAAGTCTGATTACTTAATGAGGAGCTGGCCAAATATTTTACTGTGT	743
Db	242	rLeuAsnGlySerLysIleTrieSerAsnGlyGlyLeuAlaAspIlePheThrValPh	262
Qy	744	TGCAAGACTGAGGCTGTTGAT---TCTGTGATTCAGTGAAGACAAATATCAGCATT	800
Db	262	eAlaLysThrProIleLysAspAlaAlaThrGlyAlaValLysGluLysIleThrAlaPh	282
Qy	801	CATAGTAGAAAGAGACTTTGGTGGAGTCACATAATGGGAAACCCGAGACATAAATAGGCAT	860
Db	282	eValValGluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGlyIle	302
Qy	861	TGGGGCTCCAACTTGTGAAGTCCATTTTGAATAACCAAGATACCTCTGTGGAAAAACAT	920
Db	302	eLysAlaSerAsnThrSerGluValTyPheAspGlyValLysValProAlaGluAsnVal	322
Qy	921	CTTTGAGAGGTCGAGATGGTTAAGTGCCTCATGAACTCTCTCAACGCGCGCGTT	980
Db	322	lLeuGlyGluValGlyAspGlyPheLysValAlaValAsnIleLeuAsnGlnLysArgPh	342

RESULT 3

554183

acyl-CoA dehydrogenase (EC 1.3.99.-) very-long-chain specific - human
S54.83
C:Species: Homo sapiens (man)

C;species: homo sapiens (man)
C;Date: 08-Jul-1995 #sequence revision 21-Jul-1995 #text change 09-Jul-2004

C: Accession: S54183

C, ACCESSION. 034103
R:Andresen. B.S.

K. Andersen, D.S.
submitted to the EMBL Data Library. April 1995

A:Reference number: S54183

A:Accession: S54183
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-655 <AND>
 A:Cross-references: UNIPROT:P49748; EMBL:X86556; NID:g790446; PID:g790447
 C:Genetics:
 A:Gene: GDB:ACADVL; VILCAD
 A:Cross-references: GDB:1248185; OMIM:201475
 A:Map position: 17p11.2-17p11.1
 C:Keywords: oxidoreductase

Alignment Scores:
 Pred. No.: 8.62e-78 Length: 655
 Score: 1321.00 Matches: 297
 Percent Similarity: 61.52% Conservative: 109
 Best Local Similarity: 45.00% Mismatches: 213
 Query Match: 29.33% Indels: 41
 DB: 2 Gaps: 13

US-09-945-326-1 (1-2452) x S54183 (1-655)

QY	21	GCTAAGAGGGGAGACTGAGCTGAGCTGGGGAACATCGGGCAGCATGACGGCTGGG	80
DB	8	AlaSerLeuGlyArgGlnLeuLeuArgLeuGly-----GlyGlySerSerArgLeuThr	25
QY	81	GCTCTT-----CCTCGCACACCGGCTCGGCTCGTGCCTCGG	119
DB	26	AlaLeuLeuGlyGlnProArgProGlyProAlaArg-----Pro	39
QY	120	GGTCTGTGTCTC-----TACCGGCAACCGGCG	149
DB	40	TyrAlaGlyGlyAlaAlaGlnLeuAlaLeuAspHisSerAspHisProSerAspAla	59
QY	150	GCTACTGGCACCGCCGCGC-----TGTCAGAGCTTCCCAAGAGCTTTTCT	200
DB	60	LeuThrArgIysIysProAlaLysAlaGluSer-LysSerPheAlaValGlyMetPheIy	79
QY	201	AGGCAAAATCAAGAAAGAAAGTTTCCCATTTCCAGAAAGTAGCCAAGATGAATCTAA	260
DB	79	sGlyGlnLeuThrThrAspGlnValPheProTyrProSerValLeuAsnGluGlnThr	99
QY	261	TGAA--ATCANTCAGTCTTGGACCCGCTGGAAATTTCTCCTCAAGAGGTGGACTC	317
DB	99	rGlnPheLeuGlyGlnLeuValGluProValSerArgPhePheGluGluValAsnAspPr	119
QY	318	CCGAAAAATTGACCAAGGAGGAAATCCACAGATGAAACTTTGAGAAATGGAAGACCT	377
DB	119	oAlaLysAsnAspAlaLeuGluMetValGluGluThrThrTrpGlnGlyLeuLysGluLe	139
QY	378	AGGCTTTTGGCTGCAAGTCCAGAGAAATATGTTGGCTGGCTTCTCCAAACCCAT	437
DB	139	uGlyAlaPheGlyLeuGlnValProSerGluLeuGlyGlyValGlyLeuCysAsnThrGl	159
QY	438	GTACTCAAGTAGGGGAGATCATCAGCATG---GATGGTCCATCACTGTGACCTGGC	494
DB	159	nTyrAlaArgLeuValGluLeuValGlyMetHisAspLeuGlyValGlyIleThrLeuGl	179
QY	495	AGGCACACAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGC	554
DB	179	yAlaHisGlnSerIleGlyPheIysGlyIleLeuLeuPheGlyThrIysAlaGlnIysGl	199
QY	555	CAATACCTTGCCTTAACTGGCGTCCGGGAGCACATTGAGCTTCTGCCTCAGGAGCC	614
DB	199	uLysTyrLeuProIysLeuAlaSerGlyGluThrValAlaAlaPheCysLeuThrGluPr	219
QY	615	AGCCAGTGGGAGGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAACACAGAA	674
DB	219	oserSerGlySerAspAlaIaSerIleArgThrSerAlaValProSerProCysGlyLy	239
QY	675	GCACTACATCCTCAATGGCTCCAAGTCTCGAATTACTAATGGAGGACTGCCCAATATTTT	734
DB	239	stYrThrLeuAsnGlySerIysLeuTrpIleSerAsnGlyGlyLeuAlaAspIlePh	259

QY	735	TACTGTGTTTCCAAAGACTGAGGTGCTGTGAT---TCTGATGGATCAGTGAAGACAAAT	791
DB	259	eThrValPheAlaLysThrProValThrAspProAlaThrGlyAlaValLysGluLysIl	279
QY	792	CACAGCATTCATAGTAGAAAGAGACTTTGTGTGAGTCACTAATGGGAAACCCCAAGATAA	851
DB	279	eThrAlaPheValValGluArgGlyPheGlyGlyIleThrHisGlyProGluLysLy	299
QY	852	ATTAGGCATTGGGGCTCCAAACACTTGTGAAGTCCATTTTGAANAACACCAAGATACCTGT	911
DB	299	sMetGlyIleLysAlaSerAsnThrAlaGluValPhePheAspGlyValArgValProSe	319
QY	912	GGAAAACATCCTTGGAGAGTCGAGATGGTTTAAGTGGCCATGAACATCTCCACAG	971
DB	319	rGluAsnValLeuGlyGluValGlySerGlyPheLysValAlaMetHisIleLeuAsnAs	339
QY	972	CGGCCGCTTTCAGCATGGCAGCGCTCGTGGCTGGCTGCTCAAGAGATGATTGTTGAAATGAC	1031
DB	339	nGlyArgPheGlyMetAlaAlaAlaLeuAlaGlyThrMetArgGlyIleAlaLysAl	359
QY	1032	TGCTGAGTAGCCCTGCACAGGAAACAGTTTAACAGAGGCTCAGTGAATTTGGATTGAT	1091
DB	359	aValAspHisAlaThrAsnArgThrGlnPheGlyGluLysIleHisAsnPheGlyLeuIl	379
QY	1092	TCAGAGAAATTTGCATCTGATGGCTCAGAAAGGCTTACGTTCATCGAGAGTATGACCTACCT	1151
DB	379	eGlnGluLysLeuAlaArgMetValMetLeuGlnTyrValThrGluSerMetAlaTyrMe	399
QY	1152	CACAGCAGGAGTCTCGACCAACCTCGCTTCCGACTCTCTCATCGAGGAGCCATGGT	1211
DB	399	tValSerAlaAsnMetAspGln---GlyAlaThrAspPheGlnIleGluAlaIleSe	418
QY	1212	GAAGGTGTTTCAGTCCGAGCGCCCTGGCAGTGTGTGAGTAGGGCTCGACATCTCCG	1271
DB	418	rIysIlePheGlySerGluAlaAlaIlePheValThrAspGluCysIleGlnIleMetGl	438
QY	1272	GGCTTTGGCTACACAAGGGACTATCCGTACGAGCGCATCTGCGTGACACCCGCACTCT	1331
DB	438	yGlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeuArgIlePh	458
QY	1332	CCTCATCTTCGAGGNAACCAATGAGATTTCTCGGATGTACATCGCCCTGACGGTCTGCA	1391
DB	458	eArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMe	478
QY	1392	GCATGCGCCGCGCATCCTGACTACAGGATCCATGAGTCTTAAACAG-----GCCAAAGT	1445
DB	478	tAspLysGlyLysGluLeuSerGlyLeuGlySerAlaLeuLysAsnPropheGlyAsnAl	498
QY	1446	GAGCAGTCATGGATPACCGTTGGCGGAGGCTTCGGGACTCCCTGGGCGCAACTGTGGA	1505
DB	498	aGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeuArgArgAlaGlyLeuGlySerGl	518
QY	1506	CCTGGGCTGACAGGCAACCATGGAGTTGTGCACCCAGTCTTTCGGAGACGCGCAACAA	1565
DB	518	yLeuSerLeuSer-----GlyLeuValHisProGluLeuSerArgSerGlyGluLe	535
QY	1566	GTTCGAGGAAACACCTACTGCTTCGGCGGAGCGCTGGAGACACACTGCTCTCGCTTTGG	1625
DB	535	uAlaValArgAlaLeuGluGlnPheAlaThrValValGluAlaLysLeuIleYHisIly	555
QY	1626	CAAGACCATCATGGAGGACAGCTGTACTGAAGGGGTGGCCAAACATCCTCATCAACCT	1685
DB	555	sIysGlyIleValAsnGluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLe	575
QY	1686	GTATGGCATGACGGCGTCTGTCGGGCGCAGCGCTCCATCCGATTTGGGCTCCGCAA	1745
DB	575	uTyrAlaMetValValLeuLeuSerArgAlaSerArgSerLeuSerGluGlyHisProTh	595
QY	1746	CCACGACCAAGAGTTCTTCTGGCCAACACCTTCTCGCTGGAA-----GCTTACTTCT	1799
DB	595	rAlaGlnHisGluLysMetLeuCysAspThrTrpCysIleGluAlaAlaAlaArgIleAr	615
QY	1800	GAATCTTTCAGCCTCTCTCAGCTGGACACAGTAGTATGCTCCAGNAACCTAGATGAGCAGAT	1859

Db 615 gGluGlyMetAlaAlaLeuGlnSerAspProTrpGlnGlu---LeuTyrArgAsnPh 634
 Qy 1860 TAAGAAAGTGTCCAGCAGATCTTGTAGAAGCAGACCTATATCTGTGCCACCCCTCTG 1917
 Db 634 eLysSerIleSerLysAlaLeuValGluArgGlyGlyValValThrSerAsnProLeu 653

RESULT 4

T15905

hypothetical protein E04F6.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T15905

R:Pauley, A.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid E04F6.

A:Reference number: 218427

A:Accession: T15905

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-613 <PAU>

A:Cross-references: UNIPROT:Q19057; EMBL:U28943; NID:g861333; PID:g861335; PIDN:AAA68357

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:E04F6.5

A:Introns: 55/3; 90/2; 195/3; 233/3; 472/2; 518/1; 567/3

Alignment Scores:

Pred. No.: 1,25e-70 Length: 613
 Score: 1210.50 Matches: 272
 Percent Similarity: 61.16% Conservative: 109
 Best Local Similarity: 43.66% Mismatches: 205
 Query Match: 26.88% Indels: 37
 DB: 2 Gaps: 14

US-09-945-326-1 (1-2452) x T15905 (1-613)

Qy 85 TTCCTGGCCACCGGTCGGCTGCTGCTGCGGGTCTGGTCTCTACCGCGAAC 144
 Db 16 PheIleArgLeuSerHisSerAlaAlaAlaLys-----AspAlaLysPro 31
 Qy 145 CGCGGGTACTCGCCACCGCCCTGTAGCAGCTTTCGCCAAGAGCTTTCCTAGGC 204
 Db 32 LysLysValAlaAlaValAspSerPro-----SerPheValMetAsnLeuPheArgGly 49
 Qy 205 AAAATCAAGAAGAAAGTTCCTCCATTTCCAGAGTTAGCCAAAGATGAATTAATGAA 264
 Db 50 LysAlaValThrAspGlnValPheProTy:ProLeuAsnMetThrAspGluGlnLysGlu 69
 Qy 265 ---ATCAATCAGTTCTTGGGACCGTGGAAAAATTTCTTCACTGAAGAGGTGGACTCCCGA 321
 Db 70 ThrLeuGlyMetValMetSerProLeuGluLysMetLeuValGluValAsnAspValVal 89
 Qy 322 AAAATTGACCGAGGAAATCCAGATGAATCTTGGAGAAATGAAGAGCCTAGGG 381
 Db 90 LysAsnAspGluThrSerAspIleProArgAlaValLeuAspGlnPheAlaGluLeuGly 109
 Qy 382 CTTTTCGGCTGCAAGTCCCAAGAAATATGTGGCTGGGCTTCTCCACACCATGTAC 441
 Db 110 ThrPheGlyValLeuValProGluLeuGluGlySerGlyPheAsnAsnSerGlnMet 129
 Qy 442 TCAAGACTAGGGGAGATCATC---AGCATGGATGGGTCATCTACTGTGACCCCTGGCAGCG 498
 Db 130 AlaArgValAlaGluIleValGlyAlaTyrAspLeuGlyPheGlyValValMetGlyAla 149
 Qy 499 CACGAGCTATTGGCTCAAGGGATCATCTTGGCTGGCAGCTAGGAGCAGAAAGCCAAA 558
 Db 150 HisGlnSerIleGlyTyrLysGlyIleLeuLeuGluGlyThrAspAlaGlnLysGlnLys 169
 Qy 559 TACTTGGCTAAACTGGGTCCGGGAGACACATTCACGCTTCTCCCTCAGGAGCCAGCC 618
 Db 170 TyrLeuProAspLeuAlaThrGlyArgLysPheAlaAlaPheAlaLeuThrGluProThr 189

Qy 619 AGTGGAGCGATCGAGCCTCAATCCGAGCAGAGCCACACTAAGTGAAGACAAGACAC 678
 Db 190 ThrGlySerAspAlaSerValArgThrArgAlaGluLeuSerAlaAspGlyLysHis 209
 Qy 679 TACATCTCAATGGCTCCAAGGCTGATTAATGAGGACTGGCCAAATATTTTACT 738
 Db 210 TyrValLeuAsnGlyGlyLysIleTrpIleSerAsnGlyGlyPheAlaAspValPheThr 229
 Qy 739 GTGTTTCCAAAGACTGAGTCTGTTGATTTCTGATGGATCAGTGAAGACAAAATCACAGCA 798
 Db 230 ValPheAlaGlnThrProValLysGlnAlaAspGlySerThrLysAspLysMetSerAla 249
 Qy 799 TTCATAGTACAAAGACACTTGTGGAGTCACTAATGGGAAACCCGAGATAAATTAGGC 858
 Db 250 PheIleValGluArgAlaPheGlyGlyValThrSerGlyProGlnGluLysLeuMetGly 269
 Qy 859 ATTCCGGGCTCCAAACACTTGTGAAGTCCATTTTGAACCAACCAAGATACCTGTGAAAC 918
 Db 270 IleLysGlySerAsnThrThrGluValHisPheAsnLeuLysIleProValGluAsn 289
 Qy 919 ATCTTTCGAGAGTTCGAGATGGTTTAAGTGGCCATGAACATCTCAACAGCGCGCG 978
 Db 290 LeuLeuGlyLysGluGlyGluGlyPheLysValAlaMetAsnIleLeuAsnAsnGlyArg 309
 Qy 979 TTCAGCATGGCAGCGCTGCTGGCTGCTCAAGAGATTGATTGAATGACTGCTGAG 1038
 Db 310 PheGlyIleProAlaAlaCysThrGlyAlaMetLysHisCysIleGlnLysThrValAsp 329
 Qy 1039 TAGCCTGTCACAAAGAAACAGTTTAAACAGAGGCTCAGTGAATTTGGATTGATTCAGGAG 1098
 Db 330 HisIleThrThrArgValGlnPheGlyLysLysLeuGlnGluPheGlyAsnIleGlnGlu 349
 Qy 1099 AAATTTGCATGTGCTCAGAAGCTTACGTCACTGAGAGATGATGACTACCTACCTCACAG 1158
 Db 350 LysLeuValGluMetIleSerLysLeuTyrAlaThrGluSerIleValTyrMetLeuSer 369
 Qy 1159 GGGATGCTGACCAACCTGCTTCCGACTGCTCCATCGAGGAGCCATGTTGAAGTG 1218
 Db 370 SerAsnMetAspArg---GlyIleLysGluTyrGlnLeuGluAlaIleGlyLysVal 388
 Qy 1219 TTCAGCTCCAGGCGCGCTGCGAGTGTGAGTGGCGCTGACAGATCTCGGGGGCTTG 1278
 Db 389 LeuAlaSerGluAsnAlaThrLeuValCysAspAspAlaIleGlnValHisGlyGlyMet 408
 Qy 1279 GGCTACAAAGGACTATCCGTACGAGCGCATCTGCGTGCACCCCTCCTCTCATC 1338
 Db 409 GlyPheMetArgGluThrGlyLeuGluArgValLeuArgAspLeuArgIlePheArgIle 428
 Qy 1339 TTCAGGGAACCAATGAGATCTCCGGATGTACATCCCTGACGGGTCTGCAGCATGCC 1398
 Db 429 PheGluGlyAlaAsnAspValLeuArgLeuPheIleAlaLeuThrGlyAlaGlnHisAla 448
 Qy 1399 GCGCGCATCTGACTACCAGATCCATGAGCTTAAACAGGCGCAAGTGAGCAGCATG 1458
 Db 449 GlyLys-----HisLeuAlaGluGlnAla-----SerGlyValGly 460
 Qy 1459 GATACCGTTTGGCGGAGGCTTCCGGAGCTCCTCGGCGCAACTGTGGACCTGGGCTGACA 1518
 Db 461 GlyLeuIleGlyLeuAlaValSerArgValThrGly-----GlyAsnThr 475
 Qy 1519 GGC---AACCATGGA---GTTGTGACCCCGAGTCTTGGGACAGCTGCGCAACAGTTTGAG 1572
 Db 476 GlySerAsnPheGlyGlnValValAspAlaSerLeuGlnAspSerAlaLysValLeuAsp 495
 Qy 1573 GAGAACACCTACTGCTTCGCGCGGACCGTGGAGACACTGCTGCTCCGCTTTGGCAAGACC 1632
 Db 496 GlnGlnIleAlaLeuPheGlyGlnThrValGlnGlyLeuLeuMetLysHisLysLysGly 515
 Qy 1633 ATCATGGAGGAGCAGTGTGTAAGCGGGTGGCCAACTCTCATCACTGATGATGGC 1692
 Db 516 IleIleAspArgGlnTyrGluMetHisArgValAlaAspAlaIleAsnIleTyrSer 535
 Qy 1693 ATGACGGCCGTGCTGTGCGCGGCGAGCCGCTCCATCCGCATTGGGCTCCGCAACCCAGC 1752

QY 1330 CTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGATGTACATCGCCTGACGGCTG 1389
 D 1330 CTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGATGTACATCGCCTGACGGCTG 1389
 Db 401 AsnArgIlePheGluGlyThrAsnGluIleAsnArgIleValProSerThrPheLeu 420
 QY 1390 CAGCATGCC-----GGCCGCATC---CTGACTACCAAGATCCATGAGCTTAACAGGCC 1440
 D 1390 CAGCATGCC-----GGCCGCATC---CTGACTACCAAGATCCATGAGCTTAACAGGCC 1440
 Db 421 LysLysAlaLeuLysGlyGluLeuProLeuPheGluLysAlaGlnSerLeuGlnGlu 440
 QY 1441 AAAGTGAGCAGCATGATGATACCGTTGGCCGGAGGCTCCGGAGCTCCCTGGCCGCAACT 1500
 D 1441 AAAGTGAGCAGCATGATGATACCGTTGGCCGGAGGCTCCGGAGCTCCCTGGCCGCAACT 1500
 Db 441 LeuMetMetLeuMetProGluGluProGly----- 450
 QY 1501 GTGACCTGGGGCTCACAGGCAACCATCGAGTTGTGCACCCCACTCTTGGCAGAGTGCC 1560
 D 1501 GTGACCTGGGGCTCACAGGCAACCATCGAGTTGTGCACCCCACTCTTGGCAGAGTGCC 1560
 Db 451 -----SerGlyValleu----- 454
 QY 1561 AACAAAGTTGAGGAGACACCTACTGCTCGCCGGCCGCGTGGAGACACTGCTGCTC--- 1617
 D 1561 AACAAAGTTGAGGAGACACCTACTGCTCGCCGGCCGCGTGGAGACACTGCTGCTC--- 1617
 Db 455 -----GluGlnGluLysTyIleValLysGlnAlaLysLysIleAlaLeuPheAla 471
 QY 1618 -----CGCTTTGGCAAGACCATCATGGAGGAGCAGCTGGTACTCAAG 1659
 D 1618 -----CGCTTTGGCAAGACCATCATGGAGGAGCAGCTGGTACTCAAG 1659
 Db 472 AlaGlyLeuAlaAlaGlnLysTyIleValLysGlnAlaLysLysIleAlaLeuPheAla 491
 QY 1660 CGGTGGCCCAACATCTCATCAACCTGTATGGCATGACGGCCGCTGTGTCGCGGCCGACG 1719
 D 1660 CGGTGGCCCAACATCTCATCAACCTGTATGGCATGACGGCCGCTGTGTCGCGGCCGACG 1719
 Db 492 AsnValAlaAspIleValSerAsnValTyAlaMetGluSerAlaValLeuArgThrGlu 511
 QY 1720 CGCTCCATCCGATT---GGCTCCGCAACGACGACGACGAGTTCCTTGGCCCAACACC 1776
 D 1720 CGCTCCATCCGATT---GGCTCCGCAACGACGACGACGAGTTCCTTGGCCCAACACC 1776
 Db 512 LysAlaIleAlaAlaGlnGlyAlaGluLysAlaAlaGlnLysValLeuTyIleThrGlu 531
 QY 1777 TTCTGCTGGAGCTTACTTGGAC----- 1800
 D 1777 TTCTGCTGGAGCTTACTTGGAC----- 1800
 Db 532 PheValGlnGluAlaPheAsnGluIleGluAlaHisAlaLysGluSerLeuIleAlaMet 551
 QY 1801 -----AATCTCTCAGCCTCTCTCAGCTGGCAAGATGCT 1836
 D 1801 -----AATCTCTCAGCCTCTCTCAGCTGGCAAGATGCT 1836
 Db 552 GluGluGlyAspSerLeuArgMetMetSerAlaLeuArgLysLeuThrArgValThr 571
 QY 1837 CCAGAAACCTAGTAGCAGATTAGAAAGTGTCCAGCAGATCCTTGGAGAGCAGGCC 1896
 D 1837 CCAGAAACCTAGTAGCAGATTAGAAAGTGTCCAGCAGATCCTTGGAGAGCAGGCC 1896
 Db 572 ProLysAsnValIleGlnLysLysArgGluAlaAlaAlaGlyIlePheGluAlaGluLys 591
 QY 1897 TAT 1899
 D 1897 TAT 1899
 Db 592 Tyr 592

RESULT 7
 A70817
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: A70817
 R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: A70817
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-650 <COL>
 A:Cross-references: UNIPROT:Q10538; GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA1767
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: fadE10

Alignment Scores:
 Pred. No.: 3.09e-38 Length: 650

Score: 711.50 Matches: 204
 Percent Similarity: 49.32% Conservative: 123
 Best Local Similarity: 30.77% Mismatches: 242
 Query Match: 15.80% Indels: 94
 DB: 2 Gaps: 18

US-09-945-326-1 (1-2452) x A70817 (1-650)

QY 178 GCTTTCCGCAAGAGCTTTCTTAGGCAAAATCAAGAAAGAAAGTTCCTCCATTTCCA 237
 D 178 GCTTTCCGCAAGAGCTTTCTTAGGCAAAATCAAGAAAGAAAGTTCCTCCATTTCCA 237
 Db 28 SerPheAlaLysGluLeuPheLeuGlyArgPheProLeuGlyLeuHisProPhePro 47
 QY 238 GAAGTTAGCCCAAGATCAATTAATGAATCAATCACTTTTGGGACCCGCTGGAAAAATTC 297
 D 238 GAAGTTAGCCCAAGATCAATTAATGAATCAATCACTTTTGGGACCCGCTGGAAAAATTC 297
 Db 48 LysProSerAspAlaGluAlaArgThrGluAlaPheLeuValLysLeuArgGluPhe 67
 QY 298 TTCACCTAGAGGTGACTCCCGAAAAATTTGACGAGAGGAAAAATCCAGATGAACCT 357
 D 298 TTCACCTAGAGGTGACTCCCGAAAAATTTGACGAGAGGAAAAATCCAGATGAACCT 357
 Db 68 Leu---AspThrValAspGlySerValIleGluArgAlaAlaGlnIleProAspGluTy 86
 QY 358 TTGGCAAAATTTGAAGAGCTAGGCTTTTGGCTGCAAGTCCCAAGATCCCAAGAAATATGCTGC 417
 D 358 TTGGCAAAATTTGAAGAGCTAGGCTTTTGGCTGCAAGTCCCAAGATCCCAAGAAATATGCTGC 417
 Db 87 ValLysGlyLeuAlaGluLeuGlyCysPheGlyLeuLysIleProSerGluTyGly 106
 QY 418 CTGGGCTTCTCCAAACACCATCTACTCAAGA---CTAGGGGAGATCATCATGATGGTGGG 474
 D 418 CTGGGCTTCTCCAAACACCATCTACTCAAGA---CTAGGGGAGATCATCATGATGGTGGG 474
 Db 107 LeuAsnMetSerGlnValAlaTyAsnArgValLeuMetMetValThrValHisSer 126
 QY 475 TCCATCCTGTGACCTGGCAGGCGACAGGCTATTGGCTC---AAGGGATCATCTTG 531
 D 475 TCCATCCTGTGACCTGGCAGGCGACAGGCTATTGGCTC---AAGGGATCATCTTG 531
 Db 127 SerLeuGlyAlaLeuLeuSerAlaHisGlnSerIleGlyValProGluProLeuLysLeu 146
 QY 532 GCTGGCAGCTGAGGAGAGAAAGCCAAATCTTGCCTTAACTGCGCTCCGCGGAGCACAT 591
 D 532 GCTGGCAGCTGAGGAGAGAAAGCCAAATCTTGCCTTAACTGCGCTCCGCGGAGCACAT 591
 Db 147 AlaGlyThrAlaGluGlnLysArgPheLeuProArgCysAlaIleGlyAla---Ile 165
 QY 592 GCAGCCTTCTGCTCCTCAGGAGCCAGCAGTGGAGCGATGCAGCCTCAATCCGGAGCAGA 651
 D 592 GCAGCCTTCTGCTCCTCAGGAGCCAGCAGTGGAGCGATGCAGCCTCAATCCGGAGCAGA 651
 Db 166 SerAlaPheLeuLeuThrGluProAspValGlySerAspProAlaArgMetAlaSerThr 185
 QY 652 GCACACTAAGTGAAGAGAGAGACACTACATCTCAATGGCTCCAGAGTCTGGATTACT 711
 D 652 GCACACTAAGTGAAGAGAGAGACACTACATCTCAATGGCTCCAGAGTCTGGATTACT 711
 Db 186 AlaThrProIleAspAspGlyGlnAlaTyGluLeuGluGlyValLysLeuThrThr 205
 QY 712 AATGAGGAGCTGCCAATATTTTACTGTGTTTGAAGACACTGAGTCTGATCTGAT 771
 D 712 AATGAGGAGCTGCCAATATTTTACTGTGTTTGAAGACACTGAGTCTGATCTGAT 771
 Db 206 AsnGlyValValAlaAspLeuLeuValValMetAlaArg-----ValProArgSerGlu 223
 QY 772 GGATCAGTGAAGAGCAAAATCACAGATTCATAGTAGAAGAGACTTTGGTGGAGTCACT 831
 D 772 GGATCAGTGAAGAGCAAAATCACAGATTCATAGTAGAAGAGACTTTGGTGGAGTCACT 831
 Db 224 GlyHis---ArgGlyGlyIleSerAlaPheValValGluAlaAspSerProGlyIleThr 242
 QY 832 AATGGAAACCCGAGATAAATTAGGCATTCCGGGCTCCACACTTGTGAAGTCCATTTT 891
 D 832 AATGGAAACCCGAGATAAATTAGGCATTCCGGGCTCCACACTTGTGAAGTCCATTTT 891
 Db 243 ValGluArgArgAsnLysPheMetGlyLeuArgGlyIleGluAsnGlyValThrArgLeu 262
 QY 892 GAAACACCAACAGATACCTGTGAAACACATCTTGGAGAGGTCGAGATGGGTTTAAGGTG 951
 D 892 GAAACACCAACAGATACCTGTGAAACACATCTTGGAGAGGTCGAGATGGGTTTAAGGTG 951
 Db 263 HisArgValArgValProLysAsnLeuIleGlyArgGluGlyAspGlyLeuLysIle 282
 QY 952 GCATGACATCCTCAACAGCGCGGTTTACAGATGGGAGCGCTGCTGGCTGGCTGCTC 1011
 D 952 GCATGACATCCTCAACAGCGCGGTTTACAGATGGGAGCGCTGCTGGCTGGCTGCTC 1011
 Db 283 AlaLeuThrThrLeuAsnAlaGlyArgLeuSerLeuProAlaIleAlaThrGlyValAla 302
 QY 1012 AAGAGATTGATTGAATGACTCTCAGTACGCTGCACAGGAAACAGTTTAAACAGAGG 1071
 D 1012 AAGAGATTGATTGAATGACTCTCAGTACGCTGCACAGGAAACAGTTTAAACAGAGG 1071
 Db 303 LysGlnAlaLeuLysIleAlaArgGluTrpSerValGluArgValGlnTrpGlyLysPro 322
 QY 1072 CTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCATGCTCGCTCAGAGGCTTACGTC 1131
 D 1072 CTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCATGCTCGCTCAGAGGCTTACGTC 1131
 Db 323 ValGlyGlnHisGluAlaValAlaSerLysIleSerPheIleAlaAlaThrAsnTyAla 342
 QY 1132 ATGGAGAGTATGACCTACCTCACAGCAGGAGTGTGGACCAACCTGGCTTTCCCGACTGC 1191

.....
343 LeuAspAlaValValGluLeuSerSerGlnMetAlaAspGlu---GlyArgAsnAspIle 361
QY 1192 TCCATCCAGGAGCAGCATGGTGAAGCTTTCAGCTCCGAGCGCGCTCGCAGTGTGTCAGT 1251
Db 362 ArgIleGluAlaLeuAlaLeuAlaLeuTrpSerSerGluMetAlaCysLeuValGlyAsp 381
QY 1252 GAGCGCTCAGATCTCCGCGGGCTTCGGCTAC----- 1284
Db 382 GluLeuLeuGlnIleArgGlyGlyArgGlyTyrgluThrAlaGluSerLeuAlaAlaArg 401
QY 1285 ---ACAAGGACTATCCGTAGGAGCGCATACTGCGTCACACCCGCATCTCTCATCTTC 1341
Db 402 GlyGluAlaValProValGluGlnMetValArgAspLeuArgIleAsnArgIlePhe 421
QY 1342 GAGGGAACCAATGAGATTCTCCGAGATACATCCCTCGCGGT-----CTG 1389
Db 422 GluGlySerSerGluIleMetArgLeuLeuIleAlaArgGluAlaValAlaHisLeu 441
QY 1390 CAGCATGCCGCGCATCTCTGACTACACAGGATCCATGAGCTTAACAGGCCAACAGTGAGC 1449
Db 442 ThrAlaAlaGlyAspLeuAlaAsnProLysAla---AspLeuArgGlnLysAlaAlaAla 460
QY 1450 ACAGTCATGATACCTGTGCGCGAGCGCTCGGGACTCCCTGCGCCGAACCTGTGGACCTG 1509
Db 461 AlaAla----- 462
QY 1510 GGGCTGACAGCGCAACCATGGAGTTGTGACCCCGAGTCTTGG----- 1551
Db 463 GlyAlaSerGlyPheTyAlaLysTrpLeuProLysLeuValPheGlyGluGlyGlnLeu 482
QY 1552 -----GACAGT 1557
Db 483 ProThrThrTrpArgGluPheGlyAlaLeuAlaThrHisLeuArgPheValGluArgSer 502
QY 1558 GCCAACAGTTTGGAGGAACACCTACTGCTTGGCGCGGACCGTGGAGACACTGCTGCTC 1617
Db 503 SerArgLysLeuAlaArgAsnThrPhe---TyrGly-----MetAla 515
QY 1618 CGCTTTGGCAAGACCATCATGGAGGAGCAGTGTACTGAAGCGGGTGGCCACATCCTC 1677
Db 516 ArgTrpGlnAlaSerLeuGluLysLysGlnGlyPheLeuGlyArgIleValAspIleGly 535
QY 1678 ATCAACCTGTATGGCATGACGCGCGTCTCTGCGGGCGCCAGCGCTCCATCCGCAATTGGG 1737
Db 536 AlaGluLeuPheAlaIleSerAlaAlaCysValArgAlaGluAlaGlnArgThrAlaAsp 555
QY 1738 CTCGCGCAACCGACGACGAGGTCTCTTGGCCAAACCTTCTGC----- 1782
Db 556 ProValGluGlyGlnAlaTyrgluLeuAlaGluAlaPheCysGlnGlnAlaThrLeu 575
QY 1783 ---GTGGAAGCTTACTTGCAGATCTCTCAGCTCTCTCAGCTGGCAAGATGCTCCA 1839
Db 576 ArgValGluAlaLeuPheAspAlaLeuTrpSer----- 586
QY 1840 GAAACACCTAGATGACGAGATTAGAAAGTGTCCAGCAGATCTCTTGAGAAGCGA---GCC 1896
Db 587 ---AsnThrAspSerIleAspValArgLeuAlaAsnAspValLeuGluGlyArgTyThr 605
QY 1897 TATATCTGTGCCACCTCTGGACAGACATGCTGAGCGGAGGAGCAGTGTCCCTGCTA 1956
Db 606 TrpLeuGluGlnGlyIleLeuAspGlnSer-GluGlyThrGlyProTrpIleAlaSerTr 625
QY 1957 CCGCCG-----CCCTACCATGCGCGGTGTGGATGATGCTTACTCTTTT 2004
Db 625 pGluProGlyProSerThrGluAlaAsnLeuAlaArgPheLeuThrValSerProse 645
QY 2005 TTCAGAA 2011
Db 645 rSerGlu 647

RESULT 8
B87302

acyl-CoA dehydrogenase, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87302
R;Niernman, W.C.; Feildbilyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: B87249; MUID:21173698; PMID:11259647
A;Accession: B87302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-382 <STO>
A;Cross-references: UNIPROT:Q9AB07; GB:AE005673; NID:g13421592; PIDN:AAK22414.1; GSPDB:GB
C;Genetics:
A;Gene: CC0427
C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.: 1,7e-37 Length: 382
Score: 699.00 Matches: 155
Percent Similarity: 58.31% Conservative: 80
Best Local Similarity: 38.46% Mismatches: 124
Query Match: 15.52% Indels: 44
DB: 2 Gaps: 8
US-09-945-326-1 (1-2452) x B87302 (1-382)
QY 253 GAACCTTAATGAATCAATCAATGTTCTTGGGACCGTGGAAAAATCTTCACTGAGAGGTG 312
Db 4 AspLeuGluThrArgGluGlnLeuIleAspThrValAlaArgPheValAlaGluArgLeu 23
QY 313 GAC-----TCCCGAAAAATTGACAGGAGGAGGAAAAATCCAGATGAAATCTTGGAGAAA 366
Db 24 ArgProIleGluAlaGlnValAlaGluAsnAspAlaValProAspAspValIleGluGlu 43
QY 367 TTCAGAGCGCTAGCGCTTTTGGCTGCAAGTCCCAAGAACAAATATGTGGCTGGCTTC 426
Db 44 MetLysGlyLeuGlyLeuPheGlyLeuThrIleProGluGluPheGlyGlyLeuGly--- 62
QY 427 TCCAACACCATGTACTCAGACTAGGGAGATCATCAGCATGGTGGTCCATCATCTGTG 486
Db 63 -----LeuThrMetGluGluAlaLeuVal 71
QY 487 ACCCTGCGCGCCACCGAGCT----- 507
Db 72 AlaIleGluLeuGlyArgAlaSerProAlaPheArgSerValPheGlyThrAsnValGly 91
QY 508 ATTGGCTCAAGGGGATCATCTTGGCTGGCAGTGGAGGAGAGAAAGCAATATCTTCCT 567
Db 92 IleGlySerGlnGlyLeuValMetPheGlyAsnAspGluGlnLysAlaLysTrpLeuPro 111
QY 568 AAATGGCTCCCGGAGCAGCATTTGAGCTTCTGCTCAGGAGCCAGCCAGTGGGAGC 627
Db 112 GlyIleAlaSerGlyAlaValIleThrSerPheAlaLeuThrGluProGluAlaGlySer 131
QY 628 GATGCGCTCAATCCGAGCAGCAGCACACTAAGTGAAGACAAAGAGCACTACATCCTC 687
Db 132 AspSerAlaAlaValGlnThrArgAlaThr-----ArgAspGlyAspAspTyTrpIleLeu 149
QY 688 AATGGCTCCAGGCTCTGGATTACTATGGAGGATGGCCCAATATTTTACTGTGTTTGA 747
Db 150 AsnGlySerLysArgTyTrpIleThrAsnAlaGlyLysAlaSerLeuPheThrValMetAla 169
QY 748 AACACTGAGTCTTGTGATCTGTGATCATCAGTCAAGACAAATATCAGCATTCATAGTA 807
Db 170 ArgThrAsn---ProAspAlaLysGlyGlyAla-----GlyValSerAlaPheLeuVal 186
QY 808 GAAAGAGACTTTGTTGGAGTCACATAATGGGAAACCCGAGATAAATAGGCACTTCGGGGC 867
Db 187 ProArgAspLeuProGlyLeuThrValGlyLeuProGluLysLysMetGlyGlnGlnGly 206

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Qy 868 TCCACACTTGTGAAGTCCATTTTGAACACCAAGATACCTGTGGAAACATCCTTGA 927
Db : : : : :
207 AlaHisIleHisAspValThrPheAspAsnValArgValProAlaTyrAsnArgLeuGly 226
Qy 928 GAGTCCGAGATGGTTTAAGGTGGCCATGAACATCTCTCAACAGCGCGGTTCAGCATG 987
Db : : : : :
227 AlaGluGlyGluGlyPheLeysValAlaMetGlnValLeuAspArgGlyArgLeuHisIle 246
Qy 988 GGCAGCGTGGTGGCTCTCAAGAGATTGTAATGAGTCTGCTGAGTACGCGCTGC 1047
Db : : : : :
247 AlaAlaValCysValGlyValAlaGluArgLeuIleAlaAspCysValAlaTyrAlaSer 266
Qy 1048 ACAAGAAACAGTTTAAACAAGAGCTCAGTGAATTTGGATTGATTCAG----- 1095
Db : : : : :
267 GluArgLysGlnPheGlyGlnProIleAlaSerPheGlnLeuIleGlnAlaMetIleAla 286
Qy 1096 ---CAGAAATTTGCACTGATGGCTCAGAGGCTTACGTATGAGATGATGACCTCTC 1152
Db : : : : :
287 AspSerLysThrGluAlaLeuAlaAlaLysAlaLeuValLeuGluThrAlaAlaArgLysArg 306
Qy 1153 ACAGCAGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCGCATGGTG 1212
Db : : : : :
307 AspAlaGlyVal-----AsnValThrLeuGluAlaAlaSerSer 319
Qy 1213 AAGGTGTTACGCTCCGAGCGCGCTGCGAGTGTGTGAGTGAGGCGCTGCGAGATCCTCGG 1272
Db : : : : :
320 LysLeuPheAlaSerGluMetValGlyArgValAlaAlaAspArgAlaValGlnValPheGly 339
Qy 1273 GGCTTGGCTACACAAGGGACTATCCGTACGAGCGCATCTGCGTGACACCCGATCCTC 1332
Db : : : : :
340 GlyAlaGlyTyrValAlaAlaAspTyrGlyLeuGluArgLeuTyrArgAspValArgIlePhe 359
Qy 1333 CTACATCTTCAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTGCAG 1392
Db : : : : :
360 ArgIleTyrGluGlyThrSerGlnValGlnGlnLeuIleAlaArgGluThrLeuLys 379
Qy 1393 CATGCCGCGC 1401
Db : : : : :
380 ArgGlyGly 382

RESULT 9
B83443
Probable acyl-CoA dehydrogenase P1631 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83443
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83443
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-384 <STO>
A:Cross-references: UNIPROT:Q91391; GB:AB004590; GB:AB004091; NID:g9947587; PIDN:AAG0502
A:Experimental source: strain PA01
C:Genetics:
A:Gene: P1631
C:Superfamily: acyl-CoA dehydrogenase

Alignment Scores:
Pred. No.: 5,22e-37 Length: 384
Score: 691.50 Matches: 147
Percent Similarity: 58.87% Conservative: 82
Best Local Similarity: 37.79% Mismatches: 121
Query Match: 13.35% Indels: 39
DB: 2 Gaps: 8

US-09-945-326-1 (1-2452) x B83443 (1-384)
Qy 265 ATCAATCAGTTCTTGGACCCGCGGAAATAATTTCTTCACTGAAGAGGTG-----GACTCG 318
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Db : : : : :
8 LeuAsnLeuLeuLeuAspSerIleArgGlnPheValArgGluSerLeuValProHisGlu 27
Qy 319 CGAAATATTGACCGAAGGGAATAATCCAGATGAAACTTTGGAGAAATTTGAAGAGCCTA 378
Db : : : : :
28 GlnGluValAlaGluThrAspArgIleProGluAlaIleAlaArgMetArgGluMet 47
Qy 379 GGCCTTTTGGGCTGCAAGTCCAGAGATATGTTGGCTGGCTTCTCCACACCATG 438
Db : : : : :
48 GlyLeuPheGlyLeuSerIleProGluAlaTyrGlyGlyLeuGly----- 62
Qy 439 TACTCAAGACTAGGGGAGATCATCAGCATGGTGGTCCATCATCTGTGACC----- 489
Db : : : : :
63 -----ValThrMetGluGluValSerIleAlaPheGluLeu 75
Qy 490 -----CTGGCAGCGCACCCAGGCTATTGGCCTCAAG 519
Db : : : : :
76 GlyArgThrSerProAlaPheArgSerLeuLeuGlyThrAsnAsnGlyIleGlySerGln 95
Qy 520 GGGATCATCTTGGCTGCGCACTGAGGAGCAGAAACCAATACTTGGCTAAACTGGCGTCC 579
Db : : : : :
96 GlyIleValIleAspGlyThrGluGluGlnLysArgArgIyrLeuProArgLeuAlaSer 115
Qy 580 GGGAGCACATTCAGCCTTCTGCTCACGGAGCCAGCCAGTGGGAGCGATGCGAGCTCA 639
Db : : : : :
116 GlyGluLeuLeuSerSerPheCysLeuThrGluProAspSerGlySerAspAlaAlaSer 135
Qy 640 ATCCGAGCAGAGCCACACTAAGTGAAGACAAGACACTACATCTCAATGCTGCTCAAG 699
Db : : : : :
136 LeuLysThrThrAlaVal-----ArgAspGlyGluHisTyrValLeuAsnGlyThrLys 153
Qy 700 GTCTGATTAATAATGGAGGACTGGCCAAATATTTTACTGTGTGTTTCAAGAGACTGAGTC 759
Db : : : : :
154 ArgPheIleThrAsnAlaProGlnAlaGlyIleTyrThrValMetAlaArgThr----- 171
Qy 760 GTTGATTTCTGATGATCAGTGAAGACAAA-----ATCACAGCATTTCTAGTAGAAAGA 813
Db : : : : :
172 -----AspProAlaIleArgGlyAlaGlyGlyIleSerAlaPheValValGluArg 188
Qy 814 GACTTTGGTGGAGTCACTAATGGGAACCCGAGATAAATTAGGCATTCGGGCTCCAAC 873
Db : : : : :
189 GlyThrProGlyLeuSerLeuGlyLysProAspArgLysMetGlyGlnLysGlyAlaHis 208
Qy 874 ACTTGTGAAGTCCATTTTCAAAACACCAAGATACCTGTGGAACCAATCTCTGGAGAGGTC 933
Db : : : : :
209 ThrCysAspValIlePheAspCysArgValProAlaSerGlnLeuIleGlyVal 228
Qy 934 ---GGAGATGGTTTAAGTGGCCATGAACATCTCTCAACAGCGCGGTTCAGATGGC 990
Db : : : : :
229 GluGlyValGlyPheLysThrAlaMetLysValLeuAspLysGlyArgLeuHisIleAla 248
Qy 991 AGCGTCGTGGCTGGCTGCTCAAGAGATTGATTGAATGACTGCTGAGTACCGCTGCACA 1050
Db : : : : :
249 AlaValCysValGlyValAlaGluArgMetLeuGluAspAlaLeuArgTyrAlaLeuGlu 268
Qy 1051 AGGAACACAGTTTAAACAAGGCTCAGTGAATTTGGATTGATTTCAGGAGAAATTTGACTG 1110
Db : : : : :
269 ArgLysGlnPheGlyGlnProIleAlaGluPheGlnLeuIleGlnAlaMetLeuAlaAsp 288
Qy 1111 ATGGCTCAGAAGCTTACGTCATGAGAGTATGACTTACCTCAGCAGCGGATGCTGGAC 1170
Db : : : : :
289 SerLysAlaGluAlaTyrAlaAlaArgCysMetValIleAspAlaAlaArgGlnArgAsp 308
Qy 1171 CAACCTGGCTTTCCCGACTGCTCCATCGAGCGGCATCGTGAAGGTGTTTCAGCTCCGAG 1230
Db : : : : :
309 GluGly-----ArgAspValGlyThrGluAlaSerCysAlaLysLeuPheAlaSerGlu 326
Qy 1231 GCCGCTGGCAGTGTGTGAGTGGCGCTGCAGATCTCTGGGGGTCTGGGCTTACACAAG 1290
Db : : : : :
327 MetCysGlyArgValAlaAlaAspArgAlaValGlnIlePheGlyGlyValGlyTyrIleGly 346
Qy 1291 GACTATCGTACGAGCGCATCTCGTGACACCCGATCTCTCTCATCTTCGAGGGAACC 1350
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1291 GACTATCGTACGAGCGCATCTCGTGACACCCGATCTCTCTCATCTTCGAGGGAACC 1350
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Db 347 AspTyrGlyIleGluAurPheThyArgAspValArgLeuPheArgIleTyrGluGlyThr 366
 Qy 1351 AATGAGATTCTCCGGATGATCATCGCC 1377
 Db 367 ThrGlnIleGlnLeuLeuIleAala 375
 RESULT 10
 G84124
 acyl-CoA dehydrogenase mmGC [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: G84124
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Puji, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: G84124
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-379 <STO>
 A:Cross-references: UNIPROT:Q9K6D0; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BA075
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: mmGC
 C:Superfamily: acyl-CoA dehydrogenase
 Alignment Scores:
 Pred. No.: 6.51e-37 Length: 379
 Score: 690.00 Matches: 147
 Percent Similarity: 61.39% Conservative: 74
 Best Local Similarity: 40.83% Mismatches: 125
 Query Match: 15.32% Indels: 14
 DB: 2 Gaps: 6
 US-09-945-326-1 (1-2452) x G84124 (1-379)
 Qy 298 TTCACTGAAGGTGGACTCCGAAAAATTGACCAGGAAGGAAAAATCCCGAGATGAAC 357
 Db 27 PheValGluMetGluThr-----AenAspThrPheProMetHisIle 41
 Qy 358 TTGAGAAATGAGAGCCTAGGCTTTTGGGTGCAAGTCCCGAGAGATATGGTGGC 417
 Db 42 ValLysGluMetGlyLeuGlyLeuMetGlyIleProIleProGluAlaTyrGlyGly 61
 Qy 418 CTGGGCTTCTCCACACCATGTAC---TCAAGACTAGGGAGATCATCAGCATGGTGGG 474
 Db 62 AlaGluMetAspPheThrSerTyrIleIleAlaIleHisGluLeuSerLysValSerAla 81
 Qy 475 TCCATCACTGTGACCCCTGGCAGCGCACAGGCTATTGGCTTCAAGGGGATCATCTTGGCT 534
 Db 82 ThrValGlyValIleLeuSerValHisThrSerValGlyThrAsnProIleLeuPhePhe 101
 Qy 535 GGCCTAGGNGCAGAAAGCCAAATACTTGCCTAACTGGCGTCCGGGGAGCACATTGCA 594
 Db 102 GlyThrGluGluGlnLysSerArgPheIleProLysLeuAlaLysGlyGlyTyrLeuGly 121
 Qy 595 GCCTTCTGCTCCACGAGCAGCAGTGGAGCGCATCGAGCTCAATCCGGAGCAGAGCC 654
 Db 122 AlaPheGlyLeuThrGluProSerAlaGlySerAspAlaAlaLeuLysThrAla 141
 Qy 655 ACATAAGTGAAGACAAAGACACTACATCTCAATGGCTCCAAAGGTCTGGATTACTAAT 714
 Db 142 LeuLysGlnGlyAsp-----HisTyrArgLeuAsnGlySerLysValPheIleThrAsn 159
 Qy 715 GGAGGACTGGCAATATTTTACTGTGTTTGCAGAGACTGAGTGGTGTGATTGATGGA 774
 Db 160 GlyGlyAlaAlaAspThrTyrValValPheAlaSerThr-----AsnProSer 175
 Qy 775 TCAGTGAAGACAAATACACAGCATTCATAGTAAAGAGACTTTGGTGGAGTCACTAAT 834
 Db 176 AlaGlyArgLysGlyIleSerAlaPheIleValGluLysGluThrProGlyPheThrVal 195
 Qy 835 GGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAAACACTTGTGAAGTCCATTTTGA 894

Db 196 GlyLysLysGluLysLysMetGlyLeuHisGlySerAsnThrThrGluLeuIlePheGlu 215
 Qy 895 AACACCAAGATACCTGTGGAAAAACATCCTTGGAGAGGTGCGAGATGGTGTAAAGTGCC 954
 Db 216 AspAlaLeuValProLysGluAsnLeuLeuGlyValGluGlyAspGlyTyrLysIleAla 235
 Qy 955 ATGAACATCTCAACACGCGCGCTTCCAGCATGCGCAGCGCTGGTGGTGGCTGCTCAAG 1014
 Db 236 MetAlaAsnLeuGluAlaGlyArgIleGlyIleAlaAlaGlnSerLeuGlyIleAlaGlu 255
 Qy 1015 AGATTGATTGAATGACTGCTGAGTACGCTGCACACGAGGAACAGTTTAAACAAGGCTC 1074
 Db 256 AlaAlaLeuGluAlaAlaThrSerTyrAlaLysGluArgLysGlnPheGlyLysSerIle 275
 Qy 1075 AGTGAATTTGGATTGATTCAGGAGAAATTTGCACATGATGCTCAGAGGCTTACGTGTC 1134
 Db 276 GlyGlnGlnGlnAlaIleAlaPheLysLeuAlaAspLeuAlaThrGlnValGluAlaAla 295
 Qy 1135 GAGAGTATGACCTTACCTCACAGCAGGATGCTGGACCAACTGCTGCTTCCGAGTCTCC 1194
 Db 296 LysLeuLeuThrTyr---ArgAlaAlaGlnLysGlnGlnGlyIle---SerCysAla 313
 Qy 1195 ATCGAGCGCCCATGGTGAAGGTCTTCAGCTCCGAGCGCCCTGGCAGTGTGTGAGTGAG 1254
 Db 314 LysGluSerSerMetAlaLysLeuPheAlaSerLysThrAlaMetLysAlaAlaIleGlu 333
 Qy 1255 GCGCTGCAGATCCTCGGGGCTTGGCTTACACAGGAGTATCCGTACGAGCGGATAC 1314
 Db 334 AlaValGlnIlePheGlyGlyTyrGlyTyrThrLysGluTyrProValGluArgTyrPhe 353
 Qy 1315 CGTGACACCCGATCTCTCTCATCTTCGAGGGGAACCAATGAGATTCCTCGGATGTACATC 1374
 Db 354 ArgAspAlaLysValCysGluIleTyrGluGlyThrSerGluIleGlnArgIleValIle 373
 RESULT 11
 D69658
 acyl-CoA dehydrogenase mmGC - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: D69658
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Arevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holeappel, S.; Hosono, S.; Hullo, M.F.;
 Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maugel,
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror,
 akeuchi, M.; Tamakoishi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: D69658
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-378 <KUN>
 A:Cross-references: UNIPROT:P45857; GB:Z99116; GB:AL009126; NID:g2634723; PIDN:CAB14346.1
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: mmGC
 C:Superfamily: acyl-CoA dehydrogenase
 Alignment Scores:
 Pred. No.: 2.15e-36 Length: 378
 Score: 682.00 Matches: 157
 Percent Similarity: 56.33% Conservative: 70
 Best Local Similarity: 38.96% Mismatches: 130
 Query Match: 15.14% Indels: 46


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DB:                2                Gaps:                8
US-09-945-326-1 (1-2452) x D69658 (1-378)
QY 172 GTACGAGCTTTCCGCAAGAGCTTTTCTAGCGCAAAATCAAGAAAGAAAGATTTCCTCCA 231
DB 14 ValArgAspPheAla-:::|||||:::|
QY 232 TTTCCAGAAGTTAGCCAAAGATGAACCTTAATGAATCAATCAGTTCTTGGGACCCGCGTGA 291
DB 25 AlaAlaGluIle-:::|||||:::|
QY 292 AAATTCTTCACTGAAGAGGTGGACTCCCGAAAAAATTCACAGGAAGGAAAAATCCAGAT 351
DB 29 -----MetGluLysThrAspGluPheProPhe 37
QY 352 GAAACTTTGGAGAAATTCGAAGAGCTAGGGCTTTTGGCTGCAAGTCCCGAAGAAATAT 411
DB 38 GlnLeuIleLysLysMetGlyLysHisGlyLeuMetGlyIleProValProGluGlnTyr 57
QY 412 GGTGGCTGGGCTTCTCCAAACACCATGTAC---TCAAGACTAGGGAGATCATCAGCATG 468
DB 58 GlyGlyAlaGlyAlaAspValValSerTyrIleLeuAlaIleHisGluIleSerArgIle 77
QY 469 GATGGTCCATCACTGTGACCTCGCAGCGCACAGGCTATTGGCTTCAAGGGATCATC 528
DB 78 SerAlaAlaValGlyValIleLeuSerValHisThrSerValGlyThrAsnProIleLeu 97
QY 529 TTGGCTGGCACTAGGAGCAAGAACCAATACTTGTGCTTCAAGTGGCTCGGGGAGCAC 588
DB 98 TyrPheGlyAsnGluGluGlnLysMetLysTyrIleProAsnLeuAlaSerGlyAspHis 117
QY 589 ATTGCAGCTTCTCCCTCACGAGCCAGCCAGTGGGAGCGTCAAGCTCAATCCGGAGC 648
DB 118 LeuGlyAlaPheAlaLeuThrGluProHisSerGlySerAspAlaGlySerLeuArgThr 137
QY 649 AGACCCACACTAAGTGAAGACAAGACACTACATCTCAATGCTCAAGGCTCGGATT 708
DB 138 ThrAlaIleLysLysAsnGlyLys-----TyrLeuLeuAsnGlySerLysIlePheIle 155
QY 709 ACTAATGGAGGACTGGCCAAATATTTTACTGTGCTTTCGAAAGACTGAGGCTGATTCT 768
DB 156 ThrAsnGlyGlyAlaAlaAspIleTyrIleThrPheAlaLeuThr-----Ala 171
QY 769 GATGGATCAGTGAAGACAAATCACAGCATTCATAGTAAAGAGACTTGTGGTGATC 828
DB 172 ProAspGlnGlyArgHisGlyIleSerAlaPheIleValGluLysAsnThrProGlyPhe 191
QY 829 ACTAATGGGAAACCCGAAGATAAATTAAGCATTCGGGCTCCAAACACTTGTGAAGTCCAT 888
DB 192 ThrValGlyLysLysGluArgLysLeuGlyLeuTyrGlySerAsnThrThrGluLeuIle 211
QY 889 TTTGAAACACCAAGATACCTGTGGAAACATCTTGGAGAGTTCGAGATGGGTTTAA 948
DB 212 PheAspAsnAlaGluValProGluAlaAsnLeuLeuGlyLysGluGlyAspGlyPheHis 231
QY 949 GTGGCCATGAACATCTCTCAACAGCGCGCTTCAGCATCGGCGAGCTCGTGGCTGGCTG 1008
DB 232 IleAlaMetAlaAsnLeuAsnValGlyArgIleGlyIleAlaAlaGlnAlaLeuGlyIle 251
QY 1009 CTCAGAGATTGATTGAATACCTGTGAGTACGCTGAGCTGCAAGGAAACAGTTTAA 1068
DB 252 AlaGluAlaAlaLeuGluHisAlaValAspTyrAlaLysGlnArgValGlnPheGlyArg 271
QY 1069 AGGCTCAGTGAATTTGGATTGATTTCAGGAGAAATTTGCACTGATGCTCAGAGGCTTAC 1128
DB 272 ProIleAlaAlaAsnGlnGlyIleSerPheLysLeuAlaAspMetAlaThrArgAlaGlu 291
QY 1129 GTCATGAGAGTATGACCTACCTACACAGGAGGATGCTGGACCAACCTGGCTTCCCGC 1188
DB 292 AlaAlaArgHisLeuValTyrHisAlaAlaAsp---LeuHisAsnArgGlyLeu---Asn 309
QY 1189 TGTCTCATCGAGCAGCCATGGTGAAGGTGTTTCAGCTCCGAGGCCCGCTGGCAGTGTG 1248
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DB 310 CysGlyLysGluAlaSerMetalLysGlnPheAlaSerAspAlaAlaValLysAlaLeu 329
QY 1249 AGTGAGCGCTCGAGATCTCTGGGGCTTGGGTACAAAGGAGCTATCGTACGAGCGC 1308
DB 330 ---AspAlaValGlnIleTyrGlyIleTyrGlyTyrMetLysAspTyrProValGluArg 348
QY 1309 ATACTCGGTGACACCCGCATCTCTCTATCTTCGAGGAGCAACATGAGATTCTCCGATG 1368
DB 349 LeuLeuArgAspAlaLysValThrGlnIleTyrGluGlyThrAsnGluIleGlnArgLeu 368
QY 1369 TACATCGCC 1377
DB 369 IleIleSer 371
RESULT 12
AC3536
butyryl-CoA dehydrogenase (EC 1.3.99.2) [imported] - Brucella melitensis (strain 16M)
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C/Accession: AC3536
R/Delvecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.;
Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A/Reference number: AD3252; PMID:11756688
A/Accession: AC3536
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-381 <KUR>
A/Cross-references: UNIPROT:Q8YDG3; GB:AE008918; PIDN:AAL53454.1; PID:gl7984354; GSPDB:GN
A/Experimental source: strain 16M
A/Genetics:
A/Map position: II
C/Superfamily: acyl-CoA dehydrogenase
C/Keywords: oxidoreductase
Alignment Scores:
Pred. No.: 2,15e-36 Length: 381
Score: 682.00 Matches: 151
Percent Similarity: 60.70% Conservative: 73
Best Local Similarity: 40.92% Mismatches: 131
Query Match: 15.14% Indels: 14
DB: 2 Gaps: 7
US-09-945-326-1 (1-2452) x AC3536 (1-381)
QY 286 GTGAAAATTTCTTCACTGAAGAGGTG-----GACTCCGAAAAAATTGACCAGAA 336
DB 16 ValArgArgPheValArgGluArgLeuValProAlaGluSerArg---ValGluGluThr 34
QY 337 GGGAAAATCCAGATGAACCTTTGGAGAAATTAAGAGAGCTTAGGCTTTTGGCTGCAA 396
DB 35 AsnArgIleProAspAspIleIleGluGluMetArgAlaMetGlyLeuPheGlyLeuSer 54
QY 397 GTCCAGAGAAATATGGTGGCTGCTTCTCAACACCATGACTCAAGACTAGG--- 453
DB 55 IleProGluGluTyrGlyLeuGlyLeuThrMetGluGluGluValArgValGlyPhe 74
QY 454 GAGATCATCAGCATGGATGGGTCCATCATGTGACCTTGGCAGCGCACCCAGGCTATTGGC 513
DB 75 GluLeuGlyTyrThrSerProAlaPheArgSerValIleGlyThrAsnAsnGlyIleGly 94
QY 514 CTCAGGGGATCATCTTGGCTGGCACTGAGGAGCAAGAACCAATACTTGCCTAAACTG 573
DB 95 SerGlnGlyIleIleAlaAspGlyThrAspAspGlnLysLysTyrTrpLeuProArgLeu 114
QY 574 GGTCCCGGGGAGCACATTGCACTTCTGCTCCAGGAGCAGCGCAGTGGGAGCGCATGCA 633
DB 115 AlaSerGlyGlyIleIleAlaSerPheAlaLeuThrGluProAspValGlySerAspAla 134
QY 634 GCCTCAATCCGAGCAGAGCCACACTAAGTGAAGACAAGAGCACTACATCTCTCAATGGC 693
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Db 135 GlyAlaValArgThr-----ThrAlaGluArgAspGlyAspSerfyrilleleAsnGly 152
Qy 694 TCCAAAGTCTGGATTACTTAATGGAGGAGTCCCAATATTTTACTGCTGTGGTTCAGAAAGACT 753
Db 153 ThrLysArgPheIleThrAsnAlaProValAlaGlyValPheThrLeuMetAlaArg--- 171
Qy 754 GAGTCTGTTGATTCGTGATGATCAGTGAAGACAAATACACAGATTCATCATAGTAGAAGA 813
Db 172 -----MetGlyGlySerGlyProSerGlyIleSerAlaPheLeuAlaGluArg 187
Qy 814 GACTTTGGTGGAGTCACTAATGGGAACCCGAGATTAATTAGCATTCGGGGCTCCCAAC 873
Db 188 AspLeuProGlyLeuThrValGlyThrProAspHisLysMetGlyGlnArgGlyThrGln 207
Qy 874 ACTTGTGAAGTCCATTTTGAACACCAAGATACCTGTGGAACACATCTTGGAGAGGTC 933
Db 208 ThrCysAspValTyLeuGluAsnValArgValProAlaThrSerIleIleGlyGlyVal 227
Qy 934 ---GGAGATGGTTTAAGGTGGCCATCAACATCTCAACAGCGCCGGTTCAGCATGGGC 990
Db 228 GluGlyArgGlyPheTyThrAlaMetLysValLeuAsnArgGlyArgLeuHisIleSer 247
Qy 991 AGCGTCTGGTGGCTGCTCAAGAGATTCGTAATGTAATGATGCTGAGTACGCTGCACACA 1050
Db 248 SerValCysAlaGlyThrAlaGluArgProIleGluSerValGlyPheAlaGlySer 267
Qy 1051 AGGAAACAGTTTAAACAGAGGCTCAGTGAATTTGGATTTGATTCAGGAGAAATTTGCAC 1110
Db 268 ArgValGlnPheGlyLysArgIleAlaGluHisGlnMetIleGlnAlaMetLeuAlaAsp 287
Qy 1111 ATGGCTCAGAGGCTTACGTTCATGAGAGATGATGACCTACCTCAGCAGGAGATGCTGCAC 1170
Db 288 MetSerThrGluAlaTyAlaGlyArgCysMetValLeuAspAlaAlaArgAlaPheAsp 307
Qy 1171 CAACCTGGCTTCCCGACTCTCATCGAGCGCCATGTGTGAAGTGTTCAGCTCCGAG 1230
Db 308 GluSerAsnVal---AspIleIleArgLysAlaAlaSerCysLysLeuPheCysSerGlu 326
Qy 1231 GCCCGCTGGAGTGTGTGAGTGAGCGCTGCAGATCTCCGGGGCTGGGCTACACAAAG 1290
Db 327 MetValGlyArgValAlaAspAsnAlaValGlnIleHisGlySerGlyTyMetGln 346
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Db 347 AsnTyProValGluHisPheTyArgAspValArgLeuPheArgLeuTyGluGlyThr 366
Qy 1351 AATGAGATTCCTCGGATGTACATGCC 1377
Db 367 SerGlnIleGlnArgIleIleAla 375

RESULT 13
B87472
acyl-CoA dehydrogenase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87472
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eise, J.; Heidelberg, J.
n, J.; Leub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: B87249; MUID:21173698; PMID:11259647
A:Accession: B87472
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-381 <STO>
A:Cross-references: UNIPROT:Q9A7C6; GB:AB005673; NID:g13423230; PIDN:AAK23774.1; GSPDB:G
C:Genetics:
A:Gene: CCI798
C:Superfamily: acyl-CoA dehydrogenase
Alignment Scores:
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Pred. No.: 3,92e-36 Length: 381
Score: 678.00 Matches: 149
Percent Similarity: 59.13% Conservative: 81
Best Local Similarity: 38.30% Mismatches: 135
Query Match: 15.05% Indels: 24
DB: 7 Gaps: 7

US-09-945-326-1 (1-2452) x B87472 (1-381)
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Db 7 LeuSerAlaLeuLeuAspValIleGlnArgPheValAlaGluArgLeuArgProIleGlu 26
Qy 325 -----ATTGACCGAGGAGGAAATCCAGATGAATCTTGGAGAAATTTGAAGAGCCTA 378
Db 27 GlyLeuValSerGluThrAspGluValProGlySerIleIleGluGluMetLysGlnLeu 46
Qy 379 GCGCTTTTGGGCTGCAAGTCCAGAGATATAGTGGCTGGCTTCTCCAAACCCATG 438
Db 47 GlyLeuPheGlyLeuSerIleProGlySerfyrGlyGlyLeuGlyLeuSerLeuGluGlu 66
Qy 439 TACTCAAGACTAGGGAGATCATCAGCATG-----GATGGTCCATCCTGTGACC 489
Db 67 GluAlaArgVal-----IleValAlaPheCysHisThrAlaProAlaPheArgSerThr 84
Qy 490 CTGGCAGCGCACCGAGCTATTGGCTCAAGGGGATCATCTTGGCTGGCCTGAGGAGCAG 549
Db 85 PheGlyThrAsnValGlyIleGlySerGlnGlyLeuValMetPheGlyAspGluAlaGln 104
Qy 550 AAGCCAAATACTTGTCTAACTGGCTCGGGGAGCAGCATTCGAGCTTCTGCTCAGC 609
Db 105 LysAlaArgTrpLeuProSerIleAlaSerGlyGluThrIleThrAlaPheAlaLeuThr 124
Qy 610 GAGCCAGCCAGTGGGAGCATGCGCTCAATCCGAGCAGAGCCACACATAAGTGAAGAC 669
Db 125 GluAlaGluAlaGlySerAspSerAlaSerValGlnThrArgAlaVal-----ArgAsp 142
Qy 670 AAGAAGCCTACATCTCAATGGCTCCAGGTCTGGATTACTTAATGAGGACTGGCCAA 729
Db 143 GlyAspHisfyrValLeuAsnGlyValLysArgfyrIleThrAsnAlaGlyArgAlaAsn 162
Qy 730 ATTTTACTGTGTTCGAAAGACTGAGTGGTGTGATCTGATGATCAGTCGAAAGACAA 789
Db 163 LeuPheThrValMetAlaArgThrAspProAsnThrLysGlyGlyAla-----Gly 179
Qy 790 ATCAGCAGCTTATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAGAG 849
Db 180 ValSerAlaPheLeuValProAlaAspLeuProGlyLeuSerValGlyLysProGluLys 199
Qy 850 AAATTAGGCATTCGGGGCTCCAACTTGTGAAGTCCATTTGAAACACCAAGATACCT 909
Db 200 LysMetGlyGlnGlnGlyAlaHisIleHisAspValValPheGluAspValArgValPro 219
Qy 910 GTGAAAACATCTCTGGAGAGTGGAGAGTGGTGAAGTGGTGGCTCAAGAGATGATTGAAATG 969
Db 220 ValGluAsnArgLeuGlyAlaGluGlyGlyGlyPheThrValAlaMetArgValLeuAsp 239
Qy 970 AGCGCGGGTTCAGCATGGGAGCGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1029
Db 240 ArgGlyArgValHisIleSerAlaValCysValGlyValAlaGluArgLeuIleAlaAsp 259
Qy 1030 ACTGCTGAGTACCCCTGCACAGGAAACAGTCTTAACAGAGGCTCAGTGAATTTGGATTG 1089
Db 260 CysValAlaTyAlaSerGluArgLysGlnPheGlyGlnProIleAlaSerPheGlnLeu 279
Qy 1090 ATTCAG-----GAGAAATTTGCACTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1134
Db 280 IleGlnAlaMetIleAlaAspSerLysThrGluAlaLeuAlaAlaLysAlaLeuAlaPhe 299
Qy 1135 GAGAGTATGACCTTACCTCAGCAGGAGGATGCTGGACCAACCTGGCTTTCCTCCGACTGCTCC 1194
Db 300 AspThrAlaArgLysArgAspAlaGly-----AlaAsnValThr 312
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QY 847 GATAAATTAGCATTCGGGCTCAACACATTTGTGAAGTCCATTTTGAAACACCAAGATA 906
Db |
QY 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
Db |
QY 907 CCTGTGAAACATCCTTGGAGAGTCGGAGATGGGTTTAAGGTGGCCATGACATCCTC 966
Db |
QY 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
Db |
QY 967 AACAGCGCGCGTTTCAGCATCGGCGAGCGTGGTGGCTGGCTGCTCAAGAGATTGATTGAA 1026
Db |
QY 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
Db |
QY 1027 ATGACTCTGAGTACGCTGCACACAGGAACAGTTTAAAGAGGCTCAGTGAATTTGGA 1086
Db |
QY 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
Db |
QY 1087 TTGATTTCAGGAGAAATTTGACACTGATCGCTCAGAGGCTTACGTCATGGAGAGTATGACC 1146
Db |
QY 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
Db |
QY 1147 TACTCTCACAGCAGGATGCTGGACCACTGGCTTTCCCGACTGCTCCATCGAGGCGAGCC 1206
Db |
QY 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
Db |
QY 1207 ATGGTGAAGGTGTTACGCTCCGAGGCGCTGGCAGTGTGTGAGTGAAGGCGCTGCAGATC 1266
Db |
QY 381 MetValLysValPheSerSerGluAlaAlaTyrGlnCysValSerGluAlaLeuGlnIle 400
Db |
QY 1267 CTGGGGGCTGGCTACACAGGAGTATCCGTACGAGGCGATCTGCTGACACCCGCG 1326
Db |
QY 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
Db |
QY 1327 ATCTCTCTCATCTTCGAGGAACCAATGAGATCTCCGGAGTGATACATCGCCCTGACGGGT 1386
Db |
QY 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
Db |
QY 1387 CTCGAGCATCCCGCGCATCTCTGACTACAGGATCCATCAGCTTAAACAGGCCAAAGTG 1446
Db |
QY 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
Db |
QY 1447 AGCACAGTCATGATACCTTGGCGGAGGCTTCGGGACTCCCTGGCGCCCACTGGGAC 1506
Db |
QY 461 SerThrValMetAspThrValGlyArgLeuArgAspSerLeuGlyArgThrValAsp 480
Db |
QY 1507 CTGGGCTGACGCAACCATGAGTTGTGCACCCAGTCTTGGGACAGTGCACCAACAG 1566
Db |
QY 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
Db |
QY 1567 TTTGAGGAGAACACTACTGCTTTCGGCGGACCGTGGAGACACTGTGCTCCGCTTTGGC 1626
Db |
QY 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuArgPheGly 520
Db |
QY 1627 AAGACCATCATGAGGAGAGCTGTTACTGAAGCGGTGGCCAACTCCTCATCAACCTG 1686
Db |
QY 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
Db |
QY 1687 TATGGCATGACGCGCTGTGTCGGGCGCAGCGCTCCATCGCATTTGGCTCCGCAAC 1746
Db |
QY 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
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QY 1747 CAGCACCAAGAGGTTCTCTTGGCCAAACACCTCTCTGCTGGAAGCTTACTTGCAGATCTC 1806
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QY 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
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QY 1807 TTGAGCTCTCTCAGCTGGACAGATGATGCTCCAGAAAACCTAGATGAGCAGATTAGAAA 1866
Db |
QY 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
Db |
QY 1867 GTCTCCAGCAGATCCTTTGAGAGCGAGCTATATCTGTGCCACCTCTGGGACAGACA 1926
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Db |
QY 1927 TGC 1929
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Db 621 Cys 621
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RESULT 2
ACD9_MOUSE STANDARD; PRT; 625 AA.
AC Q8JZNS; Q8BK76; Q8C0B5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acyl-CoA dehydrogenase family member 9, mitochondrial precursor
DE (SC 1.3.99.-) (ACAD-9).
GN Name=Acad9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojbori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirimi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierzki R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RN Nature 420:563-573 (2002).
[2]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strauss R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Has a dehydrogenase activity on palmitoyl-CoA (C16:0)
CC and stearyl-CoA (C18:0). It is three times more active on
CC palmitoyl-CoA than on stearyl-CoA. Has little activity on
CC octanoyl-CoA (C8:0), butyryl-CoA (C4:0) or isovaleryl-CoA (5:0)
CC (by similarity).
CC -!- COFACTOR: FAD (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AK01820; BAC27565.1; -
CC EMBL; AK075984; BAC36096.1; -
CC EMBL; BC031137; AAH31137.1; -
CC EMBL; BC032213; AAH32213.1; -
CC EMBL; BC033277; AAH33277.1; -
CC PIR; PT0697; PT0697.
CC PIR; PT0721; PT0721.
CC HSSP; P15651; 1JQ1.
CC MGD; MGI:1914272; Acad9.
CC InterPro; IPR006089; Acyl-CoA dh.
CC InterPro; IPR006090; Acyl-CoA dh.C.
CC InterPro; IPR006091; Acyl-CoA dh.M.
CC InterPro; IPR006092; Acyl-CoA dh.N.
CC InterPro; IPR009100; AcylCoA dehyd.NM.
CC InterPro; IPR009075; AcylCoADH_C_like.
CC Pfam; PF00441; Acyl-CoA dh; 1.
CC Pfam; PF02770; Acyl-CoA dh.M; 1.
CC Pfam; PF02771; Acyl-CoA dh.N; 1.
CC PROSITE; PS00072; ACYL_COA_DH_1; 1.
CC PROSITE; PS00073; ACYL_COA_DH_2; 1.
CC PROSITE; PS00074; ACYL_COA_DH_3; 1.
CC TRANSIT ? Mitochondrion (Potential).
CC TRANSIT ? Mitochondrion (Potential).
CC FT CHAIN 1 625 Acyl-CoA dehydrogenase family member 9.
CC FT SITE 430 430 Proton acceptor (By similarity).
CC FT CONFLICT 15 15 A -> G (in Ref. 1; BAC27565).
CC FT CONFLICT 53 53 K -> E (in Ref. 1).
CC FT CONFLICT 163 163 D -> E (in Ref. 1).
CC FT CONFLICT 540 540 I -> V (in Ref. 1; BAC27565).
CC SQ SEQUENCE 625 AA; 68707 MW; 4F06FFBF82F022 CRC64;

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Alignment Scores:

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Pred. No.: 1,21e-168 Length: 625
Score: 2704.00 Matches: 534
Percent Similarity: 91.81% Conservative: 38
Best Local Similarity: 85.71% Mismatches: 47
Query Match: 60.04% Indels: 4
DB: 1 Gaps: 1

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US-09-945-326-1 (1-2452) x AC09_MOUSE (1-625)

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QY 295 TTCTTCACTCAAGAGGTGGACTCCGAAAAATTTGACGAGGAAGGAAAAATCCAGATGAA 354
Db 81 PhePheThrGluGluValAspSerArgLysIleAspGlnGlyLysIleProValAsp 100
QY 355 ACTTTGGAGAAATTTGAAGAGCCTAGGCTTTTGGGCTGCAAGTCCGAGGAAGAAATATGGT 414
Db 101 ThrLeuGluLysLeuLysSerLeuGlyLeuPheGlyIleGlnValProGluGluTyrGly 120
QY 415 GGCTTGGCTTCTCCAAACACCATGTACTCAAGACTAGGGAGATCATCATCATGGATGGG 474
Db 121 GlyLeuGlyLeuSerAsnThrMetTyrAlaArgLeuGlyGlyIleSerLeuAspAla 140
QY 475 TCCATCACTGTGACCTGCGCAGCGCACAGGCTATTGGCTCAAGGGATCATCTGGCT 534
Db 141 SerIleThrValThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleLeuVal 160
QY 535 GGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAACTTGGCTCCGGGGAGCACATTGCA 594
Db 161 GlyAsnAspGluGlnLysAlaLysTyrLeuProLysLeuSerSerGlyGluHisIleAla 180
QY 595 GCCTTCTGCTCAGCGAGCCAGCCAGTGGAGGAGTGCAGCTCAATCCGGAGCAGAGCC 654
Db 181 AlaPheCysLeuThrGluProAlaSerGlySerAspAlaAlaSerIleGlnThrArgAla 200
QY 655 ACATAAGTGAAGACAAAGACACTACATCCTCAATGGCTCCAAAGTCTGGATTACTAAT 714
Db 201 ThrLeuSerGluAspLysLysTyrPheIleLeuAsnGlySerLysValTrpIleThrAsn 220
QY 715 GGAGGACTGCGCAATATTTTACTGTGTGTGCAAGACTGAGTCTGTTGATTCTGATGA 774
Db 221 GlyGlyLeuAlaAsnIlePheThrValPheAlaLysThrGluValValAspSerAspGly 240
QY 775 TCAGTCAAAAGACAAAATCACAGCATTCATAGTAAGAAGAGACTTTGGTGAGTCACTAAT 834
Db 241 SerLysThrAspLysMetThrAlaPheIleValGluArgAspPheGlyGlyIleThrAsn 260
QY 835 GGGAAACCCGAAGATAAATTAGGCATTTCGGGGCTCCAAACACTTGTGAAGTCCATTGTA 894
Db 261 GlyLysProGluAspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGlu 280
QY 895 ACACCAAGATACCTGTGTGAAAACATCTTGGAGAGTTCGGAGATGGTTTAAAGTGGCC 954
Db 281 AsnThrArgValProValGluAsnValLeuGlyGluValGlyGlyLysValAla 300
QY 955 ATGAACATCTCAACAGCGCGCTTCAGCATGGGCGAGTCTGCTGGCTGGCTGCTCAAG 1014
Db 301 MetAsnIleLeuAsnSerGlyArgPheSerMetGlySerAlaValAlaGlyMetLeuLys 320
QY 1015 AGATTGATTGAAATGACTGCTGAGTACGCTCACAAGGAAACAGTTTAAACAGAGGCTC 1074
Db 321 LysLeuIleGluLeuThrAlaGluTyrAlaCysThrArgLysGlnPheAsnArgAsnLeu 340
QY 1075 AGTGAATTTGGATTGATTCAGGAGAAATTTGGACTGATGGCTCAGAGGCTTACGTGATG 1134
Db 341 SerGluPheGlyLeuIleGlnLysPheAlaLeuMetAlaGlnLysAlaTyrValMet 360
QY 1135 GAGAGTATGACCTACTCTCAGCAGCAGGATGTGGACCAACCTGGCTTCCCGACTGCTCC 1194
Db 361 GluSerMetAlaTyrLeuThrSerGlyMetLeuAspGlnProGlyPheProAspCysSer 380
QY 1195 ATCGAGGAGCCCATGGTGAAGGTGTGAGTCTCAGCTCCGAGGCGCTTGGCAGTGTGTGATG 1254
Db 381 IleGluAlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGlu 400
QY 1255 GCGCTCGAGATCTCGGGGCTTGGGCTTGGCTTACACAGGACTATCCGTACAGGCGCATCTG 1314
Db 401 AlaLeuGlnIleLeuGlySerGlyTyrMetLysAspTyrProTyrGluArgMetLeu 420
QY 1315 CTGTACACCCGCTCCTCTCATCTTCAGGAGGAACCAATGAGATCTCCGAGTGTACATC 1374
Db 421 ArgAspAlaArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgLeuPheIle 440

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Qy 1375 GCCTGAGCGGTGTCAGCATGTCGGCGCGCATCTGACTACAGGATCCATGAGCTTTAAA 1434
Db 441 AlalaLeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrSerArgIleLeuGlyLeuLys 460
Qy 1435 CAGGCCAAAGTCAGCACAGTCATGATACCGTTCGGCGGAGGCTTCGGGACTCCCTGGGC 1494
Db 461 SerGlyAsnValThrValMetGluThrIleGlyArgLysLeuArgAspSerLeuGly 480
Qy 1495 CGAACTGTGACCTTGGCGGCTGACAGGCAACCATGAGTGTGACCCCGAGCTTTGGCGAC 1554
Db 481 ArgThrValAspLeuGlyLeuThrGlyAspLeuGlyValValHisProSerLeuGlyAsp 500
Qy 1555 AGTGCCCAACAGTTTGAGAGAACACCTACTCTTCGGCGGAGCGGTGGCCCAACATC 1614
Db 501 SerAlaAsnLysLeuGluGluAsnValHisIleThrPheGlyArgThrValGluThrLeu 520
Qy 1615 CTCGCTTTCGACAGACCATCATGAGGAGCGTGTCTGCGGGCGGCGCTGAGCGGTGGCCCAACATC 1674
Db 521 LeuArgPheGlyLysAsnIleValGluGluGlnLeuValLeuLysArgValAlaAsnIle 540
Qy 1675 CTCATCAACCTGTATGTCATGACGCGCGTGTCTGCGGGCGGCGCTGATCCATCCGCAAT 1734
Db 541 LeuIleAsnLeuThrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIle 560
Qy 1735 GGGCTCCGCAACACGACGACGAGGTCTCTTGGCCCAACCTTCTGCGGTGGAGCTTAC 1794
Db 561 GlyLeuArgAsnHisAspHisGluValLeuLeuAlaAsnMetPheCysValGluAlaTyr 580
Qy 1795 TTGAGATCTCTTACGCTCTCTCAGTGGACAGTATCTCAGACAGTATCTCAGAAACCTAGATGAG 1854
Db 581 PheGlnAsnLeuPheSerLeuSerGlnLeuAspLysAsnAlaProGluAsnLeuAspGlu 600
Qy 1855 CAGATTAAAGAAAGTGTCCACGAGATCTTGGAGAGCGAGCTATATCTGTGCCACCCCT 1914
Db 601 GlnIleLysLysValSerArgGlnIleLeuGluLysArgAlaTyrIleCysAlaHisPro 620
Qy 1915 CTGACAGG 1923
Db 621 LeuAspArg 623
RESULT 3
Q9H9W4 PRELIMINARY; PRT; 498 AA.
ID Q9H9W4
AC Q9H9W4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ12506.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Ohtsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosiiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Iehibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hoshino T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Mueshino K., Yuuki H., Oshima A., Sasaki N., Aotseuka S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
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RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isoqai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
CC -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
EMBL; AK022568; BAB14104.1; -;
DR HSP; Q06319; 1BUC.
DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006089; Acyl-CoA dh.
DR InterPro; IPR006090; Acyl-CoA dh C.
DR InterPro; IPR006091; Acyl-CoA dh M.
DR InterPro; IPR006092; Acyl-CoA dh N.
DR InterPro; IPR009075; AcylCoADH C-like.
DR InterPro; IPR009100; AcylCoA dehyd_NM.
DR InterPro; IPR005829; Sug transporter.
DR Pfam; PF00441; Acyl-CoA dh; 1.
DR Pfam; PF02770; Acyl-CoA dh M; 1.
DR Pfam; PF02771; Acyl-CoA dh N; 1.
DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
KW FAD; Flavoprotein; Oxidoreductase.
SQ SEQUENCE 498 AA; 55083 MW; A57B7121B8FB1310 CRC64;
Alignment Scores:
Pred. No.: 5,25e-157 Length: 498
Score: 2526.00 Matches: 498
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 56.08% Indels: 0
DB: 2 Gaps: 0
US-09-945-326-1 (1-2452) x Q9H9W4 (1-498)
Qy 436 ATGTACTCAAGACTAGGGAGATCATCAGCATGGATGGTCCATCTACTGTGACCTGGCA 495
Db 1 MetTy-SerArgLeuGlyGluIleSerMetAspGlySerIleThrValThrLeuAla 20
Qy 496 GCCCACCAGCTATTCGCTCAAGGGGATCATCTTGGCTGGCAGTGGAGGAGGAGGCC 555
Db 21 AlaHisGlnAlaIleGlyLeuLysGlyIleLeuAlaGlyThrGluGluGlnLysAla 40
Qy 556 AATACTTGCCTAACTGGCGTCCGGGAGACATTCGACGCTTCTGCTCAGCGAGCCA 615
Db 41 LysTyLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeuThrGluPro 60
Qy 616 GCCAGTGGGAGCGATGCAGCTCAATCCGAGCAGAGCCACACTTAAGTGAAGACAAGAAG 675
Db 61 AlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGluAspLysAla 80
Qy 676 CACTACATCTCTCAATGGCTCCAAGGTCTGAGTACTTAATGAGGAGCTGGCCCAATATTTT 735
Db 81 HisTyIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAlaAsnIlePhe 100
Qy 736 ACTGTGTTTCCAAGACTAGGGTCTGTGATTCGTGATTCGTGATTCGTGATTCGTGATTC 795
Db 101 ThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAspLysIleThr 120
Qy 796 GCATTTCATAGTAGAAGAGACTTTTGGTGGAGTCACTAATGGGAAACCCGGAAGATAAATTA 855
Db 121 AlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGluAspLysLeu 140
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QY 856 GCATTTCGGGGCTCAACACTTGTGAGTCCATTTTGAAACACCAAGATACCTGTGGAA 915
Db 141 GylleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIleProValGlu 160
QY 916 AACATCCTTGGAGAGGTGGAGATGGTTAAGTGGCCATGAACATCCTCAACAGCGGC 975
Db 161 AsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeuAsnSerGly 180
QY 976 CGGTTTCAGATGGGCGAGCGTGTGGCTGGCTGCTCAAGAGATTGATTGAATCAGTCT 1035
Db 181 ArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGluMetThrAla 200
QY 1036 GAGTACGCTGCACAAAGAAACAGTTTAAACAAGAGCTCACTGAATTTGGATTGATTCAG 1095
Db 201 GluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGlyLeuIleGln 220
QY 1096 GAGAAATTTGCATGATGGCTCAGAGCTTACGTATCATGGAGATATGACCTACCTCACA 1155
Db 221 GluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThrTyrLeuThr 240
QY 1156 GCAGGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCGCATGCTGAAG 1215
Db 241 AlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaMetValLys 260
QY 1216 GTGTTTCAGCTCCGAGCGGCTGGAGTGTGAGTGAGCGGCTGCAGATCCTCGGGGGC 1275
Db 261 ValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIleLeuGlyGly 280
QY 1276 TTGGGCTACACAAGGGACTATCCGTACGAGCGCATATCGGTGACACCCCATCCTCCTC 1335
Db 281 LeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArgIleLeuLeu 300
QY 1336 ATCTTCAGGGAACCAATGAGATTCTCCGGATGTACATCCGCTCGCGGTCTGCAGCAT 1395
Db 301 IlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGlyLeuGlnHis 320
QY 1396 GCCGGCGCATCTGACTACAGATCCATGAGCTTAAACAGGCCAAAGTGAACACAGTC 1455
Db 321 AlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysValSerThrVal 340
QY 1456 ATGATACCGTTGGCGGAGCTTCGGGACTCCCTGGCGCGCACTGTGGACCTGGGGCTG 1515
Db 341 MetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAspLeuGlyLeu 360
QY 1516 ACAGGCAACCATGAGTTGTGCCACCCAGTCTTCGGGACAGTCCCAACAGTTTGGAGAG 1575
Db 361 ThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLysPheGluGlu 380
QY 1576 AACACCTACTGCTTCGGCGGACCGTGGAGACACTGCTGCTCGCTTGGCAAGACCATC 1635
Db 381 AsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGlyLysThrIle 400
QY 1636 ATGAGGAGCAGCTGGTACTGAAGCGGCTGGCCAAACATCTCTCACTCACTGTATGTCATG 1695
Db 401 MetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeuTyrGlyMet 420
QY 1696 ACGCGCTGTGTCGGCGGCGCACCGCTCATCCGATTCGCTGGTCCGCAACCAACACACAC 1755
Db 421 ThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsnHisAspHis 440
QY 1756 GAGGTTCTCTTGGCCCAACCTTCTCGTGGAAGCTTACTTGAGATCTCTTCAGCTTC 1815
Db 441 GluValLeuLeuAlaAsnThrPheCysValGluLysValGluLysLeuGlnAsnLeuPheSerLeu 460
QY 1816 TCTCAGCTGGAAGATGTCTCCAGAAAACTAGATGAGCAGATTAAAGAAAGTGTCCACAG 1875
Db 461 SerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLysValSerGln 480
QY 1876 CAGATCCTTGAAGGAGCGCTTATATCTGTGCCACCTCTGTGACGAGCAGCATGCG 1929
Db 481 GlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThrCys 498
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RESULT 4

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Q6DDF2
ID Q6DDF2 PRELIMINARY; PRT; 622 AA.
AC Q6DDF2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Acad9-prov protein.
GN Name-acad9-prov;
OS Xenopus laevis (African clawed frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Anura; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Schmutz J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
DR EMBL; BC077618; AAH77618.1; -
DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006089; Acyl-CoA dh.
DR InterPro; IPR006090; Acyl-CoA dh.
DR InterPro; IPR006091; Acyl-CoA dh.
DR InterPro; IPR006092; Acyl-CoA dh.
DR InterPro; IPR009075; AcylCoADH C-like.
DR InterPro; IPR009100; AcylCoA dehyd_NM.
DR Pfam; PF00441; Acyl-CoA dh; 1.
DR Pfam; PF02770; Acyl-CoA dh M; 1.
DR Pfam; PF02771; Acyl-CoA dh N; 1.
DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW FAD; Flavoprotein; Oxidoreductase.
SQ SEQUENCE 622 AA; 68429 MW; 1BA5F489FF08A9C9 CRC64;
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Alignment Scores:

Pred. No.: 4, 93e-147 Length: 622

Score: 2374.50 Matches: 453

Percent Similarity: 85.41% Conservative: 74
Best Local Similarity: 73.42% Mismatches: 87
Query Match: 52.72% Indels: 3
DB: 2 Gaps: 1

US-09-945-326-1 (1-2452) x Q6DDF2 (1-622)

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Db 8 CysGly-----ArgAlaAAserLeuThrArgValTrpAlaGlyProAlaGlyPro 24

Qy 136 ACCCGAACCGCGGCTACTCGGCACACCGCGCTGTACGAGCTTTCGCCAAGAGCTT 195
Db 25 GluLeuPheProArgSerPheThrCysSerProHisArgLeuAlaTrpAlaLysGluLeu 44

Qy 196 TTCCTAGCGAAATCAAGAGAAAGAGTTTCCCATTTCCAGAAAGTTAGCCAAAGTAA 255
Db 45 PheLeuGlySerIleArgLysAspGluValPheProTyrProGluIleSerLysGluLeu 64

Qy 256 CTTAATGAAATCAATCAGTTCTTGGGACCGCTGGAAATAATCTTCACTGAAGAGTGGAC 315
Db 65 LeuGluGluIleAsnGlnPheValAlaProValGluLysPhePheAsnGluGluValAsp 84

Qy 316 TCCCGAAATTTGACAGGAGGAAATCCACATGAAATTTGGAGAAATTTGAAGAGC 375
Db 85 SerLysLeuIleAspGlnThrAlaLysIleProGluThrLeuAspGlyLeuLysAsn 104

Qy 376 CTAGGGCTTTTGGGCTCAAGTCCAGAGAAATATGGTGGCTTGGGCTTCTCCAAACACC 435
Db 105 LeuGlyLeuPheGlyMetGlnIleProGluGluTyrGlyGlyLeuGlyLeuSerAsnThr 124

Qy 436 ATGTACTCAAGACTAGGGAGATCATCAGCATGGATGGTCCATCACTGTGACCTGGCA 495
Db 125 MetTyrAlaArgLeuGlyGluIleSerLeuAspGlyAlaIleAlaValThrLeuAla 144

Qy 496 GCGCACAGGCTATTGGCTCAAGGAGATCATCTTGGCTGGCATGAGGACAGAAAGCC 555
Db 145 AlaHisGlnAlaIleGlyLeuLysGlyIleLeuIleAlaGlyAsnAspGluGlnLysAla 164

Qy 556 AATACTTGTCTAACTGGGCTCGGGGAGCACATTCAGCTTCTCCCTCAGCGAGCCA 615
Db 165 LysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaPheCysLeuThrGluPro 184

Qy 616 GCCAGTGGGAGCGATGCGAGCTCAATCCGAGCAGAGCCACACTAAGTGAAGACAAGAAG 675
Db 185 GlySerGlySerAspAlaAlaSerIleGlnSerArgAlaThrLeuThrProAspGlyLys 204

Qy 676 CACTACATCTCAATGGCTCAAGGCTCGATTAATTAATGAGGACTGGCCCAATATTTT 735
Db 205 HisPheLeuLeuAsnGlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAspIlePhe 224

Qy 736 ACTGTGTTCCAAAGACTGAGGCTGGTGTGATCTCATGATCAGTGAAGACAAATCACA 795
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Qy 796 GCATTCATAGTAAAGAGACTTTGGTGGAGTCACTAATGGAAACCCGAGATATAATTA 855
Db 245 AlaPheIleValGluArgAlaPheGlyValThrHisGlyLysProGluAspLysLeu 264

Qy 856 GGCATTCGGGGCTCCAACACTTGTGAAGTCCATTTTGAACCAACCAAGATACCTGTGAA 915
Db 265 GlyIleArgGlySerAsnThrCysGluLeuHisPheGluAsnThrLysValProValGlu 284

Qy 916 AACATCTCTGGAGAGTCCGAGATGGGTTTAAAGTGGCCATGAACATCTCAACAGCGGC 975
Db 285 AsnValIleGlyGluValGlyGlyPheLysValAlaMetAsnIleLeuAsnSerGly 304

Qy 976 CGGTTACAGCATGGGACGCTGCTGGCTGGCTGCTCAAGAGATTGATTGAATCACTGCT 1035
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Qy 1036 GAGTACCGCTTGACAAAGAAACAGTTTAAACAGAGGCTCAGTGAATTTGGATTGATTCAG 1095

Db 325 GluTyrAlaCysThrArgLysGlnPheAsnLysLysLeuSerAspPheGlnLeuIleGln 344
Qy 1096 GAGAAATTTGCACATGATGGCTCAGAAAGCTTATCATGAGAGATGATGACCTACTCACA 1155
Db 345 GluLysPheAlaLeuMetAlaGlnLysAlaPheValMetGluSerMetAlaTyrLeuThr 364

Qy 1156 GCAGGATGCTGAGCAACCACTGGCTTCCGACTGCTCCATCGAGGAGCCATGGTGAAG 1215
Db 365 AlaGlyMetMetAspArgProGlyLeuProAspCysSerValGluAlaAlaMetValLys 384

Qy 1216 GTGTTCAGCTCCGAGCGCGCTGCGAGTGTGTAGTCAGGCGCTGCAGATCCTCGGGGGC 1275
Db 385 ValPheSerSerGluGlyAlaTrpLeuCysValSerGluAlaLeuGlnIleLeuGlyGly 404

Qy 1276 TTGGGCTACACAAGGGACTATCCGTACGAGCGCATCTGCGTGCACCCCGCATCTCTCTC 1335
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Qy 1336 ATCTTCAGGGAACCAATGAGATTCTCCGATGTACATCGCCCTGAGCGGTCTCAGCAT 1395
Db 425 IlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGlyMetGlnHis 444

Qy 1396 GCGGCGCGCATCTGACTACAGATCCATGAGCTTAAACAGGCCAAAGTCGACGACAGTC 1455
Db 445 AlaGlyLysIleLeuThrGlyLysIleLysGluMetLysLysGlyAsnValGlyValAla 464

Qy 1456 ATGATATACCTTGGCGGAGGCTTCCGGACTCCCTGGGCGGAACTGTGGACCTGGGCTG 1515
Db 465 MetGluLeuPhePheLysLysLeuArgAspSerMetGlyArgAsnValAsnLeuGlyLeu 484

Qy 1516 ACAGGCAACCATGAGTTGTGCAACCCAGTCTTCGCGGACAGTGCACCAACAGTTTGAGG 1575
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Qy 1576 AACACCTTACTGCTCGCGCGAGCGTGGAGACACTGCTGCTCGCTTGGCAAGACCATC 1635
Db 505 AsnValTyrTyrPheGlyThrValGluSerLeuLeuTyrArgPheGlyLysThrIle 524

Qy 1636 ATGAGAGAGCAGCTGTGACTGAAGCGGCTGGCAACACTCTCATCAACCTGTATGGCATG 1695
Db 525 ValGluGluGlnLeuAlaLeuLysArgValAlaAspValIleIleAsnLeuTyrAlaMet 544

Qy 1696 ACGCCGCTGCTGTGCGGGCGCAGCGCTCCATCGCATTTGGGCTCCGCAACCCAGCAC 1755
Db 545 ThrAlaValIleSerArgAlaSerArgSerIleSerValGlyLeuProAsnHisAspHis 564

Qy 1756 GAGTCTCTTGGCCACACCTTCTGCTGCTGAGCTTACTTGCAGATCTCTTCAGGCTC 1815
Db 565 AspValLeuLeuAlaAsnMetPheCysSerGluValTyrPheLysAsnAsnTyrThrLeu 584

Qy 1816 TCTCAGCTGACCAAGTATGCTCCAGAAACCTAGATGAGCAGATTAAGAAGTGTCCCAG 1875
Db 585 AlaGlnLeuGlyLysHisSerProGluAsnGlnAspAspSerIleArgLysIleAlaGly 604

Qy 1876 CAGATCTCTGAGAGCGGAGCTATATCTGTGCCACCCCTCTCGAGCAGACA 1926
Db 605 HisIleLeuGluLysArgGlyTyrThrCysSerHisProLeuAspArgThr 621

RESULT 5
Q9BUX5 PRELIMINARY; PRT; 343 AA.
AC Q9BUX5; AC Q9BUX5; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ACAD9 protein (Fragment).
GN Name=ACAD9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2].
RC SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001817; AAH01817.2; --
DR HSSP; P15651; 1701.
DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR GO; GO:0006149; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006089; Acyl-CoA dh.
DR InterPro; IPR006090; Acyl-CoA dh C.
DR InterPro; IPR009075; AcylCoADH_C-like.
DR InterPro; IPR005829; Sug transporter.
DR Pfam; PF00441; Acyl-CoA dh; 1.
DR PROSITE; PS00073; ACYL COA DH 2; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 343 AA; 38569 MW; 10E1781937745C00 CRC64;
Alignment Scores:
Pred. No.: 1.9e-105 Length: 343
Score: 1739.00 Matches: 343
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 38.61% Indels: 0
DB: 2 Gaps: 0
US-09-945-326-1 (1-2452) x Q9BUX5 (1-343)
QY 901 AAGATACCTGTGAAACATCTTGGAGAGGTGGAGATGGTTAAGTGGCCATGAC 960
Db 1 LysileProValGluAsnileLeuGlygluValGlyAspGlyPheLysValAlaMetAsn 20
QY 961 ATCTCAACAGCGCCGGTTCAGCATGGCGAGGGTGTGGCTGGCTGCTCAAGAGATG 1020
Db 21 IleLeuAsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeu 40
QY 1021 ATTGAATAGTCTGAGTAGCTGCTGCAAGGAACAGTTTAAAGAGGCTCAGTGAA 1080
Db 41 IleGluMetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGlu 60
QY 1081 TTTGGATTGATTGAGGAAATTTGCACTCATGGCTCAGAGGCTTACGTCATGGAGACT 1140
Db 61 PheGlyLeuileGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSer 80
QY 1141 ATGACTTACTCAGCAGGAGATGCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAG 1200
Db 81 MetThrTyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerileGlu 100
QY 1201 GCAGCCATGGTAGGTGTTCAGCTCCGAGCGCCCTGGCAGTGTGTGAGTAGGCGCTG 1260

Db 101 AlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeu 120
QY 1261 CAGATCCTCGGGGGCTTGGCTACACAAGGAGACTATCCGTACGAGCGCATATCGGTGAC 1320
Db 121 GlnileLeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgilleLeuArgasp 140
QY 1321 ACCGGCATCCTCCTCATCTTCGAGGGAAACAATGAGATTCCTCCGATGTACATCGCCCTG 1380
Db 141 ThrArgileLeuLeuilePheGluGlyThrAsnGluileLeuArgMetTyrilleAlaLeu 160
QY 1381 ACCGGCTCGCAGCATCGCGCCGCTCCTGACTACACAGATCCATGCTTAACAGGCC 1440
Db 161 ThrGlyLeuGlnHisAlaGlyArgilleLeuThrArgilleHisGluLeuLysGlnAla 180
QY 1441 AAGTGAAGCAGCTCATGATACCTTGGCCGAGGCTTCGGGACTCCCTGGGCCCAACT 1500
Db 181 LysValSerThrValMetAspThrValGlyArgArgLeuArgaspSerLeuGlyArgThr 200
QY 1501 GTGAGACTCGGGCTGACAGGCAACCATGAGTGTGTGCACCCAGTCTTTCGGGACAGTGCC 1560
Db 201 ValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAla 220
QY 1561 AACCAAGTTTGAGGAGAACACCTACTCTCGGCCGCGACCGTGGAGACACTGTGCTCCGC 1620
Db 221 AsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArg 240
QY 1621 TTTGGCAAGCACCATCATGAGGAGCAGCTGGTACTGAAGCGGTGCCCAACATCTCATC 1680
Db 241 PheGlyLysThrileMetGluGluGlnLeuValLeuLysArgValAlaAsnileLeuile 260
QY 1681 AACCTGTATGGATGACGCGCTGCTCGCGGCGCAGCGCTCCATCCGATGGGCTC 1740
Db 261 AsnLeuTyrGlyWetThrAlaValLeuSerArgAlaSerArgSerileArgileGlyLeu 280
QY 1741 CGCAACACGACACACAGAGTTCTTTGGCCAAACACCTTCTGGCTTGAAGCTTACTTGCAG 1800
Db 281 ArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGln 300
QY 1801 AATCTTTCAGCTCTCTCAGCTGAGCAAGATGTGTCCAGAAAACCTAGATGACAGATT 1860
Db 301 AsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnile 320
QY 1861 AAGAAAGTCTCCAGCAGATCTTGAAGAGCGAGCTATATCTGTGCCACCTCTGGAC 1920
Db 321 LysLysValSerGlnGlnileLeuGluLysArgAlaTyrileCysAlaHisProLeuAsp 340
QY 1921 AGGACATGC 1929
Db 341 ArgThrCys 343
RESULT 6
ACDV_RAT ID ACDV_RAT STANDARD; PRT; 655 AA.
AC P45953;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE precursor (EC 1.3.99.-) (VICAD).
GN Name=Acadv1; Synonyms=Vlcad;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=94308174; PubMed=8034667;
RA Aoyama T., Ueno I., Kamijo T., Hashimoto T.;
RT "Rat very-long-chain acyl-CoA dehydrogenase, a novel mitochondrial
RT acyl-CoA dehydrogenase gene product, is a rate-limiting enzyme in
RT long-chain fatty acid beta-oxidation system. cDNA and deduced amino

RT acid sequence and distinct specificities of the cDNA-expressed protein." J. Biol. Chem. 269:19088-19094(1994).

CC -1- FUNCTION: Active toward esters of long-chain and very-long chain fatty acids such as palmitoyl-CoA and stearoyl-CoA.

CC -1- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced ETF.

CC -1- COFACTOR: FAD.

CC -1- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first step.

CC -1- SUBUNIT: Homodimer.

CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

CC -1- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases of different substrate specificities are present in mammalian tissues.

CC -1- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.

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DR EMBL; D30647; BAA06331.1; -.

DR PIR; A54872; A54872.

DR HSP; O06319; 1BUC.

DR RGD; 2014; Acadvl

DR InterPro; IPR006089; Acyl-CoA dh.

DR InterPro; IPR006090; Acyl-CoA dh C.

DR InterPro; IPR006091; Acyl-CoA dh N.

DR InterPro; IPR006092; Acyl-CoA dh N.

DR InterPro; IPR009100; AcylCoA dehyd NM.

DR InterPro; IPR009075; AcylCoA dh C-like.

DR Pfam; PF00441; Acyl-CoA dh; 1.

DR Pfam; PF02770; Acyl-CoA dh M; 1.

DR Pfam; PF02771; Acyl-CoA dh N; 1.

DR PROSITE; PS00072; ACYL COA DH 1; 1.

DR PROSITE; PS00073; ACYL COA DH 2; 1.

KW Direct protein sequencing; FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion; Oxidoreductase; Transit peptide.

FT TRANSIT 1 40 Mitochondrion.

FT CHAIN 41 655 Acyl-CoA dehydrogenase, very-long-chain specific.

FT DOMAIN 41 482 Catalytic.

SQ SEQUENCE 655 AA; 70749 MW; E808DEB0E4595D7 CRC64;

Alignment Scores:

Pred. No.:	8.19e-81	Length:	655
Score:	1365.00	Matches:	303
Percent Similarity:	62.77%	Conservative:	110
Best Local Similarity:	46.05%	Mismatches:	202
Query Match:	30.31%	Indels:	43
DB:	1	Gaps:	13

US-09-945-326-1 (1-2452) x ACVD_RAT (1-655)

QY 30 GGGAGACTGAGCTGAGCTGGGG---ACATCGGGCAGCATGAGCGGTGGCGGCTCTT 86

Db 11 GlyArgGlnLeuLeuArgLeuGlyAlaArgSerSerArgSerAlaAlaLeuGlnGln 30

QY 87 CTGCGCCACACCGCTGCGGCTCGTCCCTGCGGGGTCTGTGCTCTACCGCGAACCG 146

Db 31 Pro-ArgProThrSerAlaGlnArg-----LeuTyAlaSerGluAlaThrG 46

QY 147 GCGGCTACTGCGC-----ACGAGCCCGCTGT 173

Db 46 nAlaValLeuGluLeuProGluThrLeuSerSerAspAlaSerThrArgGluLeuProAl 66

QY 174 ACAGCT-----TTCCCAAGAGCTTTTCTTCTAGGCAAAATCAGAGAAAGA 221

Db 66 aArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlnLeuThrThrAspG 86

QY 222 AGTTTTCCCATTTCCAGAAAGTTAGCCAAAGATGAACCTTAATGAA-----AT 266

Db 86 nValPheProTyProSerVal-----LeuAsnGluGlyGlnThrGlnPheLe 102

QY 267 CAATCAAGTTCTTGGGACCCGTGGAAAAAATCTTCACTGAAGAGGTGGACTCCCGAAAAAT 326

Db 102 uLysGluLeuValGlyProValAlaArgPhePheGluGluValAsnAspProAlaLys 122

QY 327 TGACCAAGGAGGAAAAATCCAGATCAAACTTTGGAGAAATTCGAAGAGCTTAGCGCTTTT 386

Db 122 nAspSerLeuGluLysValGluGluAspThrLeuGlnGlyLeuLysGluLeuGlyAlaPh 142

QY 387 TGGGCTGCAAGTCCCAAGAAATATGTTGGCTTCTTCCAAACACCATGTTACTCAAG 446

Db 142 eGlyLeuGlnValProSerGluLeuGlyLeuGlyLeuSerAsnThrGlnTyAlaAr 162

QY 447 ACTAGGGGAGATCATCAGCATG---GATGGTCCATCATCTGTGACCTGGCAGCGCACCA 503

Db 162 GluAlaGluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisG 182

QY 504 GGTATTGGCTCAAGGGGATCATCTTGGCTGCTGAGGACGAGAGCAGAAAGCCAAATACTT 563

Db 182 nSerIleGlyPheLysGlyLeuLeuTyThrGlyThrLysAlaGlnLysGluLysTyLe 202

QY 564 GCCTAAACTGGCTCCGGGAGCACATTCAGCCTTCTGCCTCACGGAGCCAGCCAGTGG 623

Db 202 uProArgValAlaSerGlyGlnAlaLeuAlaPheCysLeuThrGluProSerSerG 222

QY 624 GAGCGATGAGCTCAATCCGAGCAGACGACACACTAAGTGAAGACAGACAGACACTACAT 683

Db 222 ySerAspValAlaSerIleArgSerSerAlaValProSerProCysGlyLysTyThr 242

QY 684 CCTCAATGGCTCAAGGCTCTGGATTACTAATGAGGACTGGCCAAATATTTTACTGTGT 743

Db 242 rLeuAsnGlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAspIlePheThrValPh 262

QY 744 TGCAAAAGACTGAGTCTGTTGAT---TCTGATGATCAGTGAAGACAAAATCAAGCAT 800

Db 262 eAlaLysThrProIleLysAspAlaAlaThrGlyAlaValLysGluLysIleThrAlaPh 282

QY 801 CATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAGAGATAAATAGGCAT 860

Db 282 eValValGluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGly 302

QY 861 TCGGGCTCCAAACACTTGTGAAGTCCATTTTGAACAACACCAAGATACCTGTGAAAACAT 920

Db 302 eLysAlaSerAsnThrSerGluValTyThrPheAspGlyValLysValProAlaGluAsnVa 322

QY 921 CCTTGGAGAGTGGGATGGGTTTAAGGTGGCCATGAACATCCTCAACAGCGCGCGTT 980

Db 322 lLeuGlyGluValGlyAspGlyPheLysValAlaValAsnIleLeuAsnAsnGlyArgPh 342

QY 981 CAGCATGGCAGCGTCTGGCTGGCTGCTCAAGAGATTGATTGAATGACTGCTGAGTA 1040

Db 342 eGlyMetAlaAlaThrLeuAlaGlyThrMetLysAlaIleIleAlaLysAlaValAspHi 362

QY 1041 CGCTCCACAAGAAACAGTTTAAACAAGAGGCTCAGTGAATTTGGATTGATTTCAGAGAA 1100

Db 362 sAlaThrAsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGlu 382

QY 1101 ATTTGCACTGATGGCTCAGAAGGCTTACGTCATGGAGAGTATGACCTACTCATCAGCAGG 1160

Db 382 sLeuAlaArgMetAlaIleLeuGlnTyThrGluSerMetAlaTyMetLeuSerAl 402

QY 1161 GATGCTGGAACCACTGGCTTTCCCGACTGCTCCATCGAGGCGGCGCATGGTGAAGTGT 1220

Db 402 aAsnMetAspGln---GlyPheLysAspPheGlnIleGluAlaAlaIleSerLysIlePh 421

QY 1221 CAGCTCCGAGGCGCTGGCAGTGTGTGAGTGCAGGCGCTGCAGATCCTCGGGGCTTGGG 1280

Db 421 eGlySerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGlyMetG 441

QY 508 ATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAGCCAAATACCTTGCT 567
 Db 189 IleglyPheLySgLyIleLeuLeuPheGlyAsnProGlnGlnLySgLyLeuTyLeuPro 208
 QY 568 AAATCGCTCCGGGGAGCATTGCGCTTCTGCTCCCTCAGGAGCCAGCCAGTGGGAGC 627
 Db 209 LysLeuAlaThrGlyGluAsnIleAlaAlaPheCysLeuThrGluProAlaSerGlySer 228
 QY 628 GATCAGCCTCAATCCGAGCAGAGCCACACTAAGTGAAGACAAGAAGCACTACATCCTC 687
 Db 229 AspAlaAlaSerIleLeuThrAlaValArgSerProCysGlyGlnTyTyThrMet 248
 QY 688 AATGGCTCCAAAGTCTGATTAATGAGGAGCTGGCCAAATATTTACTGTGTTGCA 747
 Db 249 AsnGlySerLySgLyIlePheLeuAlaGlyThrAlaGluIlePheThrValPheAla 268
 QY 748 AAGACTGAGTGGTGTAT--TCTGATGATCAGTGAAGACAAGCAAAATCACAGCATTCATA 804
 Db 269 LysThrProValLySgLyPheGluMetLySgLyIleThrAlaPheIle 288
 QY 805 GTAGAAAGAGACTTTGTGGAGTCACTAATGGGAACCCGGAAGATAAATAGGCAATCGG 864
 Db 289 ValGluArgSerPheGlyGlyValSerSerGlyProProGluLySgLyMetGlyIleLyS 308
 QY 865 GGCTCCAACTTGTGAAGTCCATTTGAAACACCAAGATACCTGTGGAAACATCCTT 924
 Db 309 AlaSerAsnThrAlaGluValTyPheGluAsnValArgValProAlaAspCysValLeu 328
 QY 925 GGAGAGCTCGAGATGGTGTAAAGTGGCCATGAACATCTCCACAGCGCCGCTTCAGC 984
 Db 329 GlyGluValGlyGlyPheLySgLyAlaMetAsnIleLeuAsnGlnGlyArgPheGly 348
 QY 985 ATGGGCAAGCTGGTGGCTCTCAAGAGATGTGATGAATGACTGTGAGTACGCC 1044
 Db 349 MetAlaAlaAlaLeuSerGlyThrMetLySgLyIleThrLySgLyAlaValAspIleAla 368
 QY 1045 TGCAAGAGAAACAGTTTAAACAGAGGCTCAGTGAATTTGGATGATTCAGGAGAAATTT 1104
 Db 369 AlaAsnArgThrGlnPheGlyAsnLySgLyIleHisAsnTyTyGlyAlaIleGlnGluLyMet 388
 QY 1105 GCATGTGCTCAGAGGCTTAGCTCATGAGAGATGATGATCCTACCTCAGCAGAGGATG 1164
 Db 389 AlaArgMetAlaMetLeuGlnTyTyValThrGluSerMetAlaTyMetValSerGlyAsn 408
 QY 1165 CTGACCAACCTGCTTCCCGCTCTCCATCAGGAGCAGCATGGTGAAGCTGTCAGC 1224
 Db 409 MetAspSer---GlyAlaThrGluPheGlnIleGluAlaIleSerLySgLyIlePheAla 427
 QY 1225 TCCGAGCCGCTGGCAGTGTGAGTGAGGCGCTGAGAGCTCCTCGGGGGCTTGGGCTAC 1284
 Db 428 SerGluAlaAlaTrpLeuValThrAspGluCysIleGlnValMetGlyGlyMetGlyPhe 447
 QY 1285 ACAGGCACTATCCGTAGGCGCATCTGGTGACACCCGATCCTCCTCATCTTCGAG 1344
 Db 448 MetLySgLyAlaGlyValGluArgValLeuArgAspLeuArgIlePheArgIlePheGlu 467
 QY 1345 GGAACCAATGAGTTCTCCGATGTACATCCCTCGAGCTGCGAGCATCCGCGCCG 1404
 Db 468 GlyThrAsnAspIleLeuArgLeuPheValAlaLeuAsnGlyPheGlnAsnAlaGlyAsn 487
 QY 1405 ATCTGCTACTACAGGATTCATGACTTAACAG-----GCCAAGGTGAGCAGCATG 1458
 Db 488 GlnLeuLySgLySerLeuGlnLySgLyAlaLeuLySgLyAsnProLeuGlyAsnAlaGlyMetLeuAla 507
 QY 1459 GATACCTTGGCGGAGCTTCGGGACTCCTTGGCGGCACTGGACCTGGGCTGCA 1518
 Db 508 GlyGluIleThrLySgLyAlaLySgLyArgAlaGly-----LeuGlySerGlyLeuThr 525
 QY 1519 GGCAACCATGAGTTGTGACCCCGCTTTCGGGACAGTCCCAACAGTTTGGAGGAGAAC 1578
 Db 526 ---LeuGlnGlyThrValHisProGluLeuAsnHisSerGlyGluLeuThrValLySgLyAla 544
 QY 1579 ACCTACTGCTTTCGGCGGAGCGGTGGAGACACTGTGCTCGCTTTCGCAAGACCATCATG 1638

Db 545 IleGluGlnPheGlyAlaValIleGluLeuLeuLeuLySgLyIleIle 564
 QY 1639 GAGGAGCAGCTGGTACTGAAGCGGTGCCCAACATCTCATCAACCTGTATGGTACG 1698
 Db 565 AspGluGlnPheValLeuLySgLyArgValAlaAspCysAlaIleAspLeuTyAlaMetVal 584
 QY 1699 GCGGTGTGTGGCGGCGCAGCCGCTCATCGCATGGCTCCGCAACACGACGACGAG 1758
 Db 585 ValValLeuSerArgAlaSerArgSerLeuAsnGlnGlyHisSerSerAlaGlnHisGlu 604
 QY 1759 GTTCTCTTGGCCACACCTTCTCGTGGAGCTTACTTGCAGATCTCTTCCAGCTCTCT 1818
 Db 605 LysMetLeuCysGluThrTyPheThrGluAlaHisGluArgValMetGlnAspIleLyS 624
 QY 1819 CAGCTGCACCAAGTATGCTCCAGAAACCTAGATGAGCAGATTAAGAAGTGTCTCCAGCAG 1878
 Db 625 PheLeuArgSerGlyThrSerLySgLyGlnThrPheLySgLyAsnLeuArgAlaIleSerAlaAla 644
 QY 1879 ATCTTGAAGAGCGAGCTATATCTGTGCCACCTCTG 1917
 Db 645 ValValGluAsnGlyGlyValValAlaProHisProLeu 657
 RESULT 8
 ACIDV_MOUSE STANDARD; PRT; 656 AA.
 ID ACIDV_MOUSE STANDARD; PRT; 656 AA.
 AC P50544; O35289; O55133;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial precursor (EC 1.3.99.-) (VLCAD) (MVLCAD).
 GN Name=Acadvl; Synonyms=Vlcad;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=Blood;
 RA Andresen B.S., Lund H., Broes P., Gregersen N.;
 RT "Mouse very-long-chain acyl-CoA dehydrogenase (VLCAD) gene.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Heart;
 RA Andresen B., Lund H., Broes P., Corydon M., Gregersen N.;
 RT "Cloning and characterization of mouse very-long-chain acyl-CoA dehydrogenase.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Czech II; TISSUE=Mammary gland;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Caplenton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[4]
SEQUENCE OF 84-656 FROM N.A.
STRAIN=ICR; TISSUE=Liver;
MEDLINE=98345418; PubMed=9680378;
Cox K.B., Johnson K.R., Wood P.A.;
"Chromosomal locations of the mouse fatty acid oxidation genes Cpt1a, Cpt1b, Cpt2, Acadvl, and metabolically related Crat gene."; Mamm. Genome 9:608-610(1998).
[5]
SEQUENCE OF 339-656 FROM N.A.
Rao G., Krimer D., Krasikov T., Austin C., Skoultschi A.I.; Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Active toward esters of long-chain and very-long chain fatty acids such as palmitoyl-CoA and stearoyl-CoA.
-1- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced ETF.
-1- PATHWAY: FAD.
-1- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first step.
-1- SUBUNIT: Homodimer (By similarity).
-1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
-1- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases of different substrate specificities are present in mammalian tissues.
-1- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.

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EMBL; Y11770; CAA72435.1; -.
DR EMBL; Z71189; CAA94919.2; -.
DR EMBL; BC026559; AAH26559.1; -.
DR EMBL; AF017176; AAC31642.1; -.
DR EMBL; U41497; AAA85185.1; -.
DR HSSP; O6319; 1BUC.
DR SWISS-2DPAGE; P50544; MOUSE.
DR MGD; MGI:1895149; Acadvl.
DR InterPro; IPR006089; Acyl-CoA dh.
DR InterPro; IPR006090; Acyl-CoA dh C.
DR InterPro; IPR006091; Acyl-CoA dh M.
DR InterPro; IPR006092; Acyl-CoA dh N.
DR InterPro; IPR009100; AcylCoA dehyd NM.
DR InterPro; IPR009075; AcylCoADH C like.
DR Pfam; PF00441; Acyl-CoA dh; 1.
DR Pfam; PF02770; Acyl-CoA dh M; 1.
DR Pfam; PF02771; Acyl-CoA dh N; 1.
DR PROSITE; PS00072; ACYL COA DH 1; 1.
DR PROSITE; PS00073; ACYL COA DH 2; 1.
FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
KW Oxidoreductase;
KW Transactinase;
FT TRANSIT 1 41 Mitochondrion (By similarity).
FT CHAIN 42 656 Acyl-CoA dehydrogenase, very-long-chain specific.
FT DOMAIN 42 483 Catalytic.
FT TRANSIT 339 341 NNG -> GTR (in Ref. 5).
FT FT CONFLICT 423 423 C -> W (in Ref. 5).
FT FT CONFLICT 427 427 A -> G (in Ref. 5).
FT FT CONFLICT 441 441 M -> I (in Ref. 5).
FT FT CONFLICT 507 507 G -> A (in Ref. 5).
FT FT CONFLICT 532 532 R -> P (in Ref. 5).
FT FT CONFLICT 567 567 Q -> K (in Ref. 5).
FT FT CONFLICT 570 571 AD -> GG (in Ref. 5).
FT FT CONFLICT 573 573 A -> P (in Ref. 5).
FT FT CONFLICT 593 593 G -> A (in Ref. 5).
FT FT CONFLICT 596 596 T -> A (in Ref. 5).
FT FT CONFLICT 612 612 A -> P (in Ref. 5).
FT FT CONFLICT 628 628 H -> O (in Ref. 4).
FT FT

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Db      366 AsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLysLeuAla 385
QY      1108 CTGATGCTTCAGAGGGCTTACGTCATCGAGAGATGATGACCTACCTCCACGACGGGATCGT 1167
Db      386 ArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAlaAsnMet 405
QY      1168 GACCACTCGCTTCCCGACTGCTCCATCGAGCAGCCATGTTGAAGGTGTTCAAGTCC 1227
Db      406 AspGln---GlyPheLysAspPheGlnIleGluAlaIleSerLysIlePheCysSer 424
QY      1228 GAGCGCCCTGGGAGTGTGTGAGTGAGCGCTGCAGATCTCCGGGCTTGGGCTACACA 1287
Db      425 GluAlaAlaIleLysValAlaAspGluCysIleGlnIleMetGlyGlyMetGlyPheMet 444
QY      1288 AGGAGTATCCGTACGACGCTACTCGTCGACACCGCGATCTCTCTCATCTTCGAGGGA 1347
Db      445 LysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePheGluGly 464
QY      1348 ACCAATGAGATTCCTCGATGTATACCTCGCTGACGGGTCTGCAGCATCGCGCGCATC 1407
Db      465 AlaAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysGlyLysGlu 484
QY      1408 CTGACTACCAAGGATCCATGAGCTTAACAG-----GCCAAAGTGACACAGTCATGGAT 1461
Db      485 LeuThrGlyLeuGlyAsnAlaLeuLysAsnProPheGlyAsnValGlyLeuLeuMetGly 504
QY      1462 ACCGTTGGCGGAGGCTTCCGGACTCTCCGCGCGAAGTCTGGACCTGGGGCTTGACAGGC 1521
Db      505 GluAlaGlyLysGlnLeuArgArgThrGlyIleGlySerGlyLeuSerLeuSer--- 523
QY      1522 AACCATGGAGTTGTGACCCAGCTTTTGGCGAGCATGTCGCCAACAAAGTTTGGAGAGAACACC 1581
Db      524 -----GlyIleValHisProGluLeuSerArgSerGlyGluLeuAlaValGlnAlaLeu 541
QY      1582 TACTGCTTCGGCGGACCGTGGAGACTCTGCTCGCTTGGCAGACCATCATGGAG 1641
Db      542 AspGlnPheAlaThrValValGluAlaLysLeuValLysHisLysLysGlyIleValAsn 561
QY      1642 GACGAGCTGCTACTGAAGCGGGTGGCAACATCTCATCACTGTATGATGATGATGATGATGAT 1701
Db      562 GluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetValVal 581
QY      1702 GTCTGTGCGCGGCGGACCGCTCCATCGCATTTGGCTCGCGACCAACACGACGAGGTT 1761
Db      582 ValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHisGluLys 601
QY      1762 CTCTTGGCCCAACCTTCTCGTGGAGCT-----TACTTGCAGATCTCTTCAGC 1812
Db      602 MetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMetAlaSer 621
QY      1813 CTCTCTCAGCTGGACAGTATGCTCCAGAAACCTAGATGACGAGATTAAGAAGTGTCC 1872
Db      622 LeuGlnSerSerProGlnHis-----GlnGluLeuPheArgAsnPheArgSerIleSer 639
QY      1873 CAGCAGATCTCTGAGAGCGAGCTATATCTGTGCCACCCCTCTG 1917
Db      640 LysAlaMetValGluAsnGlyGlyLeuValThrGlyAsnProLeu 654

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RESULT 9

```

ACDV_BOVIN
ID ACDV_BOVIN STANDARD; PRT; 655 AA.
AC P48818;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
GN precursor (BC 1.3.99.-) (VLICAD).
OS Bos taurus (Bovine)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.

```

```

OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Liu W., Zhu H., Sun X.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC ETF.
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC of different substrate specificities are present in mammalian
CC tissues.
CC -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U10817; AAA74051.1; --
CC HSSP; Q06319; 1BUC.
CC InterPro; IPR006089; Acyl-CoA dh.
CC InterPro; IPR006090; Acyl-CoA dh.
CC InterPro; IPR006091; Acyl-CoA dh.
CC InterPro; IPR006092; Acyl-CoA dh.
CC InterPro; IPR009100; AcylCoA dehyd NM.
CC InterPro; IPR009075; AcylCoA dh.
CC Pfam; PF00441; Acyl-CoA dh; 1.
CC Pfam; PF02770; Acyl-CoA dh M; 1.
CC Pfam; PF02771; Acyl-CoA dh N; 1.
CC PROSITE; PS00073; ACYL COA DH 1; 1.
CC PROSITE; PS00073; ACYL COA DH 2; 1.
CC FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
CC Oxidoreductase; Transit peptide.
CC TRANSIT 1 40 Mitochondrion (By similarity).
CC CHAIN 41 655 Acyl-CoA dehydrogenase, very-long-chain
CC specific.
CC DOMAIN 41 482 Catalytic.
CC SEQUENCE 655 AA; 70520 MW; F9DC06285023CFC0 CRC64;

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Alignment Scores:

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Pred. No.: 1.68e-79 Length: 655
Score: 1345.00 Matches: 285
Percent Similarity: 65.51% Conservative: 110
Best Local Similarity: 47.26% Mismatches: 194
Query Match: 29.86% Indels: 14
DB: 1 Gaps: 9

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US-09-945-326-1 (1-2452) x ACDV_BOVIN (1-655)

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QY 133 TCTACCGGAACCGGGCTACTGCGCACCACCGCCGCTGTACGAGCTTTCCGCCAAGAG 192
Db 57 SerGluAlaSerThrArgGluLysArgAlaAsnSerValSerLysSerPheAlaValGly 76
QY 193 CTTTTCCTAGGCAAAATCAAGAAAGAAAGTTTCCCATTTTCCAGAGTT---AGCCAA 249
Db 77 ThrPheLysGlyGlnLeuThrThrAspGlnValPheProTyrProSerValLeuAsnGlu 96
QY 250 GATGAATTAATCAATCAATCAATGTTCTTGGGACCGTGGGAAATTTCTTCACTGAAGAG 309
Db 97 AspGlnThrGlnPheLeuLysGluLeuValGlyProValThrArgPheGluGluVal 116
QY 310 GTGAGTCTCCGAAATTTGACAGGAGGAAATCCACAGATGAAATTTGGAGAAATTTG 369

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Db 117 AsnAspAlaAlaLysAsnAspMetLeuGluArgValGluThrThrMetGlnGlyLeu 136
QY 370 AAGAGCCTAGGCGCTTTTGGGCTCCAGTCCAGAGAAATATGCTGGCGGCTTCTCC 429
Db 137 LysGluLeuGlyAlaPheGlyLeuGlnValProAsnGluLeuGlyGlyValGlyLeuCys 156
QY 430 AACACCATGTACTCAAGACTAGGGAGATCATACAGCATG---GATGGGTCCACTCACTGTG 486
Db 157 AsnThrGlnTyrAlaArgLeuValGluLeuValGlyMetTyrAspLeuGlyValGlyLeu 176
QY 487 ACCCTGGCAGCGCACAGGCTATTGGCTCAAGGGATCATCTTGGCTGGCAGCTTGGCCTC 546
Db 177 ValLeuGlyAlaHisGlnSerIleGlyPheLysGlyIleLeuLeuPheGlyThrLysAla 196
QY 547 CAGAAAGCCAAATCTTGCCTAAACTCGCTCGGGGAGCACATGTCAGAGCTTCTGGCTC 606
Db 197 GlnLysGluLysTyrThrLeuProLysLeuAlaSerGlyGluThrIleAlaAlaPheCysLeu 216
QY 607 ACGGAGCCAGCAGTGGGAGCGATGACGCTCAATCCGGAGCAGAGCCACACTAAGTGAA 666
Db 217 ThrGluProSerSerGlySerAspAlaAlaSerIleArgSerSerAlaValProSerPro 236
QY 667 GACNAGAACACTACATCTCAATGGCTCCAGTCTGGATTACTAATGAGGAGCTGGCC 726
Db 237 CysGlyLysTyrThrLeuAsnGlySerLysIleTrpIleSerAsnGlyGlyLeuAla 256
QY 727 AATATTTTACTGTGTTTGCAGACACTGAGTGGTTCAT---TCTGATGATCAGTGA 783
Db 257 AspIlePheThrValPheAlaLysThrProValThrAspThrAlaThrGlyAlaValLys 276
QY 784 GACAAATCA CAGCATTCATAGTAGAAGAGACTTTTGGTGGAGTCACATAATGGGAACCC 843
Db 277 GluLysIleThrAlaPheValValGluArgSerPheGlyValThrHisGlyProPro 296
QY 844 GAAGATAAATTAGGCATTCGGGCTCCACACTTGTGAAGTCCATTTTGAACACCAAG 903
Db 297 GluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheAspGlyValArg 316
QY 904 ATACCTGTGAAACATCCTTTGAGAGTCCGAGATGGGTTTAAGTGGCCATGAACATC 963
Db 317 ValProAlaGluAsnValLeuGlyValGlyValGlyGlyPheLysValAlaMetHisIle 336
QY 964 CTCACAGCGCGGTTTACAGATGGGCGAGCGTCTGGCTGGCTGCTCAAGAGATTGATT 1023
Db 337 LeuAsnAsnGlyArgPheGlyMetAlaAlaAlaLeuAlaGlyThrMetLysGlyIleIle 356
QY 1024 GAAATGACTCTGAGTACGCTGCACNAGGAACAGTTTAAACAGAGGCTCAGTGAATT 1083
Db 357 AlaLysAlaValAspHisAlaAlaAsnArgThrGlnPheGlyGluLysIleHisAsnPhe 376
QY 1084 GGATTGATTCAGAGAAATTTGCACTGATGGCTCAGAGGCTTACGTCATGGAGAGTATG 1143
Db 377 GlyLeuIleGlnGluLysLeuAlaArgMetAlaMetLeuGlnTyrValThrGluSerMet 396
QY 1144 ACCTACTCACAGAGGATGTGGACCAACCTGGCTTCCGAGCTGCTCCATCGAGGCA 1203
Db 397 AlaTyrMetValSerAlaAsnMetAspGln---GlySerThrAspPheGlnIleGluAla 415
QY 1204 GCCATGGTGAAGTGTTCAGTCCGAGGCGCTGGCAGTGTGTGAGTGGCGCTGCAG 1263
Db 416 AlaIleSerLysIlePheGlySerGluAlaAlaTrpLysValThrAspGluCysIleGln 435
QY 1264 ATCTCTGGGGCTTGGGCTACACAGGGAGTATCCGTACAGAGCGCTACTGCTGACACC 1323
Db 436 IleMetGlyGlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeu 455
QY 1324 CGCATCTCTCATCTTCAGGGAAACAATGAGATTCTCCGATGTACATCGCCCTGAGC 1383
Db 456 ArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGln 475
QY 1384 GGTCTCAGCATCCCGCGCGCATCTCTGACTTACCAGGATCCATGAGCTTAAACAG----- 1437
Db 476 GlyCysMetAspLysGlyLysGluLeuSerGlyLeuGlyAsnAlaLeuLysAsnProPhe 495

QY 1438 GCCAAAGTGAGCACAGTCATGGATACCGTTGGCGGAGGCTTCGGAGCTCCCTGGGCGGA 1497
Db 496 GlyAsnAlaGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeuArgArgAlaGlyLeu 515
QY 1498 ACTGTGACCTGGGCTGACAGGCAACCATGGAGTTGTGCACCCAGCTCTTGGGACAGT 1557
Db 516 GlySerGlyLeuSerLeuSer-----GlyIleValHisGlnGluLeuSerArgSer 532
QY 1558 GCCAACAAAGTTTGAGGAGAACACACTACTGCTTCGGCGCGGACCGTGGAGACACATCTCTC 1617
Db 533 GlyGluLeuAlaValGlnAlaLeuGluGlnPheAlaThrValValGlnAlaLysLeuIle 552
QY 1618 CGCTTTGGCAGACCATCATGGAGGAGCAGCTGGTACTGAAGCGGGTGGCCACATCTCTC 1677
Db 553 LysHisLysLysAspIleIleAsnGluGlnPheLeuLeuGlnArgLeuAlaAspSerAla 572
QY 1678 ATCAACCTGTATGGCATGACGGCGCTGCTCCGGCGCAGCGCTCCATCCGATTTGGG 1737
Db 573 IleAspLeuTyrAlaMetValValLeuLeuSerArgAlaSerArgSerLeuSerGluGly 592
QY 1738 CTCGCCAACACGACGACGAGGTTCTTCTGGCCCAACACCTTCTGCTGGGAAGCT----- 1791
Db 593 HisProThrAlaGlnHisGluLysMetLeuCysAspSerTrpCysIleGluAlaAlaAla 612
QY 1792 ---TACTTGCAGAACTCTTTCAGCTCTCTCAGCTCGACAAAGTATGCTCCAGAAAACCTA 1848
Db 613 ArgIleArgGluAsnMetThrAlaLeu---GlnSerAspProGlnGlnGlnGlu---Leu 630
QY 1849 GATGACGAGATTAAAGAAAGTGCCCGACAGATCTTTGAGAAGCGAGCCTATCTCTGCC 1908
Db 631 PheArgAsnPhenylSerIleSerLysAlaLeuValGluArgGlyGlyValValThrSer 650
QY 1909 CACCCTCTG 1917
Db 651 AsnProLeu 653
RESULT 10
ACDV HUMAN
ID ACDV_HUMAN STANDARD; PRT; 655 AA.
AC P49748; O76056; Q8WU0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE Precursor (EC 1.3.99.-) (VLCAD).
GN NamesACADVL; Synonyms=VLCAD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1) _
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95397809; PubMed=7668252;
RA Aoyama T., Souri M., Ueno I., Kamijo T., Yamaguchi S., Rhead W.J.,
RA Tanaka K., Hashimoto T.;
RT "Cloning of human very-long-chain acyl-coenzyme A dehydrogenase and
RT molecular characterization of its deficiency in two patients.";
RL Am. J. Hum. Genet. 57:273-283(1995).
RN (2)
RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND VARIANTS.
RC TISSUE=Placenta;
RX MEDLINE=96254975; PubMed=8845838; DOI=10.1093/hmg/5.4.461;
RA Andresen B.S., Bross P., Vianey-Saban C., Divry P., Zabot M.-T.,
RA Roe C.R., Nada M.A., Bykov A., Kruse T.A., Neve S., Kristiansen K.,
RA Knudsen I., Corydon M.J., Gregersen N.;
RT "Cloning and characterization of human very-long-chain acyl-CoA
RT dehydrogenase cDNA, chromosomal assignment of the gene and
RT identification in four patients of nine different mutations within the
RT VLCAD gene.";
RL Hum. Mol. Genet. 5:461-472(1996).
RN (3)
RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Peripheral blood;
RX MEDLINE=96125338; PubMed=8554625;
RA Orii K.O., Aoyama T., Souri M., Orii K.E., Kondo N., Orii T.,
RT Hashimoto T.;
RT "Genomic DNA organization of human mitochondrial very-long-chain acyl-
RT CoA dehydrogenase and mutation analysis.";
RL Biochem. Biophys. Res. Commun. 217:987-992 (1995).
RN [4]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP TISSUE=Liver, Lung, and Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Igoellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RN CHARACTERIZATION.
RX MEDLINE=95286809; PubMed=7769092;
RA Aoyama T., Souri M., Ushikubo S., Kamiyo T., Yamaguchi S.,
RA Kelley R.I., Rhead W.J., Uetake K., Tanaka K., Hashimoto T.;
RT "Purification of human very-long-chain acyl-coenzyme A dehydrogenase
RT and characterization of its deficiency in seven patients.";
RL J. Clin. Invest. 95:2465-2473 (1995).
RN [6]
RN REVIEW ON VARIANTS.
RP MEDLINE=99138660; PubMed=9973285;
RA Andreen B.S., Olpin S., Poorthuis B.J.H.M., Scholte H.R.,
RA Vianey-Saban C., Wanders R., Ijlst L., Morris A., Pourfarzam M.,
RA Bartlett K., Baumgartner E.R., de Klerk J.B.C., Schroeder L.D.,
RA Corydon T.J., Lund H., Winter V., Bross P., Bolund L., Gregersen N.,
RT "Clear correlation of genotype with disease phenotype in very-long-
RT chain acyl-CoA dehydrogenase deficiency.";
RL Am. J. Hum. Genet. 64:479-494 (1999).
RN [7]
RN VARIANTS VLCAD DEFICIENCY GLU-130 DEL; LYS-299 DEL; GLN-382 AND
RP TRP-613.
RX MEDLINE=96108970; PubMed=8554073;
RA Souri M., Aoyama T., Orii K., Yamaguchi S., Hashimoto T.;
RT "Mutation analysis of very-long-chain acyl-coenzyme A dehydrogenase
RT (VLCAD) deficiency: identification and characterization of mutant
RT VLCAD cDNAs from four patients.";
RL Am. J. Hum. Genet. 58:97-106 (1996).
RN [8]
RN VARIANT VLCAD DEFICIENCY HIS-450.
RX MEDLINE=98206416; PubMed=9546340;
RA Snelt A.H., Poorthuis B.J.H.M., Onkenhout W., Scholte H.R.,
RA Andreen B.S., van Duinen S.G., Gregersen N., Wintzen A.R.;
RT "Very long chain acyl-coenzyme A dehydrogenase deficiency with adult
RT onset.";
RL Ann. Neurol. 43:540-544 (1998).
RN [9]
RN VARIANTS VLCAD DEFICIENCY.
RX MEDLINE=99177129; PubMed=10077518;
RA Mathur A., Sims H.F., Gopalakrishnan D., Gibson B., Rinaldo P.,
RA Vockley J., Hug G., Strauss A.W.;
RT "Molecular heterogeneity in very-long-chain acyl-CoA dehydrogenase
RT deficiency causing pediatric cardiomyopathy and sudden death.";
RT

RL Circulation 99:1337-1343 (1999).
CC -1- FUNCTION: Active toward esters of long-chain and very-long chain
CC fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC -1- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC ETF.
CC -1- COFACTOR: FAD.
CC -1- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC step.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P49748-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P49748-2; Sequence=VSP_007734;
CC Note=No experimental confirmation available;
CC -1- DISEASE: Defects in ACADVL are the cause of very long chain acyl-
CC CoA dehydrogenase deficiency (VLCAD deficiency) [MIM:201475].
CC VLCAD deficiency is an autosomal recessive disease which leads to
CC impaired long-chain fatty acid beta-oxidation. It is clinically
CC heterogeneous, with three major phenotypes: a severe childhood
CC form, with early onset, high mortality, and high incidence of
CC cardiomyopathy; a milder childhood form, with later onset, usually
CC with hypoketotic hypoglycemia as the main presenting feature, low
CC mortality, and rare cardiomyopathy; and an adult form, with
CC isolated skeletal muscle involvement, rhabdomyolysis, and
CC myoglobinuria, usually triggered by exercise or fasting.
CC -1- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC of different substrate specificities are present in mammalian
CC tissues.
CC -1- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; D43682; BAA07781.1; -
CC EMBL; L46590; AAA79002.1; -
CC EMBL; X86556; CAA60253.1; -
CC EMBL; D78298; BAA29057.1; -
CC EMBL; D78279; BAA29057.1; JOINED.
CC EMBL; D78280; BAA29057.1; JOINED.
CC EMBL; D78281; BAA29057.1; JOINED.
CC EMBL; D78282; BAA29057.1; JOINED.
CC EMBL; D78283; BAA29057.1; JOINED.
CC EMBL; D78284; BAA29057.1; JOINED.
CC EMBL; D78285; BAA29057.1; JOINED.
CC EMBL; D78286; BAA29057.1; JOINED.
CC EMBL; D78287; BAA29057.1; JOINED.
CC EMBL; D78288; BAA29057.1; JOINED.
CC EMBL; D78289; BAA29057.1; JOINED.
CC EMBL; D78290; BAA29057.1; JOINED.
CC EMBL; D78291; BAA29057.1; JOINED.
CC EMBL; D78292; BAA29057.1; JOINED.
CC EMBL; D78293; BAA29057.1; JOINED.
CC EMBL; D78294; BAA29057.1; JOINED.
CC EMBL; D78295; BAA29057.1; JOINED.
CC EMBL; D78296; BAA29057.1; JOINED.
CC EMBL; D78297; BAA29057.1; JOINED.
CC EMBL; BC000399; AAA00399.1; -
CC EMBL; BC012912; AAH12912.1; -
CC EMBL; BC020218; AAH20218.1; -
CC PIR; S54183; S54183.
CC HSSP; Q06319; 1BUC.
CC Genew; HGNC.92; ACADVL.
CC H-InvDB; HIX0013488; -
CC Reactome; P49748; -
CC MIM; 201475; -

DR GO:0005739; C-mitochondrion; TAS.
 DR GO:0004466; F-long-chain-acyl-CoA dehydrogenase activity; TAS.
 DR GO:0015980; P-energy derivation by oxidation of organic c. .; TAS.
 DR GO:0006635; P-fatty acid beta-oxidation; TAS.
 DR InterPro: IPR006089; Acyl-CoA dh.
 DR InterPro: IPR006090; Acyl-CoA dh.C.
 DR InterPro: IPR006091; Acyl-CoA dh.M.
 DR InterPro: IPR006092; Acyl-CoA dh.N.
 DR InterPro: IPR009100; AcylCoA dehyd NM.
 DR InterPro: IPR009075; AcylCoA dh C-like.
 DR Pfam: PF00441; Acyl-CoA dh; 1.
 DR Pfam: PF02770; Acyl-CoA dh.M; 1.
 DR Pfam: PF02771; Acyl-CoA dh.N; 1.
 DR PROSITE: PS00072; ACYL COA DH 1; 1.
 DR PROSITE: PS00073; ACYL COA DH 2; 1.
 KW Alternative splicing; Cardiofopathy; Disease mutation; FAD;
 KW Fatty acid metabolism; Flavoprotein; Mitochondrion; Oxidoreductase;
 KW Polymorphism; Transist peptide.
 FT TRANSIT 1 40 Mitochondrion (By similarity).
 FT CHAIN 41 655 Acyl-CoA dehydrogenase, very-long-chain

Alignment Scores:
 Pred. No.: 6 3e-78 Length: 655
 Score: 1321.00 Matches: 297
 Percent Similarity: 61.52% Conservative: 109
 Best Local Similarity: 45.00% Mismatches: 213
 Query Match: 29.33% Indels: 41
 DB: 1 Gaps: 13

US-09-945-326-1 (1-2452) x ACDEV_HUMAN (1-655)

QY	21	GCTAAGAGGGGAGCTAGGCTGAGCTGGGGAACTCGGAGCATCGGCGCTGCGG	80
DB	8	AlaSerLeuGlyArgGlnLeuLeuArgLeuGly-----GlyGlySerSerArgLeuThr	25
QY	81	GCTCTT-----CCTCGCGACACCGGCTCGGCTCGTGCCTGCCG	119
DB	26	AlaLeuLeuGlyGlnProArgProGlyProAlaArg-----Pro	39
QY	120	GGGTCTGTGTCTCTC-----TACCGCGAACCGCGG	149
DB	40	TyrAlaGlyGlyAlaAlaGlnLeuAlaLeuAlaAspLysSerAspSerHisProSerAspAla	59
QY	150	GCTACTCGGCACACCGCGC-----TGACGAGCTTCGCCAAAGAGCTTTCT	200
DB	60	LeuThrArgLysLysProAlaLysAlaGlySer-LysSerPheAlaValGlyMetPhe	79
QY	201	AGCAGAAATCAAGAAGAAAGATTTCCCATTTCCAGAGTTAGCCAGACTTAA	260
DB	79	sGlyGlnLeuThrThrAspGlnValPheProTyrProSerValLeuAsnGluGlnThr	99
QY	261	TGAA---ATCAATCAGTTCTTGGGACCCGTGGAAAAATTTCTCACTGAAGAGGTG	317
DB	99	rGlnPheLeuLysGluLeuValGluProValSerArgPhePheGluGluValAsnAspPr	119
QY	318	CCGAAAAATTGACGAGAGGAAATCCAGATGAACTTTGGAGAAATTTGAGAGCCT	377
DB	119	oAlaLysAsnAspAlaLeuGluMetValGluGluThrThrTrpGlnGlyLeuLysGluLe	139
QY	378	AGGGCTTTTGGGCTGCAAGTCCAGAGAAATATGGTGGCTGGGCTTCTCCAAACACCAT	437
DB	139	uGlyAlaPheGlyLeuGlnValProSerGluLeuGlyGlyValGlyLeuGlyAsnThrG1	159
QY	438	GTACTAAGACTAGGGAGATCATACAGATG---GATGGTTCATCATCTGACCTGGC	494
DB	159	nTyrAlaArgLeuValGluLeuValGlyMetHisAspLeuGlyValGlyLeuThrLeuG1	179
QY	495	AGCGCACCGCTATGGCTCAAGGGGATCATCTTGGCTGGCCTCAGGAGCAGAGAC	554
DB	179	yAlaHisGlnSerileGlyPheLysGlyLeuLeuPheGlyThrLysAlaGlnLysG1	199
QY	555	CAAAATCTTGCTTAACTGGCGTCCGGGAGCAGCATTTGAGCGCTTCTGCTCAGCGAGCC	614

DB	199	uLysTyrLeuProLysLeuAlaSerGlyGluThrValAlaAlaPheCysLeuThrGluPr	219
QY	615	AGCAGTGGGAGCGATGACGCTCAATCCGAGCAGAGCCACACTAAGTGAAGACAAGAA	674
DB	219	oSerSerGlySerAspAlaAlaSerileArgThrSerAlaValProSerProCysGlyLy	239
QY	675	GCATCATCTCAATGGCTCCAAAGTCTGGATTACTATGGAGGACTGCCAATATTTT	734
DB	239	styTyrThrLeuAsnGlySerLysLysLeuTrpIleSerAsnGlyGlyLeuAlaAspIlePh	259
QY	735	TACTGTGTTTGCAGAGACTGAGGTCGTTGAT---TCTGATGGATCAGTGAAGACAAAAT	791
DB	259	eThrValPheAlaLysThrProValThrAspProAlaThrGlyAlaValLysGluLysI1	279
QY	792	CACAGATTCATAGTAGAAGAGACTTTGGTGGAGTCATTAATGGGAAAACCCGAAGATAA	851
DB	279	eThrAlaPheValValGluArgGlyPheGlyGlyIleThrHisGlyProProGluLysLy	299
QY	852	ATTAGGCATTCCGGGCTCCAAACACTTGTGAAGTCCATTTTGAAACACCAAGATACCTGT	911
DB	299	sMetGlyIleLysAlaSerAsnThrAlaGluValPhePheAspGlyValArgValProse	319
QY	912	GGAAAAATCTCTGGAGAGTCCGAGATGGGTTAAGGTGGCCATGAACATCTCAACAG	971
DB	319	rGluAsnValLeuGlyGluValGlySerGlyPheLysValAlaMetHisIleLeuAsnAs	339
QY	972	CGGCCGTTTCAGCATGGGCGAGCGTCTGGCTGGGCTGCTCAAGAGATTGATGAATGAC	1031
DB	339	nGlyArgPheGlyMetAlaAlaLeuAlaGlyThrMetArgGlyIleAlaLysAl	359
QY	1032	TGCTGATGATCGCTGCACAAAGGAAACAGTTTAAACAGAGGCTCAGTGAATTTGGATTGAT	1091
DB	359	aValAspHisAlaThrAsnArgThrGlnPheGlyGlyLysIleHisAsnPheGlyLeuI1	379
QY	1092	TCAGGAAATTTGCACTGATGCTCAGAAAGGCTTACGTCTGAGAGATGACCTTACCT	1151
DB	379	eGlnGluLysLeuAlaArgMetValMetLeuGlnTyrValThrGluSerMetAlaTyrMe	399
QY	1152	CACAGCAGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGGAGCGCATGCT	1211
DB	399	tValSerAlaAsnMetAspGln---GlyAlaThrAspPheGlnIleGluAlaAlaIleSe	418
QY	1212	GAAGTGTTCAGCTCCGAGCGCGCTGGCAGTGTGTGAGTGAGGCGCTGCAGATCTCGG	1271
DB	418	rlYsIlePheGlySerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGl	438
QY	1272	GGCTTGGCTACACAAGGACTATCCGTACAGGCGCATCTGCTGACACCCGATCTCT	1331
DB	438	yGlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeuArgIlePh	458
QY	1332	CCTCATCTTCGAGGGAACCAATGAGATTCTCGGATGTACATCGCCCTGACGGGCTGCA	1391
DB	458	eArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMe	478
QY	1392	GCATCCCGCGCATCTGACTACAGGATCCATGAGCTTAAACAG-----GCCAAAGT	1445
DB	478	tAspLysGlyLysGluLeuSerGlyLeuGlySerAlaLeuLysAsnProPheGlyAsnAl	498
QY	1446	GAGCACATCTGATGATACCGTTGGCGGAGCTCGGACTCCCTGGCGCCGACTGTGGA	1505
DB	498	agLysLeuLeuGlyGluAlaGlyLysGlnLeuArgArgAlaGlyLeuGlySerG1	518
QY	1506	CCTGGGCTGACAGCAACCATGGAGTTGTGCACCCCACTTTCGGGACAGTGCCCAACA	1565
DB	518	yLeuSerLeuSer-----GlyLeuValHisProGluLeuSerArgSerGlyGluLe	535
QY	1566	GTTTGGAGAGAACCTACTCTCTCGGCGGACCGTGGAGACACTGTGCTCGCTTGG	1625
DB	535	uAlaValArgAlaLeuGluGlnPheAlaThrValValGluAlaLysLeuIleLysHisLy	555
QY	1626	CAAGACCATCATGAGGAGCAGCTGTACTCAAGCGGTGGCCCAACTCTCATCAACT	1685
DB	555	sLysGlyIleValAsnGluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLe	575

DR	PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR	PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW	FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
KW	Oxidoreductase; Transit peptide.
FT	TRANSIT 1 40 Mitochondrion (By similarity).
FT	CHAIN 41 655 Acyl-CoA dehydrogenase, very-long-chain specific.
FT	DOMAIN 41 482 Catalytic.
SQ	SEQUENCE 655 AA; 70443 MW; DCC7AA989EFCB333 CRC64;
Alignment Scores:	
Pred. No.:	8 52e-78 Length: 655
Score:	1319.00 Matches: 294
Percent Similarity:	62.15% Conservative: 110
Best Local Similarity:	45.23% Mismatches: 219
Query Match:	29.29% Indels: 27
DB:	1 Gaps: 11
US-09-945-326-1 (1-2452) x ACDV_MACPA (1-655)	
Qy	30 GGGAGACTGAGGTGCGTGGGGAACATCGGCAGCATGAGCGGTGCGGGCTCTTT--- 86
Dd	11 GlyArgGlnLeuLeuArgPheGly-----GlyGlySerSerArgProThrAlaLeuLeu 28
Qy	87 -----CCTGCCACCACCGGTGCGGCTCGTCCTCGCGGGTCTGGT 128
Dd	29 GlyGlnProTrpProGlyProAlaIleArg-ProTyrrAlaGlycylAlaAlaGlnLeuAl 48
Qy	129 GGNTCTACCGCAACCGGGGGTA-----CTGCGCACGACCGCTGTACGACG 179
Dd	48 aleuAspLysSerAspSerHisLeuSerAspAlaLeuAsnLysAlaLysProAlaLysAl 68
Qy	180 T-----TTGCCCAAAGAGCTTTTCTTAGGCCAAAATCAAGAAGAAAGAGTTT 227
Dd	68 aGluSerLysSerPheAlaValAlaMetPheLysGlyGlnLeuThrThrAspGlnValPh 88
Qy	228 CCATTTCGAGAAGTT---AGCCAAGATGAACCTTAATGAATCAATCAGTCTCTGGGACC 284
Dd	88 eProTyrrProSerValLeuAsnGlnGluInThrGluPheLysGluLeuValGluPr 108
Qy	285 CGTGGAATAATCTTCACCTCAAGAGGTGGACTCCCGAAAAATGACCAGGAAGGAAAAAT 344
Dd	108 oValSerArgPhePheGluGluValIleAsnAppProAlaLysAsnAppThrLeuGluMetVa 128
Qy	345 CCCAGATGAACCTTTGGAGAAATTTGAAGAGCCCTAGGGCTTTTTGGGCTGCAAGTCCCAGA 404
Dd	128 lGluGluThrThrLeuGlnGlyLeuLysGluLeuGlyAlaPheGlyLeuGlnValProSe 148
Qy	405 AGAATATGTGGCTGGCTCTTCACACCATGTACTCAAGACTAGGGAGATCATCAG 464
Dd	148 rGluLeuGlyGlyValGlyLeuLysGluLeuGlnGluLeuValGluLeuValGlu 168
Qy	465 CATG---GATGGGTCCATCACTGTGACCTCGGCAGCGCACGAGCTATTCGCTCAAGGG 521
Dd	168 yMetHisAspLeuAlaValGlylleThrLeuGlyAlaHisGlnSerlleGlyPheLysGl 188
Qy	522 GATCATCTTGGCTGGCACTGAGCAGCAGAAAGCCAAATCTTGCTCTAACTGGCGTCCGG 581
Dd	188 ylleLeuLeuPheGlyThrLysAlaGlnLysGluLysTyrrLeuProLysLeuAlaSerGl 208
Qy	582 GGAGCACAATTCAGCCTCTTCCTCTCAGGAGCCAGCCAGTGGGAGCGATGAGCCTCAAT 641
Dd	208 yGluThrLeuAlaAlaPheCysLeuThrGluProSerSerGlySerAspAlaAlaSerIl 228
Qy	642 CCGGAGCAGCCACACTANGTGNAGCAGAGCACTACATCCTCAATCGCTCCCAAGGT 701
Dd	228 eaRgThrSerAlaValProSerProCysGlyLysTyrrThrLeuAsnGlySerLysLe 248
Qy	702 CTGGATTACTTAATGAGGACTGGCCCAATATTTTACTGTGTTTGCAAAGACTCAGGTCGT 761
Dd	248 uTPlleSerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLysThrProValTh 268
Qy	762 TGAT---TCTGATGGATCAGTGAAGAACAAAATCAGACGATTCATAGTAGAAAAGAGACTT 818

Db 268 rAspProAlaThrGlyAlaValLysGluLysIleThrAlaPheValValGluAraGlyPhe 288
QY 819 TGGTGGAGCTCAATATGGAACCGGAGATAAATAGGATTCGGGGCTCCCAACACTTG 878
Db 288 eGlyGlyValThrHisGlyProProGluLysMetGlyIleLysAlaSerAsnThrAl 308
QY 879 TGAAGTCCATTTGAAACACCAAGATACCTGTGGAAACATCTGTGAGAGGTGCGAGA 938
Db 308 aGluValLeuPheAspGlyValArgValProSerGluAsnValLeuGlyValGlySe 328
QY 939 TGGGTTAAGTGGCCATGAACTCAACAGCGCGGTTCAGCATGGGACAGCGTCGT 998
Db 328 rGlyPheLysValAlaMetHisIleLeuAsnAsnGlyArgPheGlyMetAlaAlaLe 348
QY 999 GGCTGGGCTGCTCAAGAGATTGATTGAATGCTGCTGAGTACGCTCCGACAGGAACA 1058
Db 348 uAlaGlyThrMetArgGlyIleThrLysAlaValAspTyrAlaThrAsnArgIleGl 368
QY 1059 GTTTAAACAAGAGGCTCAGTGAATTTGGATTGATTGAGGAGAAATTTGCACCTGATGGCTCA 1118
Db 368 nPheGlyGluLysIleHisAsnPheGlyLeuIleGlnGluLysLeuAlaArgMetValMe 388
QY 1119 GAAGGCTTACCTGAGAGATGACCTACCTCACAGAGGGATGCTGACCAACCTGG 1178
Db 388 tLeuGlnTyrValThrGluSerMetAlaTyrMetValSerAlaAsnMetAspGln--Gl 407
QY 1179 CTTTCCCGAGTCCATCGAGGAGCCATGGTGAAGTGTTCAGTCCCGAGCGCGCTG 1238
Db 407 ySerThrAspPheGlnIleGluAlaIleSerLysIlePheGlySerGluAlaAlaTr 427
QY 1239 GCAGTGTGAGTGAGGCGCTGCAGATCCTCGGGGGCTGGGTGTACACAGGAGCATCC 1298
Db 427 pLysValThrAspGluCysIleGlnIleMetGlyGlyMetGlyPheMetLysGluProGl 447
QY 1299 GTACGAGCGCATCTGCTGCACCCCGATCCTCCTCATCTTCAGGGAACCAATGAGAT 1358
Db 447 yValGluArgValLeuArgAspLeuArgIlePheArgIlePheGluGlyThrAsnAspIl 467
QY 1359 TCTCCGATGTACATCCCTCGCGGTCTGCAGCATCGCGCGCATCTGACTACCCAG 1418
Db 467 eLeuArgPheValAlaLeuGlnGlyCysMetAspLysGlyLysLeuSerGlyLe 487
QY 1419 GATCCATGAGCTTAAACAG-----GCCAAAGTGAGCACATGATCATCGATCCGTCGCGC 1472
Db 487 uGlySerAlaLeuLysAsnProPheGlyAsnAlaGlyLeuLeuGlyGluAlaGlyLy 507
QY 1473 GAGGCTTCGGGACTCCTCGGCGCGAAGTGGACCTGGGGCTACAGCGCAACCATGAGT 1532
Db 507 sGlnLeuArgArgAlaGlyLeuGlySerGlyLeuSerLeuSer-----GlyIl 524
QY 1533 TGTGCAACCCAGTCTTCGGGACATGTCGCAACAAAGTTTGAGGAGAACACCTTACTGCTCGG 1592
Db 524 eValHisProGluLeuSerArgSerGlyGluLeuAlaValGlnAlaLeuGlnPheAl 544
QY 1593 CCGGACCGTGGAGACTGTGCTCGCGCTTTGGCAAGACCATCATGAGGAGCAGCTGGT 1652
Db 544 aThrValValGluAlaLysLeuIleLysHisLysLysGlyIleValAsnGlnPheLe 564
QY 1653 ACTGAGCGGGTGGCAACATCTCTCATACCTGATGGATCAGCGCGTGTGTCGGG 1712
Db 564 uLeuGlnArgLeuAlaAspGlyAlaIleAepLeuTyrAlaMetValValLeuSerAr 584
QY 1713 GGCAGCGGCTCCATCCGATCGGCTCGCAACACCGACGAGGTCTCTTGGCCAA 1772
Db 584 gAlaSerArgSerLeuSerGluGlyHisHisThrAlaGlnHisGluLysMetLeuCysAs 604
QY 1773 CACTTCTGGTGGAGCTTACTTTCGAGATCTCTTCAGCGCTCTTCAGCTGCAGCAAGTA 1832
Db 604 pThrTrpCysIleGluAlaAlaAlaArgIleArgGlyMetAlaAlaLeuGlnSerAs 624
QY 1833 TGCTCCAGAAAC--CTAGATGAGCATTAAGAAAGTGTCCACGACATCTTCAGAA 1889

Db 624 pProArgGlnHisGluLeuTyrArgAsnPheLysSerIleSerLysAlaLeuValGluAr 644
QY 1890 GCAGGCTATATCTGTGCCACCCCTCTG 1917
Db 644 gGlyGlyValValThrAsnAsnProLeu 653
RESULT 12
Q9V8T1 PRELIMINARY; PRT; 655 AA.
AC Q9V8T1; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG7461-PA.
GN CRPNames=CG7461;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burtis K.C., Buschman D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris D.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spiere E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasmann D.A., Weinstein G.W., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun. Release 3 of the Drosophila
melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).

[3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Ceiniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
 [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Beriman B.P.,
 RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter A.J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
 [5]
 RN SEQUENCE FROM N.A.
 RP FlyBase;
 RG Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [6]
 RN SEQUENCE FROM N.A.
 RP FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
 DR EMBL; AE003796; AAF57579.1; -;
 DR HSSP; Q06319; 1BUC.
 DR IntAct; Q9V8T1; -;
 DR FlyBase; FBgn034432; CG7461.
 DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006089; Acyl-CoA dh.
 DR InterPro; IPR006090; Acyl-CoA dh_C.
 DR InterPro; IPR006091; Acyl-CoA dh_M.
 DR InterPro; IPR006092; Acyl-CoA dh_N.
 DR InterPro; IPR009075; AcylCoADH_C like.
 DR InterPro; IPR009100; AcylCoA dehyd_NM.
 DR Pfam; PF00441; Acyl-CoA dh; I.
 DR Pfam; PF02770; Acyl-CoA dh; M; 1.
 DR Pfam; PF02771; Acyl-CoA dh; N; 1.
 DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
 DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
 KW FAD; Flavoprotein; Oxidoreductase.
 SQ SEQUENCE 655 AA; 71326 MW; 00916BD701E127CB CRC64;

Alignment Scores:
 Pred. No.: 2.96e-76 Length: 655
 Score: 1295.50 Matches: 280
 Percent Similarity: 61.84% Conservative: 104
 Best Local Similarity: 45.09% Mismatches: 212
 Query Match: 28.76% Indels: 25
 DB: 2 Gaps: 9

US-09-945-326-1 (1-2452) x Q9V8T1 (1-655)

Qy 106 GCTCGTCCGCGGGTCTGGTGTC-----TCTACCGCAACCGG 147
 Db 44 AlaSerLeuCybArgGlnIleAlaThrHisSerProLysLeuGlyAlaGluSerAsnArg 63
 Qy 148 CGGCTACTGCGCACCGCGCTGTACGAGCTTTCGCCAAGAGCTTTTCTAGGCAAA 207
 Db 64 SerLysGluLysAlaSerGluAsn--GluSerPheMetAlaAenIlePheArgGlySer 82
 Qy 208 ATCAAGAAAGAAAGATTTTCCCATTTCCAGAGTTAGCCAGATGAATTAATGAATC 267
 Db 83 LeuValSerSerGlnValPheProTy-ProAspValLeuThrAlaGluGlnLysGluLeu 102

Qy 268 ---AATCAGTTCTTGGGACCCCGTGGAAAAATTTCTTCACTGAAGAGGTGGACTCCCGAAA 324
 Db 103 ThrAsnSerLeuIleAspProPheGluArgPheSerAspValAsnAspAlaAlaArg 122
 Qy 325 ATTGACCAAGGAAAAATCCAGATGAACATTTGGAGAAATTTGAAGAGCCTAGGGCTT 384
 Db 123 AsnAspAlaAsnSerLysIleAspAspThrThrSerThrAlaLeuTrpGluLeuGlyAla 142
 Qy 385 TTTGGGCTCAAGTCCCAGAAAGAAATATGTGGCTGGCTTCTCCACACCATCTACTCA 444
 Db 143 PheGlyIleGlnValProSerGluPheGlyGlyLeuGlyLeuAsnAsnThrGlnTyGly 162
 Qy 445 AGATGGGAGATCATCAGCATG---GATGGGTCCATCATCTGTGACCCCTGGGCGCAC 501
 Db 163 ArgLeuCybAlaIleValGlyValAsnAspLeuGlyLeuGlyIleThrIleGlyAlaHis 182
 Qy 502 CAGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACTGAGGACGAGAAAGCCAAATAC 561
 Db 183 GlnSerIleGlyPheLysGlyIleLeuLeuTyGlyThrProGluGlnLysGluLysTy 202
 Qy 562 TTGCTAAACTGGGCTCCGGGAGACATTTGCAGCCTTCTGCCTCACGAGCCAGCCAGT 621
 Db 203 LeuProLysValAlaAlaGluGlnValTyAlaAlaPheAlaLeuThrGluProSerSer 222
 Qy 622 GGGAGCGATCAOCCTCAATCCGAGCAGACCATTAAGTGAAGACAAAGAACACTAC 681
 Db 223 GlySerAspAlaGlySerIleArgCysArgAlaValLysSerAlaAspGlyLysHisTy 242
 Qy 682 ATCTCAATGGCTCCAAAGTCTCGATTACTTAATGGAGGACTGGCCATATTTTACTGTG 741
 Db 243 ValLeuAsnGlySerLysIleTrpIleSerAsnGlyGlyIleAlaGluIleMetThrVal 262
 Qy 742 TTTGCAAGACTCAGGTCTGTGAT---TCTGATGATCAGTGAAGACAAATCACAGCA 798
 Db 263 PheAlaGlnThrGluGlnValAspProLysThrGlyGlyLysLysAspLysValThrAla 282
 Qy 799 TTCATAGTAGAAAGAGACTTTTGGTGGAGTCACATAATGGGAAACCCGAGATATAATAGGC 858
 Db 283 PheIleValGluArgSerPheGlyGlyValThrAsnGlyProProGluLysLysMetGly 302
 Qy 859 ATTGGGGCTCCAACTCTGTGAAGTCCATTTTGAANAACCAAGATACCTGTGGAAAC 918
 Db 303 IleLysAlaSerAsnThrAlaGluValTyPheGluAspValLysIleProIleGluAsn 322
 Qy 919 ATCTTGGAGAGTCCGAGATGCTTTAAGTGGCCATGAACATCTCCACAGGCGCGG 978
 Db 323 ValLeuGlyLysGluGlyAspGlyPheLysValAlaMetAsnIleLeuAsnAsnGlyArg 342
 Qy 979 TTCAGCATGGGACCGCTCGTGGCTGCTCAAGAGATTTGATTGAAATGACTGCTGAG 1038
 Db 343 PheGlyMetGlyAlaThrLeuSerGlyThrMetLysLysCysIleGluGlnAlaThrGlu 362
 Qy 1039 TAGCGCTGCACAGGAAACAGTTTAAACAGAGGCTCAGTAATTTGATTTGATTCAGAG 1098
 Db 363 HisAlaAsnAsnArgValGlnPheGlyGlnLysLeuLysAsnTyArgIleGlnGlu 382
 Qy 1099 AAATTTGCACTGATGGCTCAGAGGCTTACGTATGAGAGATGACTACTTACACAGCA 1158
 Db 383 LysLeuAlaGlnMetAsnIleLeuGlnTyAlaThrGluSerMetAlaPheThrIleSer 402
 Qy 1159 GGGATGCTGACCAACCTCGCTTTTCCCGACTGCTCCATCGAGGCGAGCCATGTGAAGTG 1218
 Db 403 GlnAsnMetAsp--AlaGlySerLysAspTyHisLeuGluAlaAlaIleSerLysIle 421
 Qy 1219 TTCAGTCCGAGCGCGCTGCGAGTGTGTAGTGAGGCGCTGCAGATCTTCGGGGCTTG 1278
 Db 422 TyrAlaSerGluSerAlaTrpTyValCysAspGluAlaIleGlnIleLeuGlyGlyMet 441
 Qy 1279 GGTACACAGAGGACTATCCGTACGAGCGCATCTGCTGACACCCGCGCATCTCTCTCATC 1338
 Db 442 GlyTyMetValAspAsnGlyLeuGluArgValLeuArgAspLeuArgIlePheArgIle 461

QY 1339 TTCGAGGAACAATGAGATTCTCGGATGTACATCGCCCTGACGGGTCTGCAGTCGCC 1398
 Db PheGluGlyThrAsnAlaLeuArgLeuPheAlaLeuThrGlyIleGlnTyAla 481
 QY 1399 GCGCGCATCTGACTACAGAGATCATGAGCTTAAACAG-----GCC 1440
 Db Gly-----SerHisLeuLysGluLeuGlnArgAlaPheLysAsnProSerAla 497
 QY 1441 AAATGAGCACAGTCATGATACCTTGGCGGAGGCTTCGGGACTCCCTGGCGCGCACT 1500
 Db AsnLeuGlyLeuIlePheLysGluAlaSerArg-----AlaAlaSerThr 513
 QY 1501 GTGACCTGGGGCTGACAGCAACATGAGTGTGTGACCCCTGCTTGGGAGAGTGCC 1560
 Db ValGlyLeuGlyThrAspLeuSerGlyHisValValGlyLeuLeuLeuProTyAla 533
 QY 1561 AACAGTTTGGAGAGACACTACTCTTGGCGGAGCGGTGGAGACACTGCTGCTCGGC 1620
 Db LysLysThrAlaHisCysIleAspLeuPheGlyGlnSerValGluGluLeuLeuArg 553
 QY 1621 TTGGCAAGACCATCATGAGGAGCAGCTGTGTACTGAAGCGGTGGCCCAACATCTCTCATC 1680
 Db TyrAsnLysAsnIleValAsnGluGlnIleLeuLeuThrArgLeuAlaAlaIle 573
 QY 1681 AACCTGTATGCGCATGACGCGCGTCTGTGCGGCGCCAGCGCTCCATPCGCTTGGGCTC 1740
 Db AspIleTyAlaMetValValThrGlnSerArgSerArgAlaValAsnLeuLeuAsnLeu 593
 QY 1741 CGCAACACGACGACGAGGTCTCTTGGCCACACCTTCTGCGTGGAGCTTACTTGCAG 1800
 Db ProThrAlaGlnHisGluLeuAsnMetThrLysAlaLeuThrIleGlnAlaSerAspArg 613
 QY 1801 AATCTTTCAGCTCTCTCAGCTGCGACAGTATGCTCCAGAAACCTAGATGACGACATT 1860
 Db ValIleLysAsnLeuGlnAlaAlaThrSerSerHisHisArgSerLeuAsnGluLysIle 633
 QY 1861 AAGAAAGTCCCGACGAGATCTTGAAGAGGAGCTATATCTGTGCGCCACCTCTGAGC 1920
 Db SerThrIleAlaLysThrThrLeuLeuGluAsnGlyGlyValThrThrThrGlyIleLeuAsp 653
 QY 1921 AGG 1923
 Db 654 Gln 654

RESULT 13
 Q7Q868
 ID Q7Q868 PRELIMINARY; PRT; 639 AA.
 AC Q7Q868:
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE AGCP15352 (Fragment).
 GN Name=agCG50940; ORFNames=ENSGG0000009991;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -/- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
 CC -/- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAB01008944; EAA10216.1; -.
 DR HSSP: Q06319; 1EUC.
 DR GO: GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR006089; Acyl-CoA dh.
 DR InterPro: IPR006090; Acyl-CoA dh_c.

DR InterPro: IPR006091; Acyl-CoA dh M.
 DR InterPro: IPR009075; AcylCoA dh C-like.
 DR InterPro: IPR009100; AcylCoA dehyd_NM.
 DR Pfam: PF00441; Acyl-CoA dh; 1.
 DR Pfam: PF02770; Acyl-CoA dh M; 1.
 DR PROSITE: PS00072; ACYL COA DH 1; 1.
 DR PROSITE: PS00073; ACYL COA DH 2; 1.
 KW FAD; Flavoprotein; Oxidoreductase.
 FT NON_TER 1
 SQ SEQUENCE 639 AA; 70246 MW; 46790371AAD12CB5 CRC64;
 Alignment Scores:
 Pred. No.: 9,11e-76 Length: 639
 Score: 1288.00 Matches: 282
 Percent Similarity: 62.66% Conservative: 109
 Best Local Similarity: 45.19% Mismatches: 187
 Query Match: 28.60% Indels: 46
 DB: 2 Gaps: 11
 US-09-945-326-1 (1-2452) x Q7Q868 (1-639)
 QY 145 CGCGGCTACTGCGCACCGCCG----- 168
 Db 28 ArgArgCysLeuSerAlaAlaProGlnAlaLysGlnAlaGluAlaGlnGlnAlaThrPro 47
 QY 169 -----CCTGTACGAGCTTTCGCCAAGAGCTTTCTCTAGCAAAATC 210
 Db 48 SerGluAlaGluLysArgProAsnMetSerPheLeuThrAsnIlePheArgGlyGlnVal 67
 QY 211 AAGAAGAAAGAGTTTCCATTTCCAGAAAGTTAGCCAAAGATGAACCTTAATGAA---ATC 267
 Db 68 GlnProAlaGlnValPheProTyProGluAlaLeuAspAlaGluGlnLysGlyIle 87
 QY 268 AATCAGTTCTTGGGACCGCGTGAAGAAATCTTCTCAGAGAGGTGACCTCCCGAAAAAT 327
 Db 88 AlaSerPheValAspProValThrLysPheGluGluValAsnAspProValLysAsn 107
 QY 328 GACCAAGGAAGGAAATCCAGATGAACCTTTGGAGAAATTCAGAGCCCTAGGCGCTTTT 387
 Db 108 AspValAsnAlaSerIleAspGluLysThrCysGluAlaLeuTrpAspLeuGlyAlaPhe 127
 QY 388 GGGCTGCAAGTCCAGAGAAATATGGTGGCTTCTCCAAACCATGACTCAAGA 447
 Db 128 SerLeuMetValProAspTyArgGlyLeuGlyLeuAsnAsnThrGlnTySerArg 147
 QY 448 CTAGGGGAGATCATC---AGCATGGATGGTCCATCCTGTGACCTGCGCAGCGACACAG 504
 Db 148 MetCysAspIleIleGlyGlnAspLeuGlyLeuGlyIlePheIleGlyAlaHisGln 167
 QY 505 GCTATTGGCTCAAGGGGATCATCTTGGCTGGCAGTGGAGAGCAGAAAGCCAAATCTTG 564
 Db 168 SerIleGlyPheLysGlyIleLeuLeuTyArgAspGlnArgGlnLysGluLysTyLeu 187
 QY 565 CTTAACTGGCGTCCGGGAGCAGATTGAGCTTCTGCTCAGGAGCGACCGAGTGGG 624
 Db 188 ProMetValSerThrGlyLysValTyAlaAlaPheAlaLeuThrGluProSerSerGly 207
 QY 625 AGCGATGCGAGCTCAATCCGGAGCAGCAGCAGTAACTGAAGCAAGCAAGCACTACATC 684
 Db 208 SerAspAlaGlySerIleArgCysArgAlaValLysSerAlaAspGlyLysHisTyVal 227
 QY 685 CTCAATGCTCAAGTCTGGATTACTAATGGAGGACTGGCCAAATATTTTACTGTGTTT 744
 Db 228 LeuAsnGlySerLysIleTrpIleSerAsnGlyGlyIleAlaAspIleMetThrValPhe 247
 QY 745 GCAAGAGCTGAGTGTGTTGAT---TCTGATGGATCAGTGAAGCAAAATCACACATTC 801
 Db 248 AlaGlnThrGluValGluAspProLysThrGlyGlnLysLysAspLysValThrAlaPhe 267
 QY 802 ATAGTAGAAGAGAGCTTTGGTGGAGTCTACTAATGGAAACCCGAGATAAATTTAGGCATT 861
 Db 268 IleValGluArgGlyPheGlyValSerSerGlyProProGluAsnLysMetGlyIle 287

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QY 862 CGGGCTCCACACTTGTGAAGTCCATTTTGAACACACCAAGATACCTGTGGAAACATC 921
Db 288 LysCysSerAsnThrAlaGluValTyrPheGluAspValIleProAlaGluAsnVal 307
QY 922 CTTGGAGAGTCCGAGATGGGTTTAAGTCGGCATGAACATCTCAACAGCGCCGGTTC 981
Db 308 LeuGlyGlyGluGlyAsnGlyPheLysValAlaMetAsnIleLeuAsnGlyArgPhe 327
QY 982 AGCATGGCAGCGTGGCTGGCTCTCAAGAGATTGTAAGATGACTGCTGAGTAC 1041
Db 328 GlyMetAlaAlaThrLeuSerGlyThrMetArgAlaCysIleGlnLysAlaAlaGluHis 347
QY 1042 GCCTGCACAGGAACAGTTTACAGAGGCTCAGTGAATTTGGATTGATTCAGGAGAAA 1101
Db 348 AlaThrAsnAsnValGlnPheGlyArgLysIleGluThrPheGlyGlyValGlnGluLys 367
QY 1102 TTTGCACTGATGCTCAGAAAGGCTTACGTCTCATGGAGATGATGACCTACCTCAGCAGG 1161
Db 368 LeuAlaArgMetAlaMetHisHisTyrValThrGlnSerMetAlaTyrMetIleSerGly 387
QY 1162 ATGCTGGACCAACTGGCTTTCCCGACTGCTCCATCGAGCGACCATGTGTGAAGTGTTC 1221
Db 388 AsnMetAsp---ThrGlySerLeuAspTyrHisLeuGluAlaAlaIleSerLysValPhe 406
QY 1222 AGCTCGAGCGCCCTGGCAGTGTGTGAGTGGCGCTGCAGATCTCCGGGGCTTGGGC 1281
Db 407 AlaSerGluSerAlaTyrTyrValCysAspGluAlaIleGlnIleLeuGlyGlyMetGly 426
QY 1282 TACACAAAGGACTATCGTACGAGCGCATCTACTCGTGACACCCGCATCTCTCATCTTC 1341
Db 427 PheMetLysAspCysGlyLeuGluArgValMetArgAspLeuArgIlePheArgIlePhe 446
QY 1342 GAGGGAACCAATGAGATTCTCCGATGTATCATCGCCCTGACGGGTCTGCAGCATCCGGC 1401
Db 447 GluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuThrGlyIleGlnTyrAlaGly 466
QY 1402 CGCATCTGACTACAGGATTCATGAGTGTAAACAGGCC-----AAAGTGACACAGTC 1455
Db 467 -----SerHisLeuLysGluLeuGlnArgAlaPheLysAsnProAlaThrAsn 482
QY 1456 ATGATACCTGTCGGCGAGGCTTCGGGACTCCTCGGCGCACTGTGGACCTGGGGCTG 1515
Db 483 MetGlyLeuIlePheLysGluGlySerArgArgAlaIleArgSerIleGlyTyrGlyGly 502
QY 1516 ACAGGCAACCATGGAGTGTGACCCCGAGTCTTTCGGGACAGTGCCCAACAGTTTGAGG 1575
Db 503 ThrAspLeuSerAlaPheValAlaAspProLeuLysValProAlaLysGlnCysSerGlu 522
QY 1576 AACACTACTGCTTCGGCGGACCGTGGAGACACTGCTGCTCGCTTGGTTCGACAGCATC 1635
Db 523 CysIleAspLeuPheGlyGlnThrValGluSerLeuLeuIleLysTyrGlyLysIle 542
QY 1636 ATGGAGGAGCAGCTGCTACTGAAGCGGTGGCCCAACATCTCATCACTGTATGCATG 1695
Db 543 ValAspGluGlnPheLeuLeuAsnArgLeuAlaAspAlaAlaIleAspThrTyrAlaMet 562
QY 1696 ACGGCGGTGCTGTGCGGGCGACCGCTCCATCCGATTTGGGTTCGCGCAACACGACCCAC 1755
Db 563 AlaValValLeuSerArgAlaThrArgSerValArgLysAspLeuProSerAlaGluHis 582
QY 1756 GAGGTCTCTTGGCCCAACACTTCTGCTGGTGAAGCTTACTTGCAGATCTCTTCAGCCTC 1815
Db 583 GluValLeuMetThrLysAlaTyrCysHisGluAlaSerAspArgValArgValAsnIle 602
QY 1816 TCTCAGCTGCAGAGTATGCTCCAGAAAACCTAGATGACGACGAGTAAAGAAA-----GTG 1869
Db 603 ArgLysIle-----AsnThrAspSerPheValLysAsnTyrGlyVal 616
QY 1870 TCCACGACATCTTGCAGAGCGAGCTATATCTGTGCC-----IleCysAlaAsnAsnGlyIleAlaHisAsn 1908
Db 617 MetSerGlnIleAlaLysAsn-----IleCysAlaAsnAsnGlyIleAlaHisAsn 633
QY 1909 CACCCTCTGGAC 1920
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Db 634 AsnProLeuAsp 637
RESULT 14
Q7Q870 PRELIMINARY; PRT; 604 AA.
AC Q7Q870;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE AgCP15349 (Fragment).
GN Name=agCGS0939; ORFNames=ENSANGS0000009986;
OS Anopheles gambiae str. PST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC -I- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008944; EAA10215.1; -.
DR HSSP; Q06319; 1BUC.
DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006089; Acyl-CoA-dh.
DR InterPro; IPR006090; Acyl-CoA-dh_C.
DR InterPro; IPR006091; Acyl-CoA-dh_M.
DR InterPro; IPR006092; Acyl-CoA-dh_N.
DR InterPro; IPR009075; AcylCoADH_C-like.
DR InterPro; IPR009100; AcylCoA_dehyd_NM.
DR Pfam; PF00441; Acyl-CoA_dh; 1.
DR Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
KW FAD; Flavoprotein; Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 604 AA; 65510 MW; F48852A94F3EP51A CRC64;
Alignment Scores:
Pred. No.: 7,97e-75 Length: 604
Score: 1273.50 Matches: 269
Percent Similarity: 64.72% Conservative: 107
Best Local Similarity: 46.30% Mismatches: 170
Query Match: 28.27% Indels: 35
DB: 2 Gaps: 10
US-09-945-326-1 (1-2452) x Q7Q870 (1-604)
QY 163 AGCCGCGCTGTACGA---GCTTTCGCCAAGAGCTTTTCTAGGCAAAATCAAGAGAAA 219
Db 17 AlaProThrValAsnThrSerPheMetAlaAsnLeuPheArgGlyGluIleGluProLeu 36
QY 220 GAAGTTTTCCTCCATTTCCAGAA---GTTAGCAAGATGAACCTTAATGAAATCAATCAGTTC 276
Db 37 GlnValIlePheProPheProAspSerLeuAsnProAspGlnLysGluMetIleGlySerLeu 56
QY 277 TTGGGACCCGCGGAAATAATTCCTTCACTGAAGAGGTGGACTCCCGGAAATAATTTGACAGGAA 336
Db 57 IleAspProValThrLysPhePhe---AspGlyTyrAspProValLysAlaGluLysAsn 75
QY 337 GGGAAATCCAGATGAACAACTTTGGAGAAATTCAGAGGCTAGGCTTTTGGGCTGCAG 396
Db 76 GlyGlyProAspGluAlaThrPheGlnSerMetTyrGluMetGlyLeuMetGlyMetGln 95
QY 397 GTCCCAAGAGATATGTCGCTGGCTTCCTCAACACCATGTACTCAAGCTAGGAGGAG 456
Db 96 AlaProGluGluTyrGlyGlyLeuAlaLeuProAsnThrGlyTyrAlaArgMetGlyGlu 115
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QY 457 ATCATC---AGCATGATGGTCCATCATCTGTGACCCCTGGCAGCGCACCGACTATTGGC 513
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
116 LeuValGlyAlaAlaAspLeuGlyLeuAlaValValPheGlyAlaHisGlnSerIleGly 135
QY 514 CTCAGAGGATCATCTTGGCTGGCACTCAGGAGCAGAAAGCAATACTTCCCTAAACTG 573
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 TrpLysGlyValLeuLeuTyrGlyThrGluGluGlnLysArgLysTyrLeuProGlnVal 155
QY 574 GCGTCCGGGGAGCATTGACGCTTCTGCTCAGGAGCCAGCCAGTCAGTGGAGCGATGCA 633
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
156 ValThrGlyGlyThrIleAlaCysPheCysLeuThrGluProSerSerGlySerAspAla 175
QY 634 GCCTCAATCCGAGCAGACACACTAAGTGAAGACAAAGAGCACTACATCTCTCAATGGC 693
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
176 GlySerIleArgSerArgAlaValLysSerAlaAspGlySerHisTyrValLeuAsnGly 195
QY 694 TCCAGGTCTGGATTAATATGGAGGACTGGCCAAATATTTTACTGTGTGCAAGACT 753
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 SerLysIleTrpIleSerGlyGlyLeuAlaAspIlePheThrValPheAlaGlnThr 215
QY 754 GAGTCTGTTGAT---TCTGATGGATCAGTGAAGACAAAGAGCACTACATCTCTCAATGGC 810
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
216 GluValThrAspProLysThrGlyGlnLysAspLysValThrAlaPheIleValGlu 235
QY 811 AGAGACTTTGGTGGAGTCACATAATGGGAACCCGAGCAATAATTAGGCATTCGGGGCTCC 870
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
236 ArgGlyPheGlyGlyValThrSerGlyProGluAspLysMetGlyIleLysCysSer 255
QY 871 AACACTTGTGAAGTCCATTTTGAANAACACCAAGATACCTGTGGAACAATCTTGGAGAG 930
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 AsnThrAlaGluValTyrPheAspAspValIleProAlaGluAsnValLeuGlyGly 275
QY 931 GTCGAGATGGTTTAAGTGGCCATGAACATCTCAACAGCGCGGTTCACATGGGC 990
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
276 GluGlyAsnGlyPheLysValAlaMetAsnIleLeuAsnAsnGlyArgPheGlyMetSer 295
QY 991 AGCTCTGGCTGGCTGCTCAAGAGATTGATGAATGACTCTGAGTACGCTGCACA 1050
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296 GlyThrLeuAlaGlyThrMetAlaHisCysIleArgLysAlaAlaGluHisAlaThrThr 315
QY 1051 AGGAACAGATTTAACAGAGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCACTG 1110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
316 ArgValGlnPheGlyGlnLysIleGluAsnPheGlyAsnValGlnGluLysLeuAlaArg 335
QY 1111 ATGCTCAGAGCTTACGTATGAGAGATATGACCTACCTCAGCAGCGGATGCTGGAC 1170
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
336 MetAlaMetHisGlnTyrValSerGlnSerMetGlyTyrMetIleSerGlyAsnMetAsp 355
QY 1171 CAACCTGGCTTCCGACTCTCCATCAGGAGCCATGGTGAAGTGTTCAGCTCCGAG 1230
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
356 ---AlaGlyHisThrAspTyrHisLeuGluAlaAlaIleSerLysIlePheSerSerGlu 374
QY 1231 GCGCCTGGCAGTGTGTGAGTAGGCGCTGCAGATCTCGGGGCTTGGGCTACACAAGG 1290
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
375 AlaAlaTrpTyrValCysAspGluAlaIleGlnIleLeuGlyGlyAsnGlyPheMetLys 394
QY 1291 GACTATCCGTACAGCGCATATCGTGTACACCCGATCTCTCTCATCTTCGAGGGAACC 1350
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
395 SerSerGlyLeuGluLysPheLeuArgAspIleArgIleTyrArgIlePheGluGlyAla 414
QY 1351 AATGAGATCTCCGGATGTACATCGCCCTGACGGGTCTGCAGCATCGCGCGCATCTGTG 1410
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
415 AsnAspIleLeuArgLeuPheValThrLeuThrGlyIleGlnTyrAlaGly----- 431
QY 1411 ACTACCAAGATCCATGAGCTTAAACAG-----GCCAAAGTAGACACA 1452
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
432 ---SerHisLeuLysGluLeuGlnArgAlaPheLysAsnProThrAlaAsnLeuGlyLeu 450
QY 1453 GTCATGGATACCGTTGGCGGAGGCTTCGGGACTCTCTGGGCGCAACTGTGGACTGGGG 1512
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
451 IlePheLysGluGlySerArgAlaValArgSerIleGly-----TyrGly 466
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QY 1513 CTGACAGGCAACCATGAGTTGTGACCCAGCTCTTGGGACAGTGCCCAACAAGTTTGAG 1572
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
467 GlyThrAspLeuSerThrPheValValAspProLeuLysGluSerAlaAlaLeuCysAla 486
QY 1573 GAGAACAACCATCTACTGCTTCGGCCGACCGTGGAGACACTCTGCTCCGCTTGGCAAGACC 1632
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
487 AspSerIleAspArgPheSerIleThrIleGluAlaLeuLeuIleLysHisGlyLysGly 506
QY 1633 ATCATGAGAGAGCAGTGGTACTGAAGCGGTGGCCAAACATCTCTCAACACCTGTATGGC 1692
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
507 IleValAspGlnGlnPheLeuLeuIleArgLeuAlaAspSerAlaIleAspIleTyrGly 526
QY 1693 ATGACGCGCTGCTGCGCGGCCAGCCCTCATTCGCTGGGCTCGCAACCAAGAC 1752
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
527 MetSerCysValLeuSerArgAlaSerLysAlaValArgGluAsnAsnProSerAlaGlu 546
QY 1753 CACGAGTCTCTCTGTCGCCAACACCTTCTGCTGGGAAGCT----- 1791
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
547 HisGluLeuLeuMetAlaLysAlaTrpCysValGluAlaAsnAspArgValArgIleAsn 566
QY 1792 -----TACTTGCAGAAATCTCTTCAGCCTCTCTCAGCTGGAC 1827
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
567 IleArgArgValAsnAsnGlyValPheValLysAsnTyrAspThrMetSerAlaIleAla 586
QY 1828 AAG 1830
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
587 Lys 587

RESULT 15
Q19057
ID Q19057 PRELIMINARY; PRT; 613 AA.
AC Q19057;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein E04F6.5.
GN Name=E04F6.5; ORFNames=E04F6.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A.;
RT "The sequence of C. elegans cosmid E04F6.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RT Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
```


RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.

DR EMBL; U28943; AAA68357.1; -;
DR PIR; T15905; T15905.
DR HSP; Q06319; 1BUC.
DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006089; Acyl-CoA dh.
DR InterPro; IPR006090; Acyl-CoA dh.C.
DR InterPro; IPR006091; Acyl-CoA dh.M.
DR InterPro; IPR006092; Acyl-CoA dh.N.
DR InterPro; IPR009100; AcylCoA dehyd_NM.
DR Pfam; PF00441; Acyl-CoA dh; I.
DR Pfam; PF02770; Acyl-CoA dh.M; 1.
DR Pfam; PF02771; Acyl-CoA dh.N; 1.
DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW FAD; Flavoprotein; Hypothetical protein; Oxidoreductase.
SQ SEQUENCE 613 AA; 66171 MW; C1F2883ECE34551B CRC64;

Alignment Scores:

Pred. No.: 1,09e-70 Length: 613
Score: 1210.50 Matches: 272
Percent Similarity: 61.16% Conservative: 109
Best Local Similarity: 43.66% Mismatches: 205
Query Match: 26.88% Indels: 37
DB: 2 Gaps: 14

US-09-945-326-1 (1-2452) x Q19057 (1-613)

QY 85 TTCCTGGCCACACGGCTCGCGCTCGCTCGCGGGTCTGGTGTCTCTACCGCGAAC 144
DB 16 PheileargLeuSerHisSerAlaAlaLys-----AspAlaLysPro 31
QY 145 CGCGGCTACTGCGCACACGCGCCCTGTAGAGCTTTTCGCCAAGAGCTTTCTTAGGC 204
DB 32 LysLysValAlaAlaValAspSerPro-----SerPheValMetAsnLeuPheArgGly 49
QY 205 AAAATCAAGAAAGAAAGTTTCCCATTTCCAGAGTTAGCCAAAGATGAACTTAATGAA 264
DB 50 LysAlaValThrAspGlnValPheProTyProLeuAsnMetThrAspGluGlnLysGlu 69
QY 265 --ATCAATCAGTTCTTGGACCGCTGCAAAATTTCTTCACTAAGAGGTGGACTCCCGA 321
DB 70 ThrLeuGlyMetValMetSerProLeuGluLysMetLeuValGluValAsnAspValVal 89
QY 322 AAAATTGACAGGAAGGAAATCCAGATGAAATTTGGAGAAATTCAGAGAGCTTAGGG 381
DB 90 LysAsnAspGluThrSerAspIleProArgAlaValLeuAspGlnPheAlaGluLeuGly 109
QY 382 CTTTTTGGCTGAAGTCCAGAGAATATGGTGGCTGGCTTCTCAACACCATGTAC 441
DB 110 ThrPheGlyValLeuValProGluLeuGlySerGlyPheAsnAsnSerGlnMet 129
QY 442 TCAAGACTAGGGAGATCATC--AGCATGATGGTCCATCACTGTGACCTGGCAGCG 498
DB 130 AlaArgValAlaGluIleValGlyAlaTyAspLeuGlyPheGlyValValMetGlyAla 149
QY 499 CACGAGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCCAAA 558
DB 150 HisGlnSerIleGlyTyLysGlyIleLeuLeuGlyThrAspAlaGlnLysGlnLys 169
QY 559 TACTTGCTAACTGGGTCCGGGAGCACATTCAGGCTTCTCCCTCAGGAGCCAGCC 618
DB 170 TyrLeuProAspLeuAlaThrGlyArgLysPheAlaPheAlaLeuThrGluProThr 189
QY 619 AGTGGAGCAGTGCAGCTCAATCCGAGCAGAGCCACACTAAGTGAAGACCAAGACAC 678
DB 190 ThrGlySerAspAlaSerSerValArgThrArgAlaGluLeuSerAlaAspGlyLysHis 209
QY 679 TACATCTCAATGGCTCCAAAGGTCTGGATTACTAATGAGGACTGGCCAAATATTTTACT 738

DB 210 TyrValLeuAsnGlyGlyLysIleTrpIleSerAsnGlyGlyPheAlaAspValPheThr 229
QY 739 GTGTTTCAAAGACTGAGGTCTGTGATCGATCGATGGAAGACAAAATCACACA 798
DB 230 ValPheAlaGlnThrProValLysGlnAlaAspGlySerThrLysAspLysMetSerAla 249
QY 799 TTCATAGTAAAGAGACTTTGTGGAGTCACTAATGGGAAACCCGAGATGAATATGAGC 858
DB 250 PheIleValGluArgAlaPheGlyGlyValThrSerGlyProGlnGluLysLysMetGly 269
QY 859 ATTCCGGGCTCCACACTTGTGAAGTCCATTTGAAACACCAAGATACCTGTCGGAAC 918
DB 270 IleLysGlySerAsnThrThrGluValHisPheAspAsnLeuLysIleProValGluAsn 289
QY 919 ATCTCTGGAGAGTCCGAGATGGTGTAAAGTGGCCATGAACATCTCAACAGCGGCGG 978
DB 290 LeuLeuGlyLysGluGlyGlyPheLysValAlaMetAsnIleLeuAsnAsnGlyArg 309
QY 979 TTCAGCATGGCAGCGCTGCTGCTCAAGAGATTGATGAATGAATGACTGCTGAG 1038
DB 310 PheGlyIleProAlaAlaCysThrGlyAlaMetLysHisCysIleGlnLysThrValAsp 329
QY 1039 TAGCCTGCAACAGGAAACAGTTTAAACAGGCTCAGTGAATTTGATTTGATTCAGAG 1098
DB 330 HisIleThrThrArgValGlnPheGlyLysLeuGlnGluPheGlyAsnIleGlnGlu 349
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DB 350 LysLeuValGluMetIleSerLysLeuTyAlaThrGluSerIleValTyMetLeuSer 369
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DB 370 SerAsnMetAspArg--GlyIleLysGluTyGlnLeuGluAlaIleGlyLysVal 388
QY 1219 TTGAGTCCAGGCGCGCTGCGAGTGTGAGTGAGGCGGTGCGAGATCTCCGGGGCTTG 1278
DB 389 LeuAlaSerGluAsnAlaTrpLeuValCysAspAspAlaIleGlnValHisGlyLysMet 408
QY 1279 GGCTACACAAAGGCACTACCTGAGCGCATCTGCTGACACCCGCTCTCTCTCATC 1338
DB 409 GlyPheMetArgGluThrGlyLeuGluArgValLeuArgAspLeuArgIlePheArgIle 428
QY 1339 TTCAGGGAACCAATGAGATTCTCCGAGTGTACATCCCTCGAGCGGTGTGACAGATGCC 1398
DB 429 PheGluGlyAlaAsnAspValLeuArgPheIleAlaLeuThrGlyAlaGlnHisAla 448
QY 1399 GCGCGCATCTGACTACAGGATCCATGAGCTTAAACAGGCCAAAGTGAGCACAGTCATG 1458
DB 449 GlyLys-----HisLeuAlaGluGlnAla-----SerGlyValGly 460
QY 1459 GATACCGTTGCGCGAGGCTTCCGGAGCTCCTCGGCGCACTGTGAGCTGGGGCTGACA 1518
DB 461 GlyLeuIleGlyLeuAlaValSerArgValThrGly-----GlyAsnThr 475
QY 1519 GGC---AACCATGGA---GTTGTGACCCCGAGTTCCTGGGACAGTGCACAAAGTTTGA 1572
DB 476 GlySerAsnPheGlyGlnValValAspAlaSerLeuGlnAspSerAlaLysValLeuAsp 495
QY 1573 GAGNACACCTACTGCTTCCGCGCGAGCGGTGGAGACACTGTGCTCCCGCTTTGGCAAGAC 1632
DB 496 GlnGlnIleAlaLeuPheGlyGlnThrValGlnGlyLeuLeuMetLysHisLysLysGly 515
QY 1633 ATCATGGAGGAGGAGTGTGTAAGCGGTGGCCAACTCTCATCAACCTCTATGGC 1692
DB 516 IleIleAspArgGlnTyGluMetHisArgValAlaAspAlaIleAsnIleTySer 535
QY 1693 ATGAGCGCGCTGTGTCGCGGCGAGCGCTCCATCCGATTCGCGCTCCGCAACACGAC 1752
DB 536 SerAlaAlaValLeuSerArgAlaThrTyAlaIleLysAsnLysSerSerSerAlaAsp 555
QY 1753 CAGAGGTTCTTTGGCCAAACACCTTCTGCTGGAGCTTACTTGTGAGATCTCTTCAGC 1812

Db 556 PheGluArgLysValAla---ThrTyTyValAspLysAlaMetLys-----Ser 571
QY 1813 CTCTCTCAGCTGGACAAAGTATGCTCCAGAAACCTAGACGACAGATTAAAGAAAGTGTC 1872
Db :::: ||| ||| :::: ||| ::::
572 SerAsnArgPheLeuLysAspAlaGlySerGlyValGluAsnAlaSerLysValAlaThr 591
QY 1873 CAGCAGATCCTTCAGAAAGCGAGCCTATATCTGTGCC-----CAC 1911
Db ::: ||| ||| ::: ||| ::: |||
592 IleGluSerLeuAlaLysGlu-----ValCysGlyAsnGlyGlyLeuThrLeuGlnHis 609
QY 1912 CCTCTGGAC 1920
Db ||| ::::
610 ProValGlu 612

Search completed: May 2, 2005, 15:32:15
Job time : 455.764 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 2, 2005, 13:09:41 ; Search time 239.621 Seconds

(without alignments)
6013.950 Million cell updates/sec

Title: US-09-945-326-3

Perfect score: 3423

Sequence: 1 atgagcggctggcggtctt.....acctctggacaggacatgc 1863

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p model -DSV=xlp
-Q/cgn2_1/USPro_spool_p/US09945326/runat 02052005 135410 22344/app query.fasta_1.4686
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09945326 @CGN 1.1 662 @runat 02052005 135410 22344 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq 16Dec04.*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3153	92.1	621	AAB73691	Aab73691 Human oxi
2	3153	92.1	621	AAB94839	Aab94839 Human pro
3	3153	92.1	621	AAE21680	Aae21680 Human acy
4	3153	92.1	621	ADJ69253	Adj69253 Human hea
5	3153	92.1	621	ADJ70247	Adj70247 Human hea
6	3153	92.1	621	ADM87327	Adm87327 Human pro
7	3153	92.1	628	AAU23008	Aau23008 Novel hum
8	3129	91.4	628	ADM87776	Adm87776 Human EST
9	2864	83.7	565	AAB41800	Aab41800 Human ORF
10	2526	73.8	498	AAB94077	Aab94077 Human pro

11	1537	44.9	306	4	AAU23012	Aau23012 Novel hum
12	1360	39.7	655	5	ABB06992	Abb06992 Mouse ver
13	1356.5	39.6	653	5	ABB06991	Abb06991 Rat very
14	1356.5	39.6	655	5	ADE56093	Ade56093 Rat Prote
15	1345	39.3	655	5	ABB06993	Abb06993 Bovine ve
16	1308	38.2	655	5	ABB06988	Abb06988 Human MD2
17	1308	38.2	655	7	ADJ68728	Adj68728 Human hea
18	1308	38.2	655	8	ABM81815	Abm81815 Tumour-as
19	1299	37.9	655	7	ADJ68514	Adj68514 Human hea
20	1295.5	37.8	655	4	ABB63264	Abb63264 Drosophil
21	1284.5	37.5	618	7	ADCI14242	Adci14242 Human enz
22	1284.5	35.4	613	8	ADN22791	Adn22791 Bacterial
23	1122	32.8	527	7	ADCI14245	Adci14245 Human enz
24	980	28.6	202	4	AAU23009	Aau23009 Novel hum
25	954	27.9	188	7	ADJ70246	Adj70246 Human hea
26	954	27.9	188	7	ADJ69636	Adj69636 Human hea
27	844.5	24.7	594	8	ADS27671	Ads27671 Bacterial
28	821	24.0	594	8	ADS28396	Ads28396 Bacterial
29	818	23.9	169	6	ABP76260	Abp76260 Human GEN
30	816	23.8	581	8	ADS30391	Ads30391 Bacterial
31	815.5	23.8	360	7	ADCI14211	Adci14211 Human enz
32	815.5	23.8	594	8	ADS44855	Ads44855 Bacterial
33	799	23.3	585	8	ADN27112	Adn27112 Bacterial
34	795.5	23.2	583	8	ADN27118	Adn27118 Bacterial
35	765	22.3	583	8	ADS21350	Ads21350 Bacterial
36	704	20.6	373	8	ADS27581	Ads27581 Bacterial
37	699	20.4	382	8	ADS27762	Ads27762 Bacterial
38	691.5	20.2	390	7	ABO77312	Abow77312 Pseudomon
39	690	20.2	379	8	ADS28427	Ads28427 Bacterial
40	686.5	20.1	377	8	ADN27173	Adn27173 Bacterial
41	682	19.9	378	8	ADS44766	Ads44766 Bacterial
42	678	19.8	381	8	ADS27885	Ads27885 Bacterial
43	675.5	19.7	379	8	ADS27580	Ads27580 Bacterial
44	666	19.5	389	6	ADA35093	Ada35093 Acinetoba
45	658	19.2	380	8	ADS28426	Ads28426 Bacterial

ALIGNMENTS

RESULT 1

AAB73691
ID AAB73691 standard; protein; 621 AA.

XX AC AAB73691;

XX DT 11-SBP-2001 (first entry)

XX DE Human oxidoreductase protein ORP-24.

XX KW Human oxidoreductase protein; ORP; cell proliferative disorder;
KW arteriosclerosis; cirrhosis; psoriasis; cancer; endocrine disorder;
KW diabetes mellitus; diabetes insipidus; dwarfism; hirsutism; amenorrhea;
KW osteoporosis; metabolic disorder; obesity; phenylketonuria;
KW hypercholesterolaemia; reproductive disorder; infertility;
KW ovulatory defect; menstrual cycle defect; endometriosis;
KW polycystic ovary disease; spermatogenesis disruption; impotence;
KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; Creutzfeldt-Jakob disease;
KW meningitis; cerebral palsy; muscular dystrophy; mood disorder; anxiety;
KW schizophrenic disorder; infection; autoimmune disorder;
KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS; asthma;
KW allergy; Crohn's disease; atopic dermatitis; gout; multiple sclerosis;
KW rheumatoid arthritis; ulcerative colitis; drug screening;
KW toxicity screening; transgenic animal; SNP detection; gene therapy.

XX OS Homo sapiens.

XX WO200144448-A2.

XX PD 21-JUN-2001.

XX PF 07-DEC-2000; 2000WO-US033158.

XX

PR 16-DEC-1999; 99US-0172367P.
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 XX Yue H, Lal P, Tang YT, Hillman JL, Baughn MR, Azimzai Y, Lu DAM;
 PI WPI; 2001-390245/41.
 DR N-PSDB; AAH24246.
 XX
 XX Novel human oxidoreductase protein (ORP) useful for diagnosing, treating
 PT and preventing cell proliferative, neurological, viral, reproductive and
 PT autoimmune/inflammatory disorders associated with abnormal expression of
 PT ORP.
 XX
 XX Claim 1; Page 117-119; 136pp; English.
 XX
 XX Sequences AAB73668-AAB73694 represent 27 novel human oxidoreductase
 CC proteins, designated ORP-1 to ORP-27 respectively, and sequences AAH24223
 CC -AAH24249 represent cDNAs encoding ORP-1 to ORP-27. Human ORP proteins
 CC and nucleic acids are useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. arteriosclerosis, cirrhosis, psoriasis,
 CC cancers); endocrine disorders (e.g., type I or II diabetes mellitus,
 CC diabetes insipidus, dwarfism, hirsutism, amenorrhea, osteoporosis);
 CC metabolic disorders (e.g., obesity, phenylketonuria,
 CC hypercholesterolemia); reproductive disorders (e.g., infertility,
 CC ovulatory and menstrual cycle defects, endometriosis, polycystic ovary
 CC disease, disruption of spermatogenesis, impotence); neurological
 CC disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's
 CC disease, Parkinson's disease, meningitis, Creutzfeldt-Jakob disease,
 CC cerebral palsy, muscular dystrophy, mood, anxiety and schizophrenic
 CC disorders); viral, bacterial, fungal and parasitic infections; and
 CC autoimmune/inflammatory disorders such as acquired immunodeficiency
 CC syndrome (AIDS), allergies, asthma, Crohn's disease, atopic dermatitis,
 CC gout, multiple sclerosis, rheumatoid arthritis or ulcerative colitis.
 CC Human ORP proteins and nucleotides can be used to identify compounds
 CC which modulate their activity or expression. ORP nucleic acid sequences
 CC may also be used for assessing the toxicity of a test compound, to detect
 CC upstream sequences such as promoters and regulatory elements, and to
 CC create knock out or knock in animals or transgenic animals to model human
 CC disease. Oligonucleotide primers derived from ORP gene sequences may be
 CC used to detect single nucleotide polymorphisms (SNPs) and for mapping the
 CC naturally occurring genomic sequences. Antibodies specific for ORP
 CC proteins may be used in the diagnosis of disorders associated with
 CC aberrant ORP expression, in assays to monitor patients being treated with
 CC ORP or modulators thereof, and for assessing toxicity of potential drugs
 XX
 XX Sequence 621 AA;
 SQ
 Alignment Scores:
 Pred. No.: 1.33e-287 Length: 621
 Score: 3153.00 Matches: 621
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 92.11% Indels: 0
 DB: 4 Gaps: 0
 US-09-945-326-3 (1-1863) x AAB73691 (1-621)
 QY 1 ATCAGCGGCTGCGGGCTCTTCTCCGCGCACCGCTGCGGCTCGCTCGCGGGCTCG 60
 Db 1 MetSerGlyCysGlyLeuPheLeuArgThrThralaalaargalaCysArgGlyLeu 20
 QY 61 GTGGTCTCTACCGCAACCGGGCTACTCGCGCACCGCGCGCTGTACGAGCTTTCCGCC 120
 Db 21 ValValSerThrAlaAenArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40
 QY 121 AAGAGCTTTCTAGCGAAATCAGAGAAAGAGTTCCTCCATTTCCAGAGTTAGC 180
 Db 41 LysGluLeuPheLeuGlyLysIleLysLysLysLysLysLysLysLysLysLysLys 60
 QY 181 CAAGATGAATTAATGAATCAATCAGTTCTTGGGACCGCTGGAAAAATTTCTTCACTGAA 240
 Db 61 GlnAspGluLeuAsnGluIleAenGlnPheLeuGlyProValGluLysPhePheThrGlu 80

QY 241 GAGGTGACTCCCGAAAAAATTGACCAAGGAGGAAAAATCCAGATGAAACTTTGGAGAAA 300
 Db 81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100
 QY 301 TTCAGAGCCCTAGGGCTTTTGGGCTGCAAGTCCCGAGAGAAATATGTTGGCTCGGCTTC 360
 Db 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluGlyGlyGlyLeuGlyPhe 120
 QY 361 TCAACACCATGTTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCCATCACTGTG 420
 Db 121 SerAsnThrMetTyrSerArgLeuGlyGluIleSerMetAspGlySerIleThrVal 140
 QY 421 ACCCTGGCAGCGCACCGACTATTGGCTCAAGGGGATCATCTTGGCTGGCATCAGGAG 480
 Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleLeuAlaGlyThrGluGlu 160
 QY 481 CAGAAAGCCAAATACTTGTCTAAACTGGGCTCGGGGAGCACATTCAGGCTTCTGCCTC 540
 Db 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180
 QY 541 ACGAGCCAGCCAGTGGGAGCGATGCGCTCAATCCGAGCAGAGCCACACTAACTGAA 600
 Db 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
 QY 601 GACAAGAAGCACTACATCTCTCAATGGCTCCAGGCTCGGATTAATCGAGGACTGGCC 660
 Db 201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
 QY 661 AATATTTTACTGTGTGTTCGAAAGACTGAGGTCGTTGATTCTGATGATCAGTGAAGAC 720
 Db 221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
 QY 721 AAATCAGACGATTCATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGGAACCCGAA 780
 Db 241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260
 QY 781 GATAAATTAGGATTCGGGGCTCCAACTGTGAAGTCCATTTTCAAAACCAAGATA 840
 Db 261 AspLysLeuGlyLysArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
 QY 841 CTGTGGAAAAATCTCTGGAGAGTTCGAGATGGGTTTAAAGTGGCCATGAACATCTC 900
 Db 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
 QY 901 AACAGCGCGGCTGAGCATGGCGCTCGTGGCTGGCTGCTCAAGAGATTGATTGA 960
 Db 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLysArgLeuIleGlu 320
 QY 961 ATGACTGCTGAGTACGCTGCAAGGAAACAGTTTAAACAGAGGCTCAGTGAATTTGA 1020
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 QY 1021 TTGATTCAGGAGAAATTTGCACTGATGGCTCAGAGGCTTACGTATGAGAGATGACC 1080
 Db 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
 QY 1081 TACCTCAGACGAGGATGCTGCAACCTGGCTTTCCGACTGCTCCATCCGAGGCGAC 1140
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 QY 1141 ATGGTGAAGGTTTTCAGCTCCGAGCGCGCTGGCAGTGTGTGAGTGGCGCTGCAGATC 1200
 Db 381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400
 QY 1201 CTCGGGGCTGGGCTACACAGGAGCTATCCGTACGAGCGCATACTGGGTGACACCCGC 1260
 Db 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
 QY 1261 ATCTCTCTCATCTTCAGGAGAACCAATCAGATTCTCCGATGTACATCGCTGACGGGT 1320
 Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440

QY 1321 CTGACGATCCGCGCCGATCCTGACTACACGAGATCCATGAGCTTAACAGGCCAAAGTG 1380
Db 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY 1381 AGCACACTGATGATACCGTTGGCCGAGGCTTCGGGACTCCCTGGGCCGAACTGTGGAC 1440
Db 461 SerThrValMetAspThrValGlyArgLeuArgLeuArgSerLeuGlyArgThrValAsp 480
QY 1441 CTGGGGCTGACAGCAACCACTGAGTTGTGCACCCAGTCTTGGGACAGTGCACCAAG 1500
Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY 1501 TTTGAGGAGAACACTACTGCTTCGCGCCGACCGTGAGACATGCTGCTCCGCTTTGGC 1560
Db 501 PheGluGluAsnThrTyrcysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
QY 1561 AAGACCATCATGAGGAGGAGCTGTTACTGAAGCGGTGGCCACATCTTCATCAACCTG 1620
Db 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
QY 1621 TATGGCATGACGCGCTGCTGTGCGGGCCAGCGCTCCATCCGATTTGGGCTCCGCAAC 1680
Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY 1681 CAGCAACACGAGGTTCTCTTTGGCCAAACACTTTCGCTGGAAGCTTACTTGCAGAACTC 1740
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
QY 1741 TTCAGCCTCTCTGCTGAGCAAGTATGCTCCAGAAACCTAGATGACAGATTAGAAA 1800
Db 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
QY 1801 GTGTCCACGACAGATCCTTTGAGACGAGCCTATATCTGTGCCACCTCTGGACAGGACA 1860
Db 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
QY 1861 TGC 1863
Db 621 Cys 621

RESULT 2
AAB94839
ID AAB94839 standard; protein; 621 AA.
XX
AC AAB94839;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:16010.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
PT
PT
XX
PS Claim 8; SEQ ID NO 16010; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention
XX
SQ Sequence 621 AA;
Alignment Scores:
Pred. No.: 1.33e-287 Length: 621
Score: 3153.00 Matches: 621
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.11% Indels: 0
DB: Gaps: 0
US-09-945-326-3 (1-1863) x AAB94839 (1-621)
QY 1 ATGAGCGGTGCGGGCTCTTCCTGCGCACACCGCTGCGGCTCGTCTCCCGGGGTCTG 60
Db 1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu 20
QY 61 GTGGTCTCTACCGAACCAGCGGCTACTGCGCACCGCCGCTGTACGAGCTTTCGCC 120
Db 21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40
QY 121 AAAGAGCTTTCTCCTAGGCAAAATCAAGAGAAAGAGTTTTCCTATTTCCAGAGTTAGC 180
Db 41 LysGluLeuPheLeuGlyLysIleLysLysLysLysLysLysLysLysLysLysLys 60
QY 181 CAAGATGAATTAATCAATCAATAGTTCTTGGGACCCCTGGGAAATTTCTTCACTGAA 240
Db 61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80
QY 241 GAGGTGACTCCCGAAAAATTTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Db 81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100
QY 301 TTGAAGAGCCTTAGGGCTTTTGGGCTGCAAGTCCCAAGAAATATGTCGCTGGGCTTC 360
Db 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyLeuGlyPhe 120
QY 361 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCCATCCTGTG 420
Db 121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
QY 421 ACCCTGGCAGCGCACCGAGCTATTGGCTCAAGGGGATCATCTTGGCTGCACCTGGAG 480
Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160

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QY 481 CAGAAAGCAAATACTTGCCTAAACTGGCGTCCGGGAGCACATTGACGCCCTTCTGCCTC 540
Db 161 GlnTysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180
QY 541 ACGGAGCCAGGAGTGGAGCGATGACGCTCAATCCGGAGACAGCCACACTAAGTAA 600
Db 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
QY 601 GACAAAGAGCACTACATCCTCAATGGCTCCAAAGTCTGGATTACTAATGGAGACTGCC 660
Db 201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
QY 661 AATATTTTTACTGTGTTTGAAGACATGAGTCCGTTCATTTCTGATGGATCAGTCAAAAGAC 720
Db 221 AsnIlePheThrValPheAlaLysThrGluValAlaAspSerAspGlySerValLysAsp 240
QY 721 AAAATCACAGCAATTCATAGTAGAAGAGACATTTGGTGGAGTCACATAATGGGAACCCGAA 780
Db 241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260
QY 781 GATAAATTAGGCATTCGGGGCTCCAAACACTTGTGAAGTCCATTTTGAACACACCAAGATA 840
Db 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
QY 841 CCTGTGGAACATCCTTTGGAGAGGTCGAGATGGGTTTAAGTGGCCATCAACATCCTC 900
Db 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
QY 901 AACAGCGCGGTTTCAGCATGGGCGAGCGTGGTGGTTCAGTGGTTCAGAGCAATTCATTGAA 960
Db 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
QY 961 ATGACTGCTGAGTACGGCTCCAGCAAGAAACAGTTTAAAGAGGCTCAGTGAATTTGGA 1020
Db 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
QY 1021 TTGATTACAGGAAATTTGCATGATGGCTCAGAGGCTTACGTCATGGAGATATGACC 1080
Db 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
QY 1081 TACCTTCACAGCAGGATGCTGGACCAACCTGGCTTCCGACATTCGCTCCATCGAGGCGGCC 1140
Db 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
QY 1141 ATGTTGAAGTGTTCAGCTCCGAGCGCGCTGGCAGTGTGTGAGTGAAGCGCTGCAGATC 1200
Db 381 MetValLysValPheSerSerGluAlaAlaTyrGlnCysValSerGluAlaLeuGlnIle 400
QY 1201 CTCGGGGCTTGGGTACACAAGGCACTATCCGTACGAGCGCATACTGGGTGACACCCGC 1260
Db 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
QY 1261 ATCCTCTCATCTTCGAGGGAACCAATGAGATTCTCCGATGTACATCGCCCTGACGGGT 1320
Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY 1321 CTGAGCATCCCGCGCATCTCTGACTACAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
Db 441 LeuGlnHisAlaGlyArgIleLeuThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY 1381 AGCAGATCATGATACCGTTGGCCGAGGCTTCGGGACTCCCTGGCGCGCAACTGGGAC 1440
Db 461 SerThrValMetAspThrValGlyArgGlyLeuArgAspSerLeuGlyArgThrValAsp 480
QY 1441 CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCGAGTCTTGGGACAGTGCACCAAG 1500
Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY 1501 TTTGAGGAGAACACCTACTGCTTCGGCGCGGACCGTGGAGACACTGCTGCTCGCTTGGC 1560
Db 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
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QY 1561 AAGACCATCATGAGGAGCAGCTGTACTGAAGCGGGTGGCCCAACATCTCTCATCAACCTG 1620
Db 521 LysThrIleMetGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
QY 1621 TATGGCATGACGCGCTGTGTCTCGCGGCAGCGCTCCATCCGCAATTTGGGCTCCGCAAC 1680
Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY 1681 CAGACCCAGCAGGTTCTTCTGGCCCAACACTTCTGGTGGGAAGCTTACTTGCAGAAATCTC 1740
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
QY 1741 TTGAGCTCTCTCAGCTGGACAAAGTATGTCTCCAGAAAACCTAGATGAGCAGATTAAGAAA 1800
Db 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
QY 1801 GTTCTCCAGCAGATCTTGGAGAGCGAGGCTATATCTGTGCCACCCTCTTGGACAGGACA 1860
Db 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
QY 1861 TGC 1863
Db 621 Cys 621

RESULT 3
AAE21680
ID AAE21680 standard; protein; 621 AA.
XX
AC AAE21680;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human acyl dehydrogenase DHDR-7 (62112 protein).
XX
KW Human; dehydrogenase-7; DHDR-7; 62112 protein; CNS disorder; epilepsy;
KW Alzheimer's disease; AS; Pick's disease; differentiation disorder;
KW Huntington's disease; autonomic function disorder; hyperthyroidism;
KW depression; schizophrenia; panic migraine; cardiac related disorder;
KW anxiety; obesity; arteriosclerosis; testenosis; Parkinson's disease;
KW angina; hypertension; cardiomyopathy; arrhythmia; muscle weakness;
KW arterial inflammation; cell proliferation disorder; growth disorder;
KW diabetes mellitus; hypertension; migration disorder; gene therapy;
KW fertility disorder; autoimmune disorder; metabolic disorder; ataxia;
KW cancer; hepatic disease; acyl-CoA dehydrogenase; beta-oxidation; enzyme.
XX
OS Homo sapiens.
XX
FH Key
FT Domain
FT /note= "Dehydrogenase domain"
FT 23..123
FT /note= "Dehydrogenase precursor domain"
FT 37..426
FT /note= "Acyl-coA very long chain dehydrogenase domain"
FT 70..432
FT /note= "dehydrogenase-related long acyl-coA chain
FT oxidoreductase domain"
FT 74..448
FT /note= "Short chain related acyl-coA dehydrogenase
FT specific domain"
FT 85..438
FT /note= "Acyl CoA dehydrogenase domain"
FT 85..177
FT /note= "Acyl CoA dehydrogenase middle domain"
FT 147..431
FT /note= "ACD-3 acyl-coA dehydrogenase domain"
FT 172..549
FT /note= "Oxidoreductase acyl-coA dehydrogenase family
FT domain"
FT 179..286
FT /note= "Acyl CoA dehydrogenase C-terminal domain"
FT 179..191
FT /note= "Acyl CoA dehydrogenase signature 1"
```

FT	Domain	207. .604	
FT		/note= "Acyl-coA oxidase dehydrogenase oxidoreductase	
FT		flavoprotein domain"	
FT	Domain	290. .441	
FT		/note= "Acyl CoA dehydrogenase N-terminal domain"	
FT	Region	399. .418	
FT		/note= "Acyl CoA dehydrogenase signature 2"	
FT	Domain	408. .611	
FT		/note= "Dehydrogenase butyryl domain"	
FT	Domain	432. .580	
FT		/note= "Polysaccharide deacetylase domain"	
FT	Domain	438. .621	
FT		/note= "Very long chain dehydrogenase domain"	
FT	Region	460. .476	
FT		/note= "Sugar transport protein signature"	
XX	WO200218582-A2.		
XX			
XX	07-MAR-2002.		
XX			
XX	31-AUG-2001; 2001WO-US0271186.		
XX			
XX	31-AUG-2000; 2000US-0229831P.		
XX			
XX	(MILL-) MILLENNIUM PHARM INC.		
XX			
XX	Meyers R, Hunter JJ;		
PI			
XX			
XX	WPI; 2002-329775/36.		
DR			
DR	N-PSDB; AAD344006.		
XX			
XX	New human dehydrogenase polypeptide for diagnosing and treating		
PT	dehydrogenase-7 associated diseases and disorders e.g. Alzheimer's		
PT	disease, and to identify modulators of therapeutic use.		
XX			
XX	Claim 13; Fig 1; 124pp; English.		
XX			
XX	The invention relates to human dehydrogenase (DHDR)-7 polypeptides		
CC	referred to as 62112 and nucleic acid molecules encoding such		
CC	polypeptides. DHDR-7 is an acyl-CoA dehydrogenase, a mitochondrial		
CC	flavoprotein which catalyses the first step of fatty acid beta-		
CC	oxidation. Sequences of the invention and their antibodies are useful for		
CC	treating a disorder, disease or condition which is caused by		
CC	misregulation (e.g. downregulation or upregulation) of DHDR activity.		
CC	Examples of disorders include central nervous system (CNS) disorders e.g.		
CC	Alzheimer's disease (AS), Pick's disease, Parkinson's, Huntington's		
CC	disease, Gilles de la Tourette's syndrome, multiple sclerosis, epilepsy,		
CC	amyotrophic lateral sclerosis and Creutzfeldt-Jakob disease; autonomic		
CC	function disorders e.g. hypertension, depression, schizophrenia, panic		
CC	migraine, anxiety, obsessive-compulsive disorder and obesity; cardiac		
CC	related disorder e.g. arteriosclerosis, ischaemia reperfusion injury,		
CC	restenosis, arterial inflammation, angina, hypertension, cardiomyopathy		
CC	and arrhythmia; disorders of musculus skeletal system paralysis, muscle		
CC	weakness e.g. ataxia; cell proliferation, growth, differentiation or		
CC	migration disorders e.g. cancer, diabetes mellitus, hypothyroidism or		
CC	hyperthyroidism; reproductive or fertility disorders; autoimmune or		
CC	immune deficiency disorders; hepatic disease or dysfunction and metabolic		
CC	disorders. They are used for screening assays, predictive medicine e.g.		
CC	diagnostic assays, prognostic assays, monitoring clinical trials, and		
CC	pharmacogenetics. Polypeptides of the invention are used to identify		
CC	modulators that modulate their activity. Polynucleotides of the invention		
CC	are used in gene therapy. The present sequence is human DHDR-7		
XX			
XX	Sequence 621 AA;		
SQ			

Alignment Scores:	1.33e-287	Length:	621
Pred. No.:	353/00	Matches:	621
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	92.11%	Gaps:	0
DB:	5		

US-09-945-326-3 (1-1863) x AAE21680 (1-621)

Qy	1	ATGAGCGGCTGCGGCTCTTCTCGCGCACACGCGCTGGGCTGTGCTCTGCGGGCTCTG	60
Db	1	MetSerGlyCySgLyLeuPheLeuArgThrThrAlaAlaArgAlaCysArgGlyLeu	20
Qy	61	GTGCTCTACTACCGAACCAGCGGCTACTGCGCACCGCGCTGTACGAGCTTTCGCC	120
Db	21	ValValSerThrAlaAsnArgLeuLeuArgThrSerProProValArgAlaPheAla	40
Qy	121	AAAGAGCTTTCTTAGCCAAATCAAGAAAGAAAGTTTTCCTATTTCCAGAAAGTTAGC	180
Db	41	LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer	60
Qy	181	CAAGATGAATTAATGAATCAATCAATCTTGGGACCGGTGGGAAAATTTCTTCACTGAA	240
Db	61	GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu	80
Qy	241	GAGGTGACCTCCGCAAAATTTGACGAGGAGGAAAATCCAGATGAAACTTTCGAGAAA	300
Db	81	GluValAspSerArgLysIleAspGlnGlyLysIleProAspGluThrLeuGluLys	100
Qy	301	TTGAAAGACCTAGGCTTTTGGCTCCAAGTCCAGAAATATGTTGGCTGGGCTTC	360
Db	101	LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyGlyLeuGlyPhe	120
Qy	361	TCCAACACCATGTACTCAAGACTAGGGAGATCATCAGCATGGATGGGTCCATCACTGTG	420
Db	121	SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal	140
Qy	421	ACCTGCGACGGCNCAGGCTNTTGGCTCAAGGGATCATCTTGGCTGGGCACTGAGAG	480
Db	141	ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu	160
Qy	481	CAGAAAGCCAAATCTTGCCTAAACTGCGTCGCGGGAGCACATTGCAGCCTTCTGCCTC	540
Db	161	GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu	180
Qy	541	ACGGAGCCAGCCAGTGGGAGCGATGCAGCCTCAATCCGGAGCAGAGCCACACTAAGTGA	600
Db	181	ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu	200
Qy	601	GACAAGACACTACATCCTCAATGGCTCCAGGCTCGGATTACTATGAGGAGCTGCC	660
Db	201	AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla	220
Qy	661	AATATTTTACTGTGTTGCAAGACACTGAGTCCGTTGATTCGTGATGATCAGTGAAGAC	720
Db	221	AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp	240
Qy	721	AAAATCACAGCATTCATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAA	780
Db	241	LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu	260
Qy	781	GATAAATTAGGCATTCGGGCTCCAACACTTGTGAAGTCCCATTTTGAACACCCAGATA	840
Db	261	AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle	280
Qy	841	CCTGTGGAAACATCCTTGGAGAGCTCGGAGATGGGTTAAGTGGCCATCAACATCCCTC	900
Db	281	ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu	300
Qy	901	AACAGCGGCGGTTTCAGCATGGGCGGCTCGTGGCTGGGCTGCTCAAGAGATGATTCGA	960
Db	301	AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu	320
Qy	961	ATGACTCTCAGTAGCGCTGCACAAGGAAACAGTTTAAACAGAGGCTCAGTGAATTTGGA	1020
Db	321	MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly	340
Qy	1021	TTGATTCAAGAGAAATTTGCATGTGGCTCAGAGGCTTACGTATCGAGAGTATGACC	1080
Db	341	LeuIleGlnGlyLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr	360

QY 1081 TACCTCACAGCAGGATGCTGGACCAACCTTCCGACTGCTCCATCGAGCGAGCC 1140
 DB |||||
 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaA 380
 QY 1141 ATGGTGAAGGTGTTGAGTCCGAGGCCGCCCTGGCAGTGTGTGAGTGAAGCGCTCGAGATC 1200
 DB |||||
 381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400
 QY 1201 CTCGGGGCTTGGGCTACACAGGAGCTATCGTACGAGCGCATCTGCGTGAACACCGC 1260
 DB |||||
 401 LeuGlyGlyLeuGlyTyThrArgAspTyrProLysGluArgIleLeuArgAspThrArg 420
 QY 1261 ATCTCTCTCATCTTCGAGGGGAACCAATGAGATTCTCCGGATGTATCATCGCCCTCACCGGT 1320
 DB |||||
 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
 QY 1321 CTGAGCATGCGGGCGGATCCTGATACACAGGATCCATGAGCTTAACAGGCCAAAGTG 1380
 DB |||||
 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
 QY 1381 AGCAGCTCATGGATACCGTTGGCGGAGGCTTCGGGACTCCCTGGCGCGAATGTGGAC 1440
 DB |||||
 461 SerThrValMetAspThrValGlyArgGluArgAspSerLeuGlyArgThrValAsp 480
 QY 1441 CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCACTCTTCGGGACAGTGCCCAACAG 1500
 DB |||||
 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
 QY 1501 TTTGAGGAGACACTACTGCTTCGGCGGACCGGTGGAGACATGCTGCTCCGCTTTGGC 1560
 DB |||||
 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
 QY 1561 AAGACCATCATGGAGGACAGCTGCTACTGAAGGGGTGGCAACATCCATCAACCTG 1620
 DB |||||
 521 LysThrIleMetGluGluGlnLeuValLeuLysValValAlaAsnIleLeuIleAsnLeu 540
 QY 1621 TATGGCATGACGGCGGTGTGTGCGGGCCAGCGCTCCATCGCATTTGGGCTCCGCAAC 1680
 DB |||||
 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
 QY 1681 CAGACACACAGGTCTCTTGGCCCAACCTTCTGCTGGAAGCTTACTTGGAGATCTC 1740
 DB |||||
 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
 QY 1741 TTCAGCCTCTCTCAGCTGGACAAGTATGCTCCAGAAACCTAGATGACAGATTAAGAAA 1800
 DB |||||
 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
 QY 1801 GTGTCCAGCAGATCTTTGAGAGCGGAGCCTATATCTGTGCCCAACCTCTGGACAGGACA 1860
 DB |||||
 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
 QY 1861 TGC 1863
 DB |||||
 621 Cys 621

RESULT 4

ADJ69253
 ID ADJ69253 standard; protein; 621 AA.

AC
 XX
 AC
 XX
 DT
 XX

06-MAY-2004 (first entry)

Human heat mitochondrial protein as a therapeutic target SeqID1059.

DE
 XX
 KW
 XX

mitochondrial; human; screening assay; diabetes mellitus;

Huntington's disease; osteoarthritis;

Leber's hereditary optic neuropathy; LHON;

mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

osteopathic; ophthalmological; cytostatic.

OS Homo sapiens.

FN WO2003087768-A2.

PD 23-OCT-2003.

XX 04-APR-2003; 2003WO-US010870.

XX 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987P.

PR 20-SEP-2002; 2002US-0412418P.

XX (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI Warnock DE;

XX WPI; 2003-845369/78.

DR
 XX Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.

PS Claim 1; SEQ ID NO 1059; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.

XX Sequence 621 AA;

Alignment Scores:

Pred. No.: 1.33e-287 Length: 621
 Score: 3153.00 Matches: 621
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 92.11% Indels: 0
 DB: 7 Gaps: 0

US-09-945-326-3 (1-1863) x ADJ69253 (1-621)

QY 1 ATGAGCGGCTGGGGCTCTTCTGTCGGCACCGCTGGGCTCGTCCGCCGGGCTG 60

DB 1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaArgAlaCysArgGlyLeu 20

QY 61 GTGGTCTCTTACCGGAACCGGGGCTACTGTGGCACCAGCCCGCTGTACGAGCTTTCGCC 120

DB 21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40

QY 121 RAAGAGCTTTCTCTAGGCAAAATCAAGAAGAAGATTTTCCATTTCACAGATTAGC 180

DB 41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer 60

QY 181 CAAGATGAACCTTAATGAAATCAATCAGTTCTTGGACCCGCTGGAAAAATTTCTCACTGAA 240

DB 61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80


```
QY 241 GAGTGAGCTCCGAAAAATTGACGAGAGGAAAAATCCAGATGAACCTTTGGAGAAA 300
Db 81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100
QY 301 TTGAAGAGCTTAGGGCTTTTGGGCTCAAGTCCAGAGAATAATGTGGCTGGGCTTC 360
Db 101 LeuYsSerLeuGlyLeuPheGlyLeuGlnValProGluGluThrGlyGlyLeuGlyPhe 120
QY 361 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGGTCCATCCTGTG 420
Db 121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
QY 421 ACCCTGCGAGGACACAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCAGCTAGGAG 480
Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160
QY 481 CAGAAAGCCAAATACTTGGCTTAAACTCGCGTCCGGGAGCAGCATTCGAGCTTCTGCCTC 540
Db 161 GlnYsAlaLysTyrLeuProLysLeuAlaSerGlyGlnHisIleAlaIlePheCysLeu 180
QY 541 ACGGAGCCAGCTAGGGAGCGATGACAGCTCTCAATCCGGAGCAGAGCCACACTAAGTGAA 600
Db 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
QY 601 GACAGAGCACTACATCTCAATGGCTCAAGTCTCGAATTACTTAATGAGAGCTGGCC 660
Db 201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
QY 661 AATATTTTACTGTGTTGCAAGACTGAGTGGTTCGATTCATCTGATGATCAGTCAAGAGC 720
Db 221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
QY 721 AAAATCAGCAGCATTCATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGGAACCCGAA 780
Db 241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260
QY 781 GATAAATTAGGCATTCGGGCTCCAAACACTTGTGAAGTCCATTTTGAACACCAAGATA 840
Db 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
QY 841 CTTGTGGAACATCTCTGAGAGGTCGGAGAGTGGTTTAAGTGGCCATGAACATCCTC 900
Db 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
QY 901 AACAGCGCGCGTTTCAGCATGGCGCTGCTGGCTGCTCAAGAGATTGATTGAA 960
Db 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
QY 961 ATGACTGCTGAGTACGCTGCACAAGAAACAGTTTAAAGAGGCTCAGTGAATTGGA 1020
Db 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
QY 1021 TTGATTCAGAGAAATTTGCACTGATGGCTCAGAGGCTTACGTCATGAGAGATGACC 1080
Db 341 LeuIleGlnLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
QY 1081 TACTCTCAGCAGGAGTGTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGAGGCC 1140
Db 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaIle 380
QY 1141 ATCGTGAAGGTGTTACGCTCCGAGGCGCTGCGAGTGTGTGAGTAGGCGCTGCAGATC 1200
Db 381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400
QY 1201 CTCGGGGCTTGGCTACACAAGGACTATCCGTACGAGCGCATCTGCTGACACCCGC 1260
Db 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
QY 1261 ATCCTCTCATCTTCAGAGGAACCAATGAGATTCTCCGAGTGTACATCGCCCTGACGGGT 1320
Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY 1321 CTCAGCATCCGCGCGCATCTCTGACTACAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
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Db 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY 1381 AGCACAGTCTATGATACCGTTGGCCGAGGCTTCGGGACTCCCTGGGCGCAACTGTGGAC 1440
Db 461 SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480
QY 1441 CTGGGCTGACAGGCAACCATGAGTTGTGCACCCAGTCTTGGGACAGTGCACCAAG 1500
Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY 1501 TTTGAGGAGAACACCTACTGCTTCGCGCGACCGTGGAGACACTGCTGCTCCGCTTTGGC 1560
Db 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
QY 1561 AAGACCATCATGAGCAGCAGCTGTGTCTCGCGGCGAGCGCTCCATCCGATTTGGGCTCCGCAAC 1620
Db 521 LysThrIleMetGluGlnLeuValLeuValLeuArgValAlaAsnIleLeuIleAsnLeu 540
QY 1621 TATGGCATGACGCGCTGTGTCTCGCGGCGAGCGCTCCATCCGATTTGGGCTCCGCAAC 1680
Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY 1681 CAGACCCAGAGTTCTTCTGGCCAAACACTTCTCGTGGAGCTTACTTGCAGAACTTC 1740
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
QY 1741 TTCAGGCTCTCTCAGCTGGACAAGTAGTGTCCAGAAAACTTAGATGACAGATTAAGAAA 1800
Db 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
QY 1801 GTCTCCAGCAGATCCTTGAGAAAGCAGGCTATATCTGTCCCAACCTCTTGGACAGACA 1860
Db 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
QY 1861 TGC 1863
Db 621 Cys 621
RESULT 5
ADJ70247
ID ADJ70247 standard; protein; 621 AA.
AC ADJ70247;
XX 06-MAY-2004 (first entry)
XX
XX
XX Human heat mitochondrial protein as a therapeutic target SeqID2053.
XX mitochondrial; human; screening assay; diabetes mellitus;
XX Huntington's disease; osteoarthritis;
XX Leber's hereditary optic neuropathy; LHON;
XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
XX osteoprotectic; ophthalmological; cytostatic.
XX Homo sapiens.
XX
XX WO2003087769-A2.
XX
XX 23-OCT-2003.
XX
XX 04-APR-2003; 2003WO-US010870.
XX
XX 12-APR-2002; 2002US-0372843P.
XX 17-JUN-2002; 2002US-0389987P.
XX 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
XX (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
PI
```

PI Warnock DE;
XX WPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
XX Claim 1; SEQ ID NO 2053; 180pp; English.
XX
XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cyostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 621 AA;

Alignment Scores:
Pred. No.: 1.33e-287 Length: 621
Score: 3153.00 Matches: 621
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.11% Indels: 0
DB: 7 Gaps: 0

US-09-945-326-3 (1-1863) x ADJ70247 (1-621)

QY 1 ATGAGCGCTGCGGCTCTCTCGGCACACCGCTGCGCTGCGCTGCGGCTCTG 60
DB 1 MetSerGlyCysGlyLeuPheLeuArgThrAlaAlaAlaArgAlaCysArgGlyLeu 20
QY 61 GTGGTCTCTACCGCAACCGCGGCTACTGCGCACCGCCGCTGTACAGCTTTGCGC 120
DB 21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProValArgAlaPheAla 40
QY 121 AAGAGCTTTCTAGGCAAAATCAAGAAAGAGATTTTCCATTTCCAGAACTTAC 180
DB 41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer 60
QY 181 CAAGATCAACTTAATGAAATCAATCAGTCTTGGACCGGTGAAATTTCTCACTGAA 240
DB 61 GluAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80
QY 241 GAGGTGACTCCCGAAAAATTGACAGGAAGGAAAAATCCAGATGAAATTTGGAGAAA 300
DB 81 GluValAspSerArgLysIleAspGlnGluLysIleProAspGluThrLeuGluLys 100
QY 301 TTGAAGAGCTAGGCTTTTGGCTGCAAGTCCAGAGAAGATATGTTGGCTGGGCTTC 360
DB 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluThrGlyGlyLeuGlyPhe 120
QY 361 TCAACACCATGTACTCAAGACTAGGGAGATCATCAGCATGGATGGTCCATCACTGTG 420
DB 121 SerAsnThrMetThrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
QY 421 ACCCTGGCAGCGCACCAAGGCTATTGGCTCAAGGGATCATCTTGGCTGGCACTAGGAG 480
DB 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160
QY 481 CAGAAAGCCAAATATCTTGCTCTAACTGGCTCGGGGAGGACATTTGAGCCTTCTGCTC 540

DB 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180
QY 541 ACGGACCCAGCCAGTGGGAGCGATGAGCTCAATCCGAGAGAGAGCCACACTAAGTGAA 600
DB 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
QY 601 GACAAGAAGCAGCTACATCTCAATGGCTCAAGGTCTGAAGTCTTAATGAGGAGCTGGCC 660
DB 201 AspLysLysHisTyrIleLeuAsnGlySerLysValTyrIleThrAsnGlyGlyLeuAla 220
QY 661 AATATTTTACTGTGTTGCAAGACTGAGGTCTGTTGATTTCTCATGATGATCAGTGAAGAC 720
DB 221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
QY 721 AAAATCACAGCATTCATAGTAGAAGAGAGCTTTGGTGGAGTCACTAATGGGAACCCGAA 780
DB 241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260
QY 781 GATAAATTAGGCAATTCGGGGCTCCAAACACTGTGTGAAGTCCATTTTGAACACCAAGATA 840
DB 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
QY 841 CCTGTGAAAAACATCTCTGAGAGGTGCGAGATGGGTAAAGTGGCCATGACATCCTC 900
DB 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
QY 901 AACAGCGCGCGTTTCAGCATGGCAGCGCTCGTGGCTGGCTCAAGAGATTGATTGAA 960
DB 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
QY 961 ATGACTGCTGAGTACGCTCGACAGAAACAGTGTAAACAAGAGGCTCAGTGAATTGGA 1020
DB 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
QY 1021 TTGATTGAGAGAAATTTGCACTGATGGCTCAGAGGCTTACGTCACTGAGAGATGAGC 1080
DB 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
QY 1081 TACTCTACAGAGGAGTGTGGCAACCTGGCTTTCCGACTGCTCCATCGAGGAGGCC 1140
DB 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
QY 1141 ATGTTGAAGGTGTACGCTCCGAGCGCGCTGCGAGTGTGTAGTGAAGCGCTGCGAGATC 1200
DB 381 MetValLysValPheSerSerGluAlaAlaTyrGlnCysValSerGluAlaLeuGlnIle 400
QY 1201 CTCGGGGCTTGGCTTACACAGGGAGTATCGTACGAGCGCATCTCGGTGAGCCCGC 1260
DB 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
QY 1261 ATCCTCTCATCTTCCAGGGAAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1320
DB 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY 1321 CTGACGATCGCGCGCGCATCTCTGACTACAGATCCATGAGCTTAAACAGGCCAAAGTG 1380
DB 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY 1381 AGCAGATCATGATACCTTGGCCGGAGCTTGGGAGCTCCCTGGCGCGCACTGTGGAC 1440
DB 461 SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480
QY 1441 CTGGGCTGACAGGCAACCATGAGTGTGTGACCCCGAGTCTTGGGAGACAGTGCACCAAG 1500
DB 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY 1501 TTTGAGGAGAACACCTTACTGTCTTGGCCCGGACCGTGGAGACACTGTCTGCTCCCTTGGC 1560
DB 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
QY 1561 AAGACCATCATGAGGAGCAGCTGTGAGCGGGTGGCCAAACATCTCATCAACCTG 1620
DB 521 LysThrIleMetGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540

QY 1621 TATGGCATGACGCGCTGCTGCTCGCGGGCCAGCGCTCCATCCGATGGGCTCCGCAAC 1680
 DB 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerileArgileGlyLeuArgAsn 560
 QY 1681 CAGACCCAGCAGGTTCTTGGGCAACACCTTCTGGTGAAGCTTACTTGCAGATCTC 1740
 DB 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
 QY 1741 TTCAGCCTCTCAGCTGGACAAGTAGTGTCCAGAAACCTAGATGACGAGATTAAGAAA 1800
 DB 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
 QY 1801 GTCTCCAGCAGATCTTGAGAGCGAGCTATATCTGTCCCAACCTCTGGACAGGACA 1860
 DB 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
 QY 1861 TGC 1863
 DB 621 Cys 621
 RESULT 6
 ID ADM87327 standard; protein; 621 AA.
 XX
 AC ADM87327;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human protein SEQ ID NO:420.
 XX
 KW respiratory; cytostatic; antiarthritic; antiinflammatory;
 KW gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
 KW antirheumatic; gene therapy; molecular weight marker; chromosome marker;
 KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
 KW inflammatory condition; arthritis; inflammatory bowel disease;
 KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
 KW graft versus host disease; human.
 XX
 OS Homo sapiens.
 XX
 FN WO2004009834-A2.
 XX
 PD 29-JAN-2004.
 XX
 PF 19-JUL-2002; 2002WO-US022858.
 XX
 PR 21-JUL-2001; 2001US-0306971P.
 PR 28-MAR-2002; 2002US-00112944.
 XX
 PA (NUVE-) NUVELO INC.
 XX
 PI Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
 PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
 PI
 DR WPI; 2004-143291/14.
 DR N-PSDB; ADM87083.
 XX
 PT New isolated polynucleotides and polypeptides, useful for treating, e.g.
 PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
 PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
 PT versus host disease.
 XX
 PS Claim 20; SEQ ID NO 420; 591pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I): (a)
 CC comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
 CC which encodes a polypeptide with biological activity, where the
 CC polynucleotide hybridises to (I) under stringent hybridisation conditions
 CC or has greater than 95% sequence identity with (I). (I) has respiratory,
 CC cytostatic, antiarthritic, antiinflammatory, gastrointestinal,
 CC antibacterial, immunosuppressive, antidiabetic and antirheumatic
 CC activities, and can be used in gene therapy. (I) can be used for

CC generating polynucleotides encoding chimeric or fusion proteins and
 CC heterologous protein sequences. The polynucleotides can be used to
 CC express recombinant protein for analysis, characterisation or therapeutic
 CC use; as markers for tissues in which the corresponding protein is
 CC preferentially expressed; as molecular weight markers on gels; as
 CC chromosome markers or tags to identify chromosomes or to map related gene
 CC positions; to compare with endogenous DNA sequences in patients to
 CC identify potential genetic disorders; as probes to hybridise and discover
 CC genes, related DNA sequences; as a source of information to derive PCR
 CC primers for genetic fingerprinting; as a probe to subtract-out known
 CC sequences in the process of discovering other novel polynucleotides; for
 CC selecting and making oligomers for attachment to a gene chip or other
 CC support, including for examination of expression patterns; to raise anti-
 CC protein antibodies using DNA immunisation techniques; and as an antigen
 CC to raise anti-DNA antibodies or elicit another immune response. The
 CC polynucleotides and polypeptides can also be used as nutritional sources
 CC or supplements, e.g. as a protein or amino acid supplement, as a carbon
 CC source, as a nitrogen source or as a source of carbohydrates. The
 CC polynucleotides and polypeptides can also be used to treat cancer. The
 CC compositions are useful for promoting better or faster closure of non-
 CC healing wounds, for the generation and regeneration of tissues, for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, and conditions resulting from
 CC systemic cytokine damage. The compositions can also be used to treat
 CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
 CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
 CC or graft versus host disease. The present sequence represents a novel
 CC human polypeptide sequence from the present invention. N.B. The sequences
 CC for this patent were obtained from the USPTO web site from an equivalent
 CC US patent US20040048249A1.
 XX

Sequence 621 AA;

Alignment Scores:
 Pred. No.: 1,33e-287 Length: 621
 Score: 3153.00 Matches: 621
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 92.11% Indels: 0
 DB: Gaps: 0

US-09-945-326-3 (1-1863) x ADM87327 (1-621)

QY 1 ATGAGCGGTGCGGGCTCTTCTGCGCACACGGCTGCGGCTCGTCCGCCGGGTCTG 60
 DB 1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu 20
 QY 61 GTGGTCTCTACCGGNAACCGGGGCTACTCGGCACCGCCGCTGTACGAGCTTTGCGC 120
 DB 21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40
 QY 121 AAAGAGCTTTTCTAGGCAAAATCAAGAAGAAGAGTTTCCCATTTCCAGAAAGTTAGC 180
 DB 41 LysGluLeuPheLeuGlyLysIleLysLysLysLysGluValPheProPheProGluValSer 60
 QY 181 CAAGATGAACCTTAATCAATCAGTTCTTGGGACCGCTGGAAATAATTTCTTCACGTAA 240
 DB 61 GlnAspGluLeuAsnGlnIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80
 QY 241 GAGTGGACTCCGAAAAATTGACCAGGAGGAAAAATCCAGATGAAATTTGGAGAAA 300
 DB 81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100
 QY 301 TTGAAGAGCTAGGGCTTTTGGGCTGCAAGTCCCAAGAAGAATATGGTGGCTGGGCTTC 360
 DB 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyLeuGlyPhe 120
 QY 361 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCCATCATGTG 420
 DB 121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
 QY 421 ACCTGGACGCGCACCGAGCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTAGGAG 480

Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160
QY 481 CAGAAAGCCAAATCTTGCCTAAACTCGCTCCGGGAGACACATTCGAGCTTCTGCCTC 540
Db 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180
QY 541 ACGGAGCCAGCCAGTCGGGAGCGATGACAGCTCAATCCGGAGCAGAGCCACACTAAGTGAA 600
Db 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
QY 601 GACAAGAGCAGCTACATCTCAATGGCTCCAAAGTCTGGATTACTAATGAGAGCTGGCC 660
Db 201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
QY 661 AATATTTTACTGTGTTGAAAGACGAGTGGTTCATTCATTCGATGATCAGTGAAGAC 720
Db 221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
QY 721 AAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGGAGTCACTAATGGGAAACCCGAA 780
Db 241 LysIleThrAlaPheIleValGluArgAspPheGlyValThrAsnGlyLysProGlu 260
QY 781 GATAAATAGGCATTCGGGCTCAACACTTGTAAGTCCATTTGAAACACCAAGATA 840
Db 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
QY 841 CCTGTGGAACATCCTTGCAGAGGTCGGAGATGGGTTTAAAGTGGCCATGAACATCCTC 900
Db 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
QY 901 AACAGCGCCGGTTCAGCATGGGACGCTCGTGGCTGCTCAAGAGATTGATTGAA 960
Db 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
QY 961 ATGACTGCTGACTACGCTCTCAACAGAAACACTTTAAACAGAGGCTCAGTAATTGGA 1020
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QY 1021 TTGATTTCAGAGAAATTTGCACATGGCTCAGAGGCTTACGTCATGAGAGATATGACC 1080
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Db 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
QY 1141 ATGGTGAAGGTGTCAGTCCGAGGCGGCTGCGAGTGTGTGAGTGGCGCTGCAGATC 1200
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QY 1261 ATCCTCCTCATCTTCAGGGAACCAATGAGATTCTCCGATGTACATCCCTCGACGGGT 1320
Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY 1321 CTGCAGCATCCCGCGCATCCTGACTACAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
Db 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY 1381 AGCAGAGTCATGATACCGTTGGCCGGAGGCTTCGGGACTCCCTGGCGCGAACTGTGGAC 1440
Db 461 SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480
QY 1441 CTGGGCTCAGAGGCAACATGAGATTGTGACCCAGTCTTCGGGACAGTCCCAACAG 1500
Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY 1501 TTTGAGGAGAACACCTTACTGCTTCGGCCGGACGCTGGAGACACTGCTGCTCCGCTTGGC 1560
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QY 1561 AAGACCATCATGGAGCAGAGCTGGTACTGAACCGGGTGGCCAAACATCTCATCAACCTG 1620
Db 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
QY 1621 TATGGCATCAGCGCCGCTGTGTCGGGGCAGCGCTCCATCCGCAATTCGGCTCCGCAAC 1680
Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY 1681 CACGACCCAGAGTTCTTTCGCCCACACCTTTCGTCGTGGAAGCTTACTTCGAGAATCTC 1740
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
QY 1741 TTCAGCTCTCTCAGCTGACAGATATGCTCCAGAAAAACCTAGATGAGCAGATTAAAGAA 1800
Db 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
QY 1801 GTGTCCACAGCATCTTCGAGAAGCAGGCTATATCTGTGCCACCCCTCTGGACAGGACA 1860
Db 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
QY 1861 TGC 1863
Db 621 Cys 621
RESULT 7
AAU23008
ID AAU23008 standard; protein; 628 AA.
XX AAU23008;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human enzyme polypeptide #94.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001239.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465566/50.
XX N-PSDB; AAS40878.
XX
XX Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Claim 11; SEQ ID NO 1004; 1180pp; English.
XX
XX The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. AAU2915-AAU23814 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 628 AA;

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 Pred. No.: 1.34e-287 Length: 628
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 Best Local Similarity: 100.00% Mismatches: 0
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US-09-945-326-3 (1-1863) x AAU23008 (1-628)

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 Db 28 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 47
 Qy 121 AAAGAGCTTTTCTAGGCAAAATCAAGAAGAAAGATTTTCCCATTTCCAGAAATTTAGC 180
 Db 48 LysGluLeuPheLeuGlyLysIleLysLysLysLysValPheProPheProGluValSer 67
 Qy 181 CAAGATGAACCTTAATGAATCAATCACTTCTTGGACCCGCTGGAAAAATTTCTCACTGAA 240
 Db 68 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 87
 Qy 241 GAGTGAACCTCCGAAAAATTTGACAGAGAGGAAATCCAGATGAACCTTTGGAGAAA 300
 Db 88 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 107
 Qy 301 TTGAAGAGCTTAGGGCTTTTGGGCTGCAAGTCCAGAGAATAATGTGTGGCTTGGGCTTC 360
 Db 108 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluThrGlyGlyLeuGlyPhe 127
 Qy 361 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCCATCATCTGTG 420
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 Qy 421 ACCCTGGCAGGCGACCGGCTATTGGCTCAAGGGATCATCTTGGCTGGCAGTGGAG 480
 Db 148 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleLeuAlaGlyThrGluGlu 167
 Qy 481 CAGAAAGCCAAATCTTGCTTAAACTTGGCGTCCGGGAGCAGCATCTGAGCTTCTGCTC 540
 Db 168 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 187
 Qy 541 ACGAGCGCAGCATCTGGAGCGATGCGACCTCAATCCGGAGCAGAGCCACACTAAGTGAA 600
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 Qy 601 GACAGAGACATCATCTCAATGGCTCCNAGTCTGGATTACTAATGAGGACTGGCC 660
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 Qy 1501 TTTGAGGAGAACACCTTACTGCTTCGGCCGACCGTGGAGACACTGCTGCTCCGCTTTGGC 1560
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 Db 528 LysThrIleMetGluGlnLeuValLeuLysArgValAlaAlaAsnIleLeuIleAsnLeu 547
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 Db 548 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 567
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 ID ADM87776 standard; protein; 628 AA.
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 AC ADM87776;
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Pred. No.: 2,29e-260 Length: 565
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-09-945-326-3 (1-1863) x AAB41800 (1-565)

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DB 62 LeuGlyPheSerAsnThrMetTyrSerArgLeuGlyGluLeuLeuSerMetAspGlySer 81
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DB 282 GluPheGlyLeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGlu 301
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QY 1252 GACACCCGCAATCTCTCATCTTCGAGGGGAACCAATGAGATTTCTCCGGATGTATCATCGCC 1311
DB 362 AspThrArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAla 381
QY 1312 CTGAGCGGTCTGCAAGATGCCGCGCATCTCTGATACCAAGGATCCATGAGCTTAAACAG 1371
DB 382 LeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGln 401
QY 1372 GCCAAGTAGACACAGTCATGGATACCGTTGGCGGAGGCTTCGGGACTCCCTGGGCCGA 1431
DB 402 AlaLysValSerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArg 421
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DB 422 ThrValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSer 441
QY 1492 GCCAACAAAGTTTGAAGAGAAACACTACTGCTTGGCGCGGACCGTGGAGACACTGCTGCTC 1551
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QY 1552 CGCTTTGGCAAGACCATCATGGAGGAGCAGCTGTACTGAAGCGGTGGCCCAACATCCTC 1611
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DB 482 IleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGly 501
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DB 502 LeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeu 521
QY 1732 CAGAACTCTTTCAGCTCTCTCAGCTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAG 1791
DB 522 GlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGln 541
QY 1792 ATTAAGAAAGTGTCCCAAGCATCTTTCAGAGCGAGCTATATCTGTGCCCACTCTG 1851
DB 542 IleLysLysValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeu 561
QY 1852 GACAGGACATGC 1863
DB 562 AspArgThrCys 565
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XX AAB94077;
XX 26-JUN-2001 (first entry)
XX DE
XX Human protein sequence SEQ ID NO:14271.
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX Homo sapiens.
XX EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-00116126.
XX 29-JUL-1999; 99JP-00248036.
PR
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PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX (HELI-) HELIX RES INST.
 PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 PI WPI; 2001-318749/34.
 DR
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 XX
 PS Claim 8; SEQ ID NO 14271; 2537pp + Sequence Listing; English.
 CC
 CC The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
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 Alignment Scores:
 Pred. No.: 1,62e-228 Length: 498
 Score: 2526.00 Matches: 498
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 73.79% Indels: 0
 DB: 4 Gaps: 0
 US-09-945-326-3 (1-1863) x AAB94077 (1-498)

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 DB 121 AlaPheIleValGluAargPheGlyGlyValThrAsnGlyLysProGluAAspLysLeu 140
 QY 790 GGCATTGGGGCTCCAACTTGTGAAGTCCATTTTGAAGAACCAAGATACCTGTGGAA 849
 DB 141 GlyIleAargGlySerAsnThrCysGluValHisPheGluAsnThrLysIleProValGlu 160
 QY 850 AACATCTTGGAGAGTCCGAGATGGTTTAAAGTGCATGAACATCTCTCAACAGGGC 909
 DB 161 AsnIleGluGlyValGluAAspGlyPheLysValAlaMetAsnIleLeuAsnSerGly 180
 QY 910 CGGTTTCAGATGGGAGCGCTCGTGGCTGGGCTCTCAAGAGATTGATTGAAATGACTGCT 969
 DB 181 ArgPheSerMetGlySerValValAlaGlyLeuLeuLysAargLeuIleGluMetThrAla 200
 QY 970 GAGTAGCCCTGCACAGGAAACAGTTTAAACAGAGGCTCAGTGAATTTGGATTGATTTCAG 1029
 DB 201 GluTyrAlaCysThrArgLysGlnPheAsnLysAargLeuSerGluPheGlyLeuIleGln 220
 QY 1030 GAGAAATTTGCATGATGCTCAGAAAGGCTTACGTTCATCGAGAGTATGACCTACCTCACA 1089
 DB 221 GluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThrLysLeuThr 240
 QY 1090 GCAGGATGCTGCACCAACTGGCTTTCGACTGCTCCATCGAGCGACGCCATGTTGTAAG 1149
 DB 241 AlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAlaMetValLys 260
 QY 1150 GTGTTTCAGTCCGAGCGCCCTGGAGTCTGTGAGTGCAGCGCTGCAGATCTCTCGGGGC 1209
 DB 261 ValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIleLeuGlyGly 280
 QY 1210 TTGGGCTACCAAGGACTATCCGTACGAGCGCATCTCCGTGACACCCGCACTCTCTCCT 1269
 DB 281 LeuGlyTyrThrArgAspTyrProTyrGluAargLysLeuAargAspThrArgIleLeuLeu 300
 QY 1270 ATCTTCGAGGAAACCAATGAGATTCTCGGATGTATCATCGCTTCAGCGGTCTGCAGCAT 1329
 DB 301 IlePheGluGlyThrAsnGluIleLeuAargMetTyrIleAlaLeuThrGlyLeuGlnHis 320
 QY 1330 GCCGGCGCATCTGACTACAGGATCCATGAGTCTAAACGCGCAACTGACGACAGTC 1389
 DB 321 AlaGlyAargIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysValSerThrVal 340
 QY 1390 ATGGATACCGTTTGGCGGAGGCTTCGGGACTCCCTGGGCGCAACTGTGTGACCTGGGGCTG 1449
 DB 341 MetAspThrValGlyAargArgLeuAargPheSerLeuGlyAargThrValAspLeuGlyLeu 360
 QY 1450 ACAGCAACCATGGAGTGTGTGACCCCGAGTCTTGGGACAGTGCACCAAGTTTGAAGAG 1509
 DB 361 ThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLysPheGluGlu 380
 QY 1510 AACACTACTGCTTCGGCGGACCGTGGAGACACTGCTGCTCCGCTTTTGGCAAGCAATC 1569
 DB 381 AsnThrTyrCysPheGlyAargThrValGluThrLeuLeuAargPheGlyLysThrIle 400
 QY 1570 ATGGAGGACGACTGGTACTGAAGCGGTGGCCAACTCTCATCAACCTGTATGGCATG 1629
 DB 401 MetGluGluGlnLeuValLeuLysAargValAlaAsnIleLeuIleAsnLeuTyrGlyMet 420
 QY 1630 AGCGCGGTGCTGTCCGGCGGACCGCTCCATCCGATTTGGCTCCGCAACCAACGACCAAC 1689
 DB 421 ThrAlaValLeuSerAargAlaSerAargSerIleAargIleGlyLeuAargAsnHisAspHis 440
 QY 1690 GAGGTTCTCTTGGCCAAACACCTTCTCGGTGGGAAGCTTACTTCAGAACTCTTTCAGCCTC 1749
 DB 441 GluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeuPheSerLeu 460

Qy 1750 TCTCAGCTGCAGACAGTATGCTCCAGAAAACCTAGATGACGAGATTAGAAGTGTCCTCCAG 1809
Db 461 SerGlnLeuAspLy8tyrAlaProGluAsnLeuAspGluGlnIleLysLysValSerGln 480
Qy 1810 CAGATCTCTCAGAGACGAGCCTATATCTGTGCCACCTCTGGACAGGACATGC 1863
Db 481 GlnIleLeuGluLy8ArgAlaIlyrIleCysAlaHisProLeuAspArgThrCys 498

RESULT 11
AAU23012
ID AAU23012 standard; protein; 306 AA.
AC AAU23012;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human enzyme polypeptide #98.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001239.
XX
PR 31-JAN-2000; 2000US-0179065P.
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PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
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PR 17-NOV-2000; 2000US-0249211P.
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 PR 01-DEC-2000; 2000US-0250160P.
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 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
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 PR 08-DEC-2000; 2000US-0251869P.
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 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254037P.
 PR 03-JAN-2001; 2001US-02559678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-465566/50.
 DR N-PSDB; AAS40892.
 XX
 PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,
 PT treating neural, immune system, muscular, reproductive, pulmonary,
 PT cardiovascular, renal, proliferative disorders and cancerous diseases.
 XX
 PS Claim 11; SEQ ID NO 1008; 1180pp; English.
 XX
 CC The present invention relates to the isolation of novel human enzyme
 CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
 CC encoding them. The enzyme polypeptides of the invention may comprise the
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
 CC isomerases or ligases. The sequences of the invention are useful in the
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of
 CC disorders including hyperproliferative disorders (e.g. cancer),
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
 CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
 CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
 CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
 CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
 CC infectious disorders (e.g. Influenza). The polynucleotides of the
 CC invention can also be used in gene therapy. AAU22915-AAU23814 represent
 CC the novel human enzyme polypeptides of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 306 AA;
 XX
 Alignment Scores:
 Pred. No.: 2,34e-135 Length: 306
 Score: 1537.00 Matches: 302
 Percent Similarity: 99.34% Conservative: 0
 Best Local Similarity: 99.34% Mismatches: 2
 Query Match: 44.90% Indels: 0
 DB: 4 Gaps: 0
 XX
 US-09-945-326-3 (1-1863) x AAU23012 (1-306)
 QY 952 TTGATTCAATGACTGCTGAGTAGCGCTGCACAGGAAACAGTTTAAACAGAGCTCAGT 1011
 Db 3 Leu***GluMetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSer 22
 QY 1012 GAATTTGGATTGATTCAGGAGAAATTTGCATGATGCTCAGAGGCTTACGTCATGGAG 1071

Db 23 GluPheGlyLeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGlu 42
 QY 1072 AGTATGACCTACCTCACAGCAGGATGCTGGACCAACTGGCTTCCCGACTGCTCCATC 1131
 Db 43 SerMetThrTyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIle 62
 QY 1132 GAGGCAGCCATGGTGAAGGTGTTACAGTCCGAGCGCCCTGGCAGTGTGTGAGTGAAGCGC 1191
 Db 63 GluAlaAlaMetValLysValPheSerSerGluAlaAlaTyrGlnCysValSerGluAla 82
 QY 1192 CTGCAGATCTCTGGGGCTTGGGCTACACAAGGACTATCTCGTACGAGCGCATCTGCGT 1251
 Db 83 LeuGlnIleLeuGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArg 102
 QY 1252 GACACCGCATCTCTCTCATCTTCGAGGGAACAATAGAGATCTCCGGTGTACATCGCC 1311
 Db 103 AspThrArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuLeuArgMetTyrIleAla 122
 QY 1312 CTGACGGGTCTGCAGCATGCCGCCGCATCTCTGACTACAGGATCCATGAGCTTAAACAG 1371
 Db 123 LeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGln 142
 QY 1372 GCCAAAGTGAGCACACTATGATACCGTTTGGCCGGAGGCTTCGGGACTCCCTGGGCCGA 1431
 Db 143 AlaLysValSerThrValMetAspThrValGlyArgArg***ArgAspSerLeuGlyArg 162
 QY 1432 ACTGTGACCTGGGCTGCAGCGCAACCATGGAGTTGTGCACCCAGTCTTTCGGGACAGT 1491
 Db 163 ThrValAspLeuGlyLeuThrGlyAsnHisGlyValHisProSerLeuAlaAspSer 182
 QY 1492 GCCAAAGTTTGGAGAGAACACTACTGTTCCGGCCGGACCGTGGAGACACTGCTGCTC 1551
 Db 183 AlaAsnLysPheGluGlnAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeu 202
 QY 1552 CGTTTGGCAAGACCATCATGAGGAGCAGCTGGTACTGAGAGCGCTGGTACTGAGCGGTGGCCACATCCTC 1611
 Db 203 ArgPheGlyLysThrIleMetGluGlnLeuValLeuLysArgValAlaAsnIleLeu 222
 QY 1612 ATCAACTCTGTATGGCATGACGCCGCTGTCTCGCGCCGAGCGCTCCATCCGATGGG 1671
 Db 223 IleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGly 242
 QY 1672 CTCGCCAACACACACGAGGTTCTCTTTGGCCAAACACCTTCTCGTGGAGGCTTACTTG 1731
 Db 243 LeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeu 262
 QY 1732 CAGAATCTCTTACGCTCTCTGAGTGGACAAGTATGCTCCAGAAAACCTAGATGAGCAG 1791
 Db 263 GlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGln 282
 QY 1792 ATTAAGAAAGTGTCCAGCAGATCCCTTGAGAGCGAGCTATATCTGTGCCACCTCTG 1851
 Db 283 IleLysLysValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeu 302
 QY 1852 GACAGGACATGC 1863
 Db 303 AspArgThrCys 306
 XX
 RESULT 12
 ABB06992
 ID ABB06992 standard; protein; 655 AA.
 XX
 AC ABB06992;
 XX
 DT 20-JUN-2002 (first entry)
 XX
 DE Mouse very long chain acyl-CoA dehydrogenase (VLCAD) protein SEQ ID:10.
 XX
 KW Human; MD25; VLCAD; very long chain acyl-CoA dehydrogenase; IRAP;
 KW insulin responsive aminopeptidase; GLUT4; glucose transporter 4;
 KW antidiabetic; intracellular regulation; glucose metabolism; diabetes;
 KW glucose transport; hyperglycaemic disorder.

XX	Mus sp.
OS	
XX	
XX	WO200216428-A1.
FN	
XX	
XX	28-FEB-2002.
PD	
XX	
XX	20-AUG-2001; 2001WO-JP007117.
PF	
XX	
XX	21-AUG-2000; 2000JP-00254263.
PR	
XX	07-SEP-2000; 2000JP-00276633.
PR	
XX	(TAKE) TAKEDA CHEM IND LTD.
FA	
XX	
XX	Tojo H, Katayama N, Kakimoto S;
PI	
XX	
XX	WPI; 2002-269344/31.
DR	
XX	
XX	Protein binding to insulin-responsive aminopeptidase and glucose
PT	transporter 4, useful for prevention and treatment of diseases associated
PT	with blood sugar level disturbance.
XX	
PS	Disclosure; Page 92-95; 103pp; Japanese.
XX	
CC	The present invention describes human MD25 (very long chain acyl-CoA
CC	dehydrogenase (VLCAD), which binds to insulin-responsive aminopeptidase
CC	(IRAP) and to glucose transporter 4 (GLUT4). MD25 has antidiabetic
CC	activity. IRAP and GLUT4 are involved in the intracellular regulation of
CC	glucose metabolism and glucose transport across the cell membrane.
CC	Expression of MD25 (whose ligands are these proteins) is also involved in
CC	this regulatory process. MD25 can be used in the prevention, treatment
CC	and diagnosis of diseases involving disturbances of glucose metabolism,
CC	such as diabetes and other hyperglycaemic disorders. The present sequence
CC	represents mouse VLCAD which is given in the exemplification of the
CC	present invention
XX	
SQ	Sequence 655 AA;

Alignment Scores:

Pred. No.:	1,96e-118	Length:	655
Score:	1360.00	Matches:	287
Percent Similarity:	66.05%	Conservative:	106
Best Local Similarity:	48.24%	Mismatches:	184
Query Match:	39.73%	Indels:	18
DB:	5	Gaps:	9

US-09-945-326-3 (1-1863) x ABB05992 (1-655)

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Db	66	ProAlaArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrIle	85	
Qy	151	AAAGAGCTTTCCGATTTCCAGAGTT---	ACCCAGATGAACCTTAATGAATCAATCATCAG	207
Db	86	AspGlnValPheProTyrProSerValLeuSerGluGluGlnAlaGlnPheLeuLysGlu	105	
Qy	208	TTCTTGGGACCGTCGAAATAATCTTCTCACTGAAGAGGTGGACTCCCGAAAAATTTGACCAG	267	
Db	106	LeuValGlyProValAlaArgPhePheGluGluValAsnAspProAlaLysAsnAspAla	125	
Qy	268	GAAGGGAAATCCCAAGATCAAACTTTGGAGAAATTCAGAGCGCTAGGGCTTTTGGGGCTG	327	
Db	126	LeuGluLysValGluAspThrLeuGlnGlyLeuLysGluLeuGlyAlaPheGlyLeu	145	
Qy	328	CAAGTCCCAAGAATAATGTTGGCCCTGGGCTTCTCCAACACCATGCTACTCAAGACTAGG	387	
Db	146	GlnValProSerGluLeuGlyGlyLeuGlyLeuSerAsnThrGlnTyrAlaArgLeuAla	165	
Qy	388	GAGATCATCAGCATG--GATGGGTCATCACTGTGACCCCTCGACGCGCACCGAGCTATT	444	
Db	166	GluIleValGlyMeHisAspLeuGlyValIleValThrLeuGlyAlaHisGlnSerIle	185	
Qy	445	GGCTTCAAGGGGATCATCTTGGCTGGCATCTAGGAGGACGAGAACCAAAATACTTGGCTAAA	504	

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QY 85 CTACTGCGC-----ACGAGCCCGCTGTACGA 111
Db 48 ValLeuGluLysProGluThrLeuSerSerAspAlaSerThrArgGluLysProAlaArg 67
QY 112 GCT-----TTCCGCCAAGAGCTTTTCTTAGGCAAAATCAAGAAAGAAAGATT 159
Db 68 AlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGlnVal 87
QY 160 TTCCCATTTCCAGAGTTAGCCAGATCAACTTAATGAA-----ATCAAT 204
Db 88 PheProTyrProSerVal-----LeuAsnGluGlyGlnThrGlnPheLys 103
QY 205 CAGTTCTTGGGACCGCTGCAAAATTTCTCACTGAAGAGGTGGACTCCCGAAATATTGAC 264
Db 104 GluLeuValGlyProValAlaArgPheGluGluValAsnAspProAlaLysAsnAsp 123
QY 265 CAGGAGGGAATATCCAGATGAATTTGGAGAAATTTGAAGAGCCCTAGGGCTTTTGGG 324
Db 124 SerLeuGluLysValGluGluAspThrLeuGlnGlyLeuLysGluLysAlaPheGly 143
QY 325 CTGCAAGTCCAGAGATATGTTGGCTGGCTTCTTCCACACCATGTACTCAAGACTA 384
Db 144 LeuGlnValProSerGluLeuGlyGlyLeuGlyLeuSerAsnThrGlnTyrAlaArgLeu 163
QY 385 GGGGAGATCATCAGCATG---GATGGGTCCATCACTGTGACCTGGCAGCGCACAGGCT 441
Db 164 AlaGluLeuValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGlnSer 183
QY 442 ATTGGCTCAAGGGATCATCTTGGCTGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 501
Db 184 IleGlyPheLysGlyLeuLeuLeuTyrGlyThrLysAlaGlnLysGluLysTyrLeuPro 203
QY 502 AAATCTGGGCTCCGGAGCAGCATTTGAGCTTCTGCTCAGCGAGCAGCGAGTGGAGC 561
Db 204 ArgValAlaSerGlyGlnAlaLeuAlaPheCysLeuThrGluProSerSerGlySer 223
QY 562 GATCAGCCTCAATCCGGAGCAGGCCACACTAAGTGAAGACAGAGCACTACATCCTC 621
Db 224 AspValAlaSerIleArgSerSerAlaValProSerProCysGlyLysTyrThrLeu 243
QY 622 AATGGCTCCAGGCTCTGATTAATGAGGAGTGGCCCAATATTTTACTGTGTTGCA 681
Db 244 AsnGlySerLysIleThrPheSerAsnGlyGlyLeuAlaAspIlePheThrValPheAla 263
QY 682 AAGACTCAGGTCGTGTGAT---TCTGATGATCAGTGAAGACAAATTCACAGCATTCATA 738
Db 264 LysThrProIleLysAspAlaAlaThrGlyAlaValLysGluLysIleThrAlaPheVal 283
QY 739 GTAGAAAGAGACTTTGTGGAGTCACTAATGGGAACCCGAGATAAATTAGGCATTCGG 798
Db 284 ValGluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGlyIleLys 303
QY 799 GGCTCCACACTTGTGAGTCCATTTTGAAGAACCCGAGATACCTGTGGAAACATCCTT 858
Db 304 AlaSerAsnThrSerGluValTyrPheAspGlyValLysValProAlaGluAsnValLeu 323
QY 859 GGAGAGTCGGAGATGGTTTAAAGTGGCCATCAACATCTCTCAACAGCGCGGTTTCAGC 918
Db 324 GlyGluValGlyAspGlyPheLysValAlaValAsnIleLeuAsnAsnGlyArgPheGly 343
QY 919 ATGGGAGCGCTGCTGGCTGGCTGCTCAAGAGATTTGATTAAGATGCTGCTGAGTACGCC 978
Db 344 MetAlaAlaThrLeuAlaGlyThrMetLysAlaIleAlaLysAlaValAspHisAla 363
QY 979 TGCACAGGAAACAGTTTAAACAGAGCTCAGTGAATTTGGATTGATTCAGGAGAAATTT 1038
Db 364 ThrAsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLysLeu 383
QY 1039 GCATGATGCTCAGAGGCTTACGTATGGAGATGATGACCTACCTCAGCAGCGGATG 1098
Db 384 AlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAlaAsn 403

QY 1099 CTGGACCAACCTGGCTTCCGACTGCTCATCAGAGCAGCCATGCTGAGAGGTGTTTCAGC 1158
Db 404 MetAspGln---GlyPheLysAspPheGlnIleGluAlaIleSerLysIlePheGly 422
QY 1159 TCCGAGCCCGCTGGCAGTGTGTAGTGGCGCTGCAGATCTCGGGGCTTGGGCTAC 1218
Db 423 SerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGlyGlyMetGlyPhe 442
QY 1219 ACAAGGACTATCCGTACGAGCGCATCTGCTGTCGTCACCCGCTATCTCTTCATCTTCGAG 1278
Db 443 MetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePheGlu 462
QY 1279 GGAACCAATCAGATCTCCGATGTACATCGCTCAGCGGTCTGCAGCATCGCGCCGC 1338
Db 463 GlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysGlyLys 482
QY 1339 ATCCTGACTACCAAGGATCCATGAGCTTAAACAG-----GCCAAAGTGAGCAGCATCATG 1392
Db 483 GluLeuThrGlyLeuGlyAsnAlaLeuLysAsnProLeuGlyAsnValGlyLeuLeuIle 502
QY 1393 GATACCGTTGGCGGAGGCTTCGGACTCCCTGGGCGCAACTGTGTGACCTGGGGCTGACA 1452
Db 503 GlyGluAlaSerLysGlnLeuArgArgThrGlyIleGlySerGlyLeuSerLeuSer 522
QY 1453 GGCACCATGAGTGTGCACCCAGCTCTTGGCGAGAGTCCCAACAAGTTTGAGGAGAAC 1512
Db 523 -----GlyIleValHisProGluLeuSerArgSerGlyGluLeuAlaValGlnAla 539
QY 1513 ACCTACTGCTTGGCGCGGACCGTGAGACACTGCTCTCGCTTTGGCAAGACCATCATG 1572
Db 540 LeuGluGlnPheAlaThrValValGluAlaLysLeuMetLysHisLysGlyIleVal 559
QY 1573 GAGGAGCAGTGGTACTGAGCGGTGGCCACATCTCTCATCACTGTATGGCATGACG 1632
Db 560 AsnGluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetVal 579
QY 1633 GCGTGTCTGCTGGCGGCGCAGCGCTCCATCCGCTTGGCTCCGCAACCCAGCAGCAGG 1692
Db 580 ValValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHisGlu 599
QY 1693 GTTCTCTTGGCCCAACACCTTCTGCTGGAAGCT-----TACTTGCAGATCTCTTC 1743
Db 600 LysMetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMetAla 619
QY 1744 AGCTCTCTCAGCTGGACAGTATCTCCAGAAACCTAGATGACGACAGATTAGAAAGTG 1803
Db 620 SerLeuGlnSerAsnProGln-----GlnGlnGluLeuPheArgAsnPheArgSerIle 637
QY 1804 TCCGAGCAGATCTTTCAGAAAGCGAGCCTATATCTGTGCCACCTCTG 1851
Db 638 SerLysAlaMetValGluAsnGlyGlyLeuValThrSerAsnProLeu 653

RESULT 15

ABB06993
ID ABB06993 standard; protein; 655 AA.
XX

AC ABB06993;

XX 20-JUN-2002 (first entry)

XX Bovine very long chain acyl-CoA dehydrogenase (VLCAD) protein SEQ ID:11.

XX Human; MD25; VLCAD; very long chain acyl-CoA dehydrogenase; IRAP;

XX insulin responsive aminopeptidase; GLUT4; glucose transporter 4;

XX antidiabetic; intracellular regulation; glucose metabolism; diabetes;

XX glucose transport; hyperglycaemic disorder.

XX Bos taurus.

XX WO200216428-A1.

XX 28-FEB-2002.

XX 20-AUG-2001; 2001WO-JP007117.
 XX 21-AUG-2000; 2000JP-00254263.
 PR 07-SEP-2000; 2000JP-00276633.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX Tojo H, Katayama N, Kakimoto S;
 XX WPI; 2002-269344/31.
 XX Protein binding to insulin-responsive aminopeptidase and glucose
 PT transporter 4, useful for prevention and treatment of diseases associated
 PT with blood sugar level disturbance.
 XX Disclosure; Page 95-97; 103pp; Japanese.
 XX The present invention describes human MD25 (very long chain acyl-CoA
 CC dehydrogenase (VLCAD)), which binds to insulin-responsive aminopeptidase
 CC (IRAP) and to glucose transporter 4 (GLUT4). MD25 has antidiabetic
 CC activity. IRAP and GLUT4 are involved in the intracellular regulation of
 CC glucose metabolism and glucose transport across the cell membrane.
 CC Expression of MD25 (whose ligands are these proteins) is also involved in
 CC this regulatory process. MD25 can be used in the prevention, treatment
 CC and diagnosis of diseases involving disturbances of glucose metabolism,
 CC such as diabetes and other hyperglycaemic disorders. The present sequence
 CC represents bovine VLCAD which is given in the exemplification of the
 CC present invention
 XX Sequence 655 AA;
 SQ

Alignment Scores:
 Pred. No.: 5,09e-117 Length: 655
 Score: 1345.00 Matches: 285
 Percent Similarity: 65.51% Conservative: 110
 Best Local Similarity: 47.26% Mismatches: 194
 Query Match: 39.29% Indels: 14
 DB: 5 Gaps: 9

US-09-945-326-3 (1-1863) x ABB06993 (1-655)

QY 67 TCTACCGGACCGCGGCTACTCGCACACGCGCGCTGTACAGAGCTTTCGCCAAGAG 126
 DB 57 SerGluAlaSerThrArgGluLysArgAlaAsnSerValSerLysSerPheAlaValGly 76
 QY 127 CTTTTCCTAGCAAAATCAAGAAAGAGTTTCCCATTTCCAGAGTT--AGCCAA 183
 DB 77 ThrPheLysGlnLeuThrThrAspGlnValPheProLysProSerValLeuAsnGlu 96
 QY 184 GATGAACCTTAATGAATCAATCACTTCTTGGGACCCGTGGAAATATCTTCACCTGAAGAG 243
 DB 97 AspGlnThrGlnPheLeuLysGluLeuValGlyProValThrArgPhePheGluGluVal 116
 QY 244 GTGACCTCCGAAAAATTGACAGGAGAGGAAATCCAGATGAATCTTGGAGAAATTG 303
 DB 117 AsnAspAlaAlaLysAsnAspMetLeuGluArgValGluGluThrThrMetGlnGlyLeu 136
 QY 304 AAGAGCTAGGCTTTTGGCTCCAGTCCAGAGATATGATGGCTGGCTGGCTTCTCC 363
 DB 137 LysGluLeuGlyAlaPheGlyLeuGlnValProAsnGluLeuGlyValGlyLeuLysCys 156
 QY 364 AACACCATGTACTCAAGACTAGGGAGATCATCAGCATG--GATGGGTCCATCCTGTG 420
 DB 157 AsnThrGlnThrAlaArgLeuValGluLeuValGlyMetThrAspLeuGlyValGlyLeu 176
 QY 421 ACCCTGGCAGCGACACCGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCAGCTGGAG 480
 DB 177 ValLeuGlyAlaHisGlnSerIleGlyPheLysGlyLeuLeuPheGlyThrLysAla 196
 QY 481 CAGAAAGCCAAATCTTCCCTAACTCGCTCGCGGAGGACATTCAGGCTTCTGCTC 540
 DB 197 GlnLysGluLysThrLeuProLysLeuAlaSerGlyGluThrIleAlaPheCysLeu 216

QY 541 ACGAGCCACCGAGTGGGAGCGATGCGAGCTCAATCCGGAGCAGAGCCACACTAAGTAA 600
 DB 217 ThrGluProSerGlySerAspAlaAlaSerIleArgSerSerAlaValProSerPro 236
 QY 601 GACAAGAAGCACTACATCTCAATGGCTCCAAAGTCTGGATTACTAATGAGGAGTGGCC 660
 DB 237 CysGlyLysThrThrLeuAsnGlySerLysIleIlePheSerAsnGlyGlyLeuAla 256
 QY 661 AATATTTTACTGTGTTTGCAAAGACTGAGGTGGTGGAT--TCTGATGATCAGTAAA 717
 DB 257 AspIlePheThrValPheAlaLysThrProValThrAspThrAlaThrGlyAlaValLys 276
 QY 718 GACAAATACAGCATTCATAGTAAGAGACTTGGTCGAGTCACTAATGGAAACCC 777
 DB 277 GluLysIleThrAlaPheValGluArgSerPheGlyValThrHisGlyProPro 296
 QY 778 GAAGATAAATAGGCATTCGGGGCTCCAACTTGTGAAGTCCATTTTGAACACCAAC 837
 DB 297 GluLysMetGlyIleLysAlaSerAsnThrAlaGluValThrPheAspGlyValArg 316
 QY 838 ATACCTGTGAAACATCTCTTGGAGAGTGGGAGTGGTTTAAGTGGCCATGAACATC 897
 DB 317 ValProAlaGluAsnValLeuGlyGluValGlyGlyPheLysValAlaMetHisIle 336
 QY 898 CTCACAGCGCGGTTTACATCGGCGAGCGTCTGGCTGGCTGGCTCAAGAGATTGATT 957
 DB 337 LeuAsnAsnGlyArgPheGlyMetAlaAlaAlaLeuAlaGlyThrMetLysGlyIle 356
 QY 958 GAAATGACTCTGAGTACGCTGCACAAAGGAAACAGTTTAACAGAGGCTCAGTGAAT 1017
 DB 357 AlaLysAlaValAspHisAlaAlaAsnArgThrGlnPheGlyGluLysIleHisAsn 376
 QY 1018 GGATTGATTGAGGAGAAATTTGCATCGCTCAGAGGCTTACGTCATGAGAGATGATG 1077
 DB 377 GlyLeuIleGlnGluLysLeuAlaArgMetAlaMetLeuGlnThrValThrGluSerMet 396
 QY 1078 ACCTACCTCAGCAGGAGGATCTGGACCAACCTGGCTTCCGCTCTCTCCATCAGGCA 1137
 DB 397 AlaTyrMetValSerAlaAsnMetAspGln--GlySerThrAspPheGlnIleGluAla 415
 QY 1138 GCATGTGTGAAGTGTTCAGCTCCGAGCGCTGCGAGTGTGTGAGTGGCGCTCGAG 1197
 DB 416 AlaIleSerLysIlePheGlySerGluAlaAlaThrLysValThrAspGluCysIleGln 435
 QY 1198 ATCTCGGGGCTTGGGCTACACAAGGGGACTATCCGTACGAGCGCATCTCCGTGACACC 1257
 DB 436 IleMetGlyGlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeu 455
 QY 1258 CGATCTCTCTATCTTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACG 1317
 DB 456 ArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGln 475
 QY 1318 GGTCTGACGATCCCGCGCCATCTCTGACTACAGGATCCATGAGCTTAAACAG-- 1371
 DB 476 GlyCysMetAspLysGlyLysGluLysGlyLeuGlyAsnAlaLeuLysAsnProPhe 495
 QY 1372 GCCAAAGTCAGCAGCATCATGATACCGTTGGCGGAGGCTTCGGGACTCCCTGGGCGGA 1431
 DB 496 GlyAsnAlaGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeuArgArgAlaGlyLeu 515
 QY 1432 ACTGTGAGCTGGGCTGACAGGCAACCATGAGTGTGTGACCCCACTCTTGGGACAGT 1491
 DB 516 GlySerGlyLeuSerLeuSer-----GlyIleValHisGlnGluLeuSerArgSer 532
 QY 1492 GCCAACAGTTTTCAGGAGAACACCTACTGCTTCGGCGCGGACCTGGAGACACTGCTGCTC 1551
 DB 533 GlyGluLeuAlaValGlnAlaLeuGluGlnPheAlaThrValValGluAlaLysLeuIle 552
 QY 1552 CGCTTTGGCAAGACCATCATGAGGAGGAGCAGCTGTACTGAAGCGGGTGGCAACATCCTC 1611
 DB 553 LysHisLysAspIleIleAsnGluGlnPheLeuLeuGlnArgLeuAlaAspSerAla 572

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	824	24.1	164	4	US-09-621-976-5565	Sequence 5565, Ap
2	816	23.8	601	4	US-09-903-540-11184	Sequence 11184, A
3	783	22.9	336	4	US-09-270-767-44314	Sequence 44314, A
4	691.5	20.2	390	4	US-09-252-991A-26058	Sequence 26058, A
5	666	19.5	389	4	US-09-328-352-6380	Sequence 6380, Ap
6	650	19.0	384	4	US-09-648-004-6	Sequence 6, Appli
7	650	19.0	384	4	US-10-273-419-6	Sequence 6, Appli
8	623	18.2	387	4	US-09-328-352-6442	Sequence 6442, Ap
9	618.5	18.1	403	4	US-09-328-352-6442	Sequence 27960, A
10	608	17.8	382	4	US-09-328-352-4850	Sequence 4850, Ap
11	604	17.6	432	4	US-09-949-016-6098	Sequence 6098, Ap
12	603.5	17.6	419	4	US-09-252-991A-31097	Sequence 31097, A

Oy 1 ATGAGCGGCTGCGGGCTCTTCTTCTGCGCACACAGCGCTGCGGGCTCGTGCTGCCGGGGTCTG 60

Db 1 MetSerGlyCysGlyLeuPheLeuArgThrAlaAlaAlaArgAlaCysArgGlyLeu 20

QY 61 GTGGCTCTACCGGACCCGGCGCTACTGCGCACACCGCCGCTGTACGAGCTTTCGCC 120
 Db 21 ValValSerThrAlaAenArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40
 QY 121 AAAGAGCTTTTCCCTAGGCAAAATCAAGAAGAAAGATTTTCCCATTTCCAGAAAGTTAGC 180
 Db 41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProPheProGluValSer 60
 QY 181 CAAGATGAACCTTAATGAATCAATCAGTTCTTGGGACCCGTGGGAAAAATTTCTTCAGTAA 240
 Db 61 GlnAspGluLeuAenGluIleAenGlnPheLeuGlyProValGluLysPhePheThrGlu 80
 QY 241 GAGGTGGACTCCCGAAAAATTGACCAAGAGGGAATCCAGATGAATTTGGAGAAA 300
 Db 81 GluValAspSerArgLysIleAspGlnGluLysIleProAspGluThrLeuGluLys 100
 QY 301 TTGAAGAGCTTAGGCTTTTGGGCTGCAAGTCCAGAGAATATGCTGGCTGGGCTTC 360
 Db 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrglyGlyLeuGlyPhe 120
 QY 361 TCCAAACCACTGACTCAAGACTAGGGAGATCATCAGCATGGATGGTCCATCAGTGTG 420
 Db 121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
 QY 421 ACCCTGGCAGCGCACCGAGCTATTGGCTCAAGGGGATCATCTTGGCTGGCATGAGGAG 480
 Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160
 QY 481 CAGAAAGCCAAA 492
 Db 161 GlnLysAlaLys 164

RESULT 2

US-09-902-540-11184
 ; Sequence 11184, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 11184
 ; LENGTH: 601
 ; TYPE: PR1
 ; ORGANISM: Myxococcus xanthus
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(601)
 ; OTHER INFORMATION: unsure at all Xaa locations
 US-09-902-540-11184

Alignment Scores:
 Pred. No.: 4,73e-67 Length: 601
 Score: 816.00 Matches: 214
 Percent Similarity: 51.60% Conservative: 92
 Best Local Similarity: 36.09% Mismatches: 197
 Query Match: 23.84% Indels: 90
 DB: 4 Gaps: 16

US-09-945-326-3 (1-1863) x US-09-902-540-11184 (1-601)

QY 160 TTCCCATTTCCAGAGTTAGCCCAAGATGAACCTT-----AATGAA 198
 Db 19 PheLeuPheGluGluValGlySerAlaArgIleLeuThrProGluThrPheThrGluGlu 38

QY 199 ATCAATCAGTCTTGGGACCCCGTGGAAAAATTTCTTCACTCAAGAGGTG-----GACTCC 252
 Db 39 GlnArgLeuPhePheLysThrAlaLeuGlnPheSerArgGluGlnValLeuProLeuSer 58
 QY 253 CGAAAAAATTCAC---CAGGAAGGGAAAAATCCAGATGMAACTTTTGGAGAAAATTAAGAGC 309
 Db 59 GluArgIleGluAlaLysAspAsnAlaLeuLeuArgGlnLeuLeuArgGlnAlaGlyGlu 78
 QY 310 CTAGGGCTTTTGGGCTGCAAGTCCAGAGAATATGTTGGCTTGGCTTCTTCCAAACCC 369
 Db 79 LeuGlyLeuLeuSerValAspIleProGluAlaTyrGlyGlyThrGlyLeuAspLysThr 98
 QY 370 ATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGGTCCATCATCTGTGACCCCTGGCA 429
 Db 99 ThrSerLeuLeuLeuAlaGluAlaMetSerLeuAsnGlySerTrpSerValThrPheGly 118
 QY 430 GCCCACCAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCC 489
 Db 119 AlaHisThrGlyIleGlyThrLeuProIleValTrpPheGlyAsnAlaGluGlnLysAla 138
 QY 490 AATACTTGCCTAACTGGCTCCGGGAGCACATTCAGAGCTTCTGCTTCACGGAGCCA 549
 Db 139 LysTyrLeuProLysLeuAlaThrGlyGluTyrValAlaAlaTyrAlaLeuThrGluGln 158
 QY 550 GCCAGTGGGAGGATGCAGCCTCAATCCGAGCAGAGCCACACTAAGTGAAGCAAGAAG 609
 Db 159 GlySerGlySerAspAlaLeuGlyAlaLysThrLysAlaValLeuSerProAspGlyLys 178
 QY 610 CACTACATCTCAATGGCTCCAGGCTCTGGATTACTTAATGGAGGACTGGCCCAATATTTT 669
 Db 179 HisTrpIleLeuAsnGlySerLysLeuTyrIleThrAsnAlaAlaPheAlaAspValPhe 198
 QY 670 ACTGTGTTTGCAGAAAGACTGAGGTCTGTGATTCTGTGATGATCAGTGAAGACAAAATCACA 729
 Db 199 ValValPheAlaLysVal-----AspGly-----AspLysPheThr 210
 QY 730 GCATTCAATAGTAAGAGAGACTTTTGTGTGAGTCACTAATGGGAAACCCAGAGATAATTA 789
 Db 211 GlyPheIleValGluLysAspThrProGlyLeuThrValGlyProGluGluHisLysMet 230
 QY 790 GGCATTCGGGGCTCCAACTTGTGAAGTCCATTTTGAACCAACCAAGATACCTGTGGAA 849
 Db 231 GlyIleArgGlySerSerThrCysProLeuTyrPheGluAspAlaArgValProValGlu 250
 QY 850 AACATCTTGGAGAGTCCGAGATGGTTTAGGTGGCCATGAACATCTTCAACACGGCC 909
 Db 251 AsnGlnLeuGlyGluValGlyLysGlyHisLysIleAlaPheAsnIleLeuAsnTyrGly 270
 QY 910 CGGTTCAAGATGGGAGCGTCGTGGCTGCTCAAGAGATTTGATTGAAATGACTGCT 969
 Db 271 ArgLeuLysLeuGlyAlaGlyValLeuGlyGlyMetLysLeuGlnLeuGlnAsnAlaLeu 290
 QY 970 GAGTAGCGCTGCACAGAAACAGTTTAAACAGAGGCTCAGTGAATTTGGATTGATTCAG 1029
 Db 291 ArgPheThrGlnGluArgLysGlnPheAsnAlaProIleValGlnPheProLeuSerArg 310
 QY 1030 GAGAAATTTGCATGATGGCTCAGAGGCTTACGTTCATCGAGAGTATGACCTACCTCACA 1089
 Db 311 GluLysLeuAlaArgMetAlaAlaLeuValTyrAlaValGluSerMetThrTyrArgThr 330
 QY 1090 GCAGGGATCTG-----GACCAACCTGGCTTT----- 1116
 Db 331 AlaGlyLeuValAspAlaArgLeuGlyGlnGlyAspLysAspAlaProAspTyrGluAla 350
 QY 1117 -----CCCAGCTGCTCCATCGAGGAGCCCATGGTGAAGGTGTTTCAGC 1158
 Db 351 ArgLeuLeuGluAlaValGluGluTyrAlaIleGluSerSerIleMetLysValHisGly 370
 QY 1159 TCCGAGGCGCGCTGGCAGTGTGTGAGTGGCGCTGCAGATCCTCGGGGCTTGGGCTAC 1218
 Db 371 SerGluSerPheGlyHisLeuValAspAlaValGlnLeuHisGlyAlaGlyTyr 390
 QY 1219 ACAAGGAGCTATCCGTACGAGCGCATCTGCTGTGACACCCGCATCCTCTCATCTTCGAG 1278

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Db 391 IleGluGluProValGluArgSerTyrArgAspAlaArgIleAsnArgIlePheGlu 410
Qy 1279 GGAACCAATGAGATTCTCCGATGATACATCGCCCTGACGGGTCTGACGAGCATGCCGCGC 1338
Db 411 GlyThrAsnGluIleAsnArgMetLeuIleThrGlyMetLeuLeuIleArgAlaValArg 430
Qy 1339 ATCTGTAGTACCAGGATTCATAGCTTAAACAG---GCCAAGATGACACAGATCATGAT 1395
Db 431 -----GlyAspLeuProLeuPheAlaMetAlaGlyAsnValAlaGlu 444
Qy 1396 ACCGTTGGCCGG-----AGGCTTCGGGACCTCCCTGGGCGCCGACTGTG 1437
Db 445 GluLeuSerArgGlyGluArgProArgAlaArgValGlnAspAlaLeuAlaProGlnGlu 464
Qy 1438 GACCTGGGGCTGACAGGCAACCATGAGTGTGTGCACCCCATGCTTCGGGACAGTGCACCA 1497
Db 465 ValAlaAlaGluAlaAlaLysHisLeuAlaLeuHis----- 476
Qy 1498 AAGTTTGAGGAGAACACCTACTGCTTCGGCGGACCGTG-----GAGACATGCTGCTC 1551
Db 477 -----GlyLeuArgValAlaAlaGluThr----- 484
Qy 1552 CGTTTGGCAAGACCATCATGAGGACAGCTGTGTACTGAAGCGGTGGCCACATCCTC 1611
Db 485 ---PheGlyProGluLeuGluGlnHisGlnGluValLeuAlaAlaLeuSerAspValVal 503
Qy 1612 ATCAACCTGTATGTCATGACGGCGTCTGTCGGCGGCGCCAGCCGCTCC----- 1659
Db 504 MetAspAlaPheAlaLeuAspSerMetValThrArgThrArgGlnAlaAlaThrSerGly 523
Qy 1660 -----ATCCGCTATGGGCTC-----CGC 1677
Db 524 AlaLeuAspProValArgValAlaMetThrGlnLeuTyrAlaLeuAspAlaIleProArg 543
Qy 1678 AACACAGCACAC---GAGGTCTCTTGGCCACACCTTCCTCGTGGAGCTTACTTGCAG 1734
Db 544 AlaTyrAspArgThrArgArgAlaLeuCysAlaThrLeuIleGlyGlyAlaLeuAspGln 563
Qy 1735 AATCTCTTACGCTCTCTCAGCTGGAGCAAGTATGCTCCA 1773
Db 564 GluLeuGluArgLeuGlyThrLeuAspValPheThrPro 576

RESULT 3
US-09-270-767-44314
; Sequence 44314, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44314
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44314

Alignment Scores:
Pred. No.: 3,88e-64 Length: 336
Score: 783.00 Matches: 169
Percent Similarity: 65.01% Conservative: 54
Best Local Similarity: 49.27% Mismatches: 104
Query Match: 22.87% Indels: 16
DB: 4 Gaps: 5

US-09-945-326-3 (1-1863) x US-09-270-767-44314 (1-336)

Qy 652 GGACTGCCCAATATTTTACTGTGTTGCAAGACTGAGTGTGTGAT---TCTGTATGGA 708
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Db 3 GlyIleAlaGluIleMetThrValPheAlaGlnThrGluGlnValAspProLysThrGly 22
Qy 709 TCAGTGAAGACAAAATCAGCATTATAGTAGAAGAGACTTTGTGTGAGTCACTAAT 768
Db 23 GluLysLysAspLysValThrAlaPheIleValGluArgSerPheGlyGlyValThrAsn 42
Qy 769 GGGAAACCCGAAAGATAATTAGGCATTCGGGGCTCCACACACTTGTGAAGTCCATTTTGA 828
Db 43 GlyProGluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheGlu 62
Qy 829 AACACCAAGATACCTGTGGAACATCCTTGGAGAGGTCGGAGATGGTGTAAAGTGGCC 888
Db 63 AspValLysIleProIleGluAsnValLeuGlyLysGluGlyAspGlyPheLysValAla 82
Qy 889 ATGAACATCTCAACAGCGCGCTTCAGCATGGGACGCGTCTGGTGGTGGCTGCTCAAG 948
Db 83 MetAsnIleLeuAsnAsnGlyArgPheGlyMetGlyAlaThrLeuSerGlyThrMetLys 102
Qy 949 AGATTGATTGAATGCTGCTGAGTAGTACGCTGCACAGGAAACAGTTTAAACAGAGCTC 1008
Db 103 LysCysIleGluGlnAlaThrGluHisAlaAsnAsnArgValGlnPheGlyGlnLysLeu 122
Qy 1009 AGTGAATTTCGATTGATTTCAGGAGAAATTTGCACTGATGCTCAGAAGGCTTACGTCATG 1068
Db 123 LysAsnTyrGlySerIleGlnGluLysLeuAlaGlnMetAsnIleLeuGlnTyrAlaThr 142
Qy 1069 GAGAGTATGACCTACCTCAGCAGGAGGATGCTCGACCAACCTGGCTTCCCGACTGCTCC 1128
Db 143 GluSerMetAlaPheThrIleSerGlnAsnMetAsp---AlaGlySerLysAspTyrHis 161
Qy 1129 ATCAGGACGCCATGTGAAGTGTTCAGCTCCGAGCCCGCTGGCAGTGTGTGAGTGAG 1188
Db 162 LeuGluAlaAlaIleSerLysIleTyrAlaSerGluSerAlaTyrTyrValCysAspGlu 181
Qy 1189 GCCTCGCAGATCTCGGGCTTGGCTACACAAGGAGTATCCGTACGAGCGCATACTG 1248
Db 182 AlaIleGlnLeuGlyGlyMetGlyTyrMetValAspThrGlyLeuGluArgValLeu 201
Qy 1249 CGTGACACCCGCTATCTCTCATCTTTCGAGGGAACCAATGAGATTTCCGGATGTAGATC 1308
Db 202 ArgAspLeuArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheIle 221
Qy 1309 GCCTGACGGTCTGACGATGCGCGCGCATCTCTGACTACCAGGATCCATGACTTAAA 1368
Db 222 AlaLeuThrGlyIleGlnTyrAlaGly-----SerHisLeuLysGluLeuGln 237
Qy 1369 CAG-----GCCAAAGTGACACAGTCACTGATACCTGTCGCGCGGAGG 1410
Db 238 ArgAlaPheLysAsnProSerAlaAsnLeuGlyLeuIlePheLysGluAlaSerArgArg 257
Qy 1411 CTTTCGGGACTCCCTGGCGGAACTGTGGACCTCGGGCTGACAGGCAACCATGGAGTTGTG 1470
Db 258 -----AlaAlaSerThrValGlyLeuGlyGlyThrAspLeuSerGlyHisVal 273
Qy 1471 CACCCAGTCTTCGGACAGTGCACCAAGTTTGGAGGAGAACACCTACTCTCTCGCGCGG 1530
Db 274 ValGlyGluLeuLeuProTyrAlaLysLysThrAlaHisCysIleAspLeuPheGlyGln 293
Qy 1531 ACCGTGGAGACACTGTGCTCGCTCCGCTTGGCAAGCATTATGAGGAGGAGTGTGTACTG 1590
Db 294 SerValGluGluLeuLeuArgTyrAsnLysAsnIleValAsnGluGlnIleLeuLeu 313
Qy 1591 AAGCGGTGGCCCAACATCTCTCATCAACCTGTATGGCATGACGGCGCTGTGTCTCGCGGCC 1650
Db 314 ThrArgLeuAlaAsnAlaAlaIleAspIleTyrAlaMetValValThrGlnSerArgSer 333
Qy 1651 AGCGGCTCC 1659
Db 334 SerArgAla 336

RESULT 4
US-252-991A-26058
; Sequence 26058, Application US/09252991A
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Alignment Scores:
Pred. No.: 3.5e-53 Length: 389
Score: 666.00 Matches: 150
Percent Similarity: 58.27% Conservative: 79
Best Local Similarity: 38.17% Mismatches: 148
Query Match: 19.46% Indels: 16
DB: Gaps: 8

US-09-945-326-3 (1-1863) x US-09-328-352-6380 (1-389)

QY 172 GAAGTTAGCAAGTGAACCTTAATGAAATCAATCAGTTCTTGGGACCGGTGAAAAATTC 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 GlnMetIleArgAspGlu---GlyMetLeuGluLeuLeuSerThrIleArgAspPhe 23

QY 232 TTCACCTGAAGAGGTGACCTCCGA-----AAAATTGACGAGGAGGAAAATCCAGAT 285
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 ValLysAsnGluLeuProArgGluAsnGluValValGluLysAspLysIleProAsp 43

QY 286 GAAACTTTTCGAGAAATTGAAGAGCCCTAGGGCTTTTTGGGCTTCAAGTCCAGAGAATAT 345

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Db 44 AspIleValGlnMetArgGluLeuGluPheGlyLeuThrIleProGluGlyTyr 63
QY 346 GGTGGCTGGCTTCTCCACACCATGCTACTCAAGACTAGGG---GAGATCATCAGCATG 402
Db 64 GlyGlyLeuGlyIleThrMetGluGluValArgValAlaPheGluLeuGlyGlnThr 83
QY 403 GATGGTCCATCTGTGACCTGGCAGCGCACAGCATGTCCTCAAGGGGATCATC 462
Db 84 SerProAlaPheArgSerLeuIleGlyThrAsnAsnGlyIleGlySerSerAlaIleLeu 103
QY 463 TTGGCTGGCACTGAGGAGCAAGCAATATCTGCTAACTGCGCTCGGGGAGCAC 522
Db 104 IleAspGlyThrGluGlnGlnLysGlnLysThrLeuProArgTyrAlaSerGlyGluLe 123
QY 523 ATTGCACCTTCTGCTCAGCGGACCGCAGGTGGAGCGCATGCGCTCAATCCCGAGC 582
Db 124 IleGlySerPheCysLeuThrGluProGluSerGlySerAspAlaIleSerLeuYThr 143
QY 583 AGAGCCACATAAGTGAAGAACAAGACACTATCATCTCAATGCTCCAGGCTCGGATT 642
Db 144 SerAlaVal-----LysAspGlyAspPheTyrValLeuAsnGlyThrLysArgPheIle 161
QY 643 ACTAATGGAGCATGGCCATATTTTACTGTGTTCCTCAAGACT-----GAGTCTGT 696
Db 162 ThrAsnAlaProHisAlaAlaThrPheThrValMetAlaArgThrAsnProGluIleLys 181
QY 697 GATTCTGATGATCAGTGAAGAACAAATCACAGCATTCATAGTAGAAGAGAGCTTGGT 756
Db 182 GlySerGlyGly-----IleSerAlaPheLeuValGluAlaAsnThrPro 196
QY 757 GGAGTCACTAATGGGAACCCGAAGATAAATTAGGCATTCGGGCTCCACACTGTGAA 816
Db 197 GlyIleThrLeuGlyLysIleAspGlnLysMetGlyGlnLysGlySerHisThrCysAsp 216
QY 817 GTCCATTTTGAACACCAAGATACCTGTGTGGAACACATCTCTGGAGAGTGC---GGAGAT 873
Db 217 ValIlePheGluAsnCysArgValProAlaSerAlaLeuIleGlyGlyValGluGlyVal 236
QY 874 GGGTTTAAGTGCCATGAACATCTCAACAGCGCGGTTTCAGCATGGCGCGTCTG 933
Db 237 GlyPheLysThrAlaMetLysValLeuAspLysGlyArgLeuHisIleGlyAlaTyrSer 256
QY 934 GCTGGGCTGCTCAAGAGATTGATTGAATGACTGCTGAGTACGCTGCACAGGAACAG 993
Db 257 ValGlyValAlaGluArgMetLeuAsnAspAlaLeuAsnTyrAlaIleGluArgLysGln 276
QY 994 TTTAACAGAGGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCATGATGGCTCAG 1053
Db 277 PheGlyGlnProIleAlaAsnPheGlnLeuIleGlnAlaMetLeuAlaAspSerLysAla 296
QY 1054 AAGGCTTACGTCATGAGAGATGATGACCTACCTCACAGCAGGATGCTGGACCAACCTGGC 1113
Db 297 GluIleTyrAlaAlaLysCysMetValLeuAspAlaAlaArgArgAspAsnGly--- 315
QY 1114 TTTCCGACTGCTCCATCGAGGAGCCATGGTGAAGGTGTTCAGCTCCGAGGCGCGCTGG 1173
Db 316 ---GluAsnIleSerThrGluAlaSerCysAlaLysMetPheAlaThrGluMetCysGly 334
QY 1174 CAGTGTGTGATGAGGCGCTGAGATCCTCGGGGCTTGGGCTTACACAGGACTATCCG 1233
Db 335 ArgValAlaAspArgCysValGlnIleHisGlyGlyAlaGlyTyrIleSerGluTyrAla 354
QY 1234 TAGCAGGCGCATCTGCTGTGACACCGCATCTCTCATCTTCGAGGGAACCAATGAGATT 1293
Db 355 IleGluArgPheTyrArgAspValAlaGluPheArgLeuTyrGluGlyThrThrGlnVal 374
QY 1294 CTCGGATGTACATCGCCCTGACGGGTCTGCAGCATGCC 1332
Db 375 GlnGlnLeuIleIleAlaLysAsnMetIleArgGluAla 387
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RESULT 6

US-09-648-004-6

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; Sequence 6, Application US/09648004
; Patent No. 6498242
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; APPLICANT: NAGARAJAN, VASANTHA
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; FILE REFERENCE: CL-1341-A
; CURRENT APPLICATION NUMBER: US/09/648,004
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/252,553
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
; US-09-648-004-6
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Alignment Scores:

Pred. No.:	1,08e-51	Length:	384
Score:	650.00	Matches:	154
Percent Similarity:	57.89%	Conservative:	77
Best Local Similarity:	38.60%	Mismatches:	132
Query Match:	18.99%	Indels:	36
DB:	4	Gaps:	11

US-09-945-326-3 (1-1863) x US-09-648-004-6 (1-384)

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QY 181 CAAGATGAACCTTAATGAA-----ATCAATCAGTTCTTGGGACCCGTGGAAAAA 228
Db 5 GlnAspThrLeuAsnGlnLeuValAspMetIleArgGlnPheValAspGlyVal---Leu 23
QY 229 TTCTTCACTGAAGAGTGGACTCCCGAAAAAATTGACCAGGAAGGAATAATCCCATGAA 288
Db 24 IleProAsnGluGluIle-----ValAlaGluThrAspGluIleProAlaGlu 39
QY 289 ACTTTTCAGAAAAATTAAGAGCCCTAGGCTTTTGGGCTGCAAGTCCACAGAAATATGGT 348
Db 40 IleValGlnGlnMetLysGluLeuGluPheGlyLeuThrIleProGluGluTyrGlu 59
QY 349 GGCTGGGCTTCTCCAACACCATGTACTCAAGACTA-----GGGGAGATCATCAGC 399
Db 60 GlyLeuGlyLeu-----ThrMetGluGluGluValTyrIleAlaPheGluLeuGlyArg 77
QY 400 ATGGATGGGTCCATCACTGTGACCTGGCAGCCGACCCAGGCTATTGGCTCAAGGGATC 459
Db 78 ThrSerProAlaPheArgSerLeuIleGlyThrAsnAsnGlyIleGlySerSerGlyLeu 97
QY 460 ATCTTGGCTGGCACTCAGGAGCAGAAAGCCAAATACTTGGCTAAACTGGCGTCCGGGGAG 519
Db 98 IleIleAspGlySerGluGlnLysGlnTyrPheLeuProArgLeuAlaSerGlyGlu 117
QY 520 CACATTGACGCTTCTGCTCAGCGAGCCAGCCAGTGGGAGCGATGCGCTCAATCCGG 579
Db 118 IleIleGlySerPheCysLeuThrGluProAspSerGlySerAspAlaAlaSerLeuLys 137
QY 580 AGCAGAGCCACACTAAGTGAAGCAAGACACTACATCTCAATGCTCAAGGCTCGG 639
Db 138 ThrThrAlaVal-----LysAspGlyAspHisTyrIleLeuAsnGlyThrLysArgTyr 155
QY 640 ATTACTAATGGAGGACTGGCCAAATATTTTACTGTGTGTTCGCAAG-----ACTGAGTTC 693
Db 156 IleThrAsnAlaProHisAlaGlyValPheThrValMetAlaArgThrSerThrGluIle 175
QY 694 GTTGATTCTGATGGATCAGTGAAGCAAAATACACAGCATTCATAGTAGAAGAGACTTT 753
Db 176 LysGlyThrGlyGly-----IleSerAlaPheIleValAspSerLysThr 190
QY 754 GGTGGAGTCACTAATGGGAAACCCGGAAGATAAATTAGGCATTTCGGGCTCCACACTGT 813
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5 GlnAspThrLeuAenGlnLeuValAspMetIleArgGlnPheValAspGlyVal---Leu 23

229 TTCTTCACTGAAGAGGTGGACTCCCGAAAAAATTGACCAGGAAGGAAATCCACAGATGAA 288

24 IleProAsnGluGluIle-----ValAlaGluThrAspGluIleProAlaGlu 39

289 ACTTTGAGAAATTTGAAGAGCTTAGGCTTTTGGCTGCAAGTCCCAAGAAATATGGT 348

40 IleValGlnGlnMetLysGluLeuGlyLeuPheGlyLeuThrIleProGluGluTyrGlu 59

349 GGCCTGGGCTTCTCAACACCATGTACTCAAGACTA-----GGGAGATCATCAGC 399

60 GlyLeuGlyLeu-----ThrMetGluGluGluValTyrIleAlaPheGluLeuGlyArg 77

400 ATGGATGGGTCTCATCACTGTGACCTGGCAGCGCACCGAGGTATTGTGGCTCAAGGGATC 459

78 ThrSerProAlaPheArgSerLeuIleGlyThrAsnAsnGlyIleGlySerSerGlyLeu 97

460 ATCTTGCTGGCACTGAGGAGCAAGAACCAATACTTGTCTAAACTGGCGTCCGGGAG 519

98 IleIleAspGlySerGluGluGlnLysGlnTyrPheLeuProArgLeuAlaSerGlyGlu 117

520 CACATTCCAGCTTCTGCTCACGGAGCCAGCAGTGGGAGCGGATGCAGCTCAATCCGG 579

118 IleIleGlySerPheCysLeuThrGluProAspSerGlySerAspAlaAlaSerLeuLys 137

580 AGCAGGCCACACTAGTGAAGACAAGACGACTACATCTCAATGCTCCAAGTCTGG 639

138 ThrThrAlaVal-----LysAspGlyAspHisTyrIleLeuAsnGlyThrLysArgTyr 155

640 ATTACTAATGGAGCTGGCCAAATATTTTACTGTGTTCGCAAG-----ACTGAGGTC 693

156 IleThrAsnAlaProHisAlaGlyValPheThrValMetAlaArgThrSerThrGluIle 175

694 GTTGATTCTGATGATCGTGAAGACAAATCACAGCATTCATPAGTAGAAGACATTT 753

176 LysGlyThrGlyGly-----IleSerAlaPheIleValAspSerLysThr 190

754 GGTGGAGTCACTAATGGRAACCCGAGATAAATTAGGCATTCGGGCTCCACACTTGT 813

191 ProGlyIleSerLeuGlyLysArgAspLysMetGlyGlnLysGlyAlaHisThrCys 210

814 GAAGTCCATTTGAAACACCAAGTACCTGTGGAAAAACATCTTGAGAGGTC---GGA 870

211 AspValIlePheGluAsnCysAspIleProAlaSerAlaLeuIleGlyGlyValGluGly 230

871 GATGGTTTAAGTGGCCATGAACATCTCCACAGCGCGCGTTCAGCATGGCAGGCGTC 930

231 ValGlyPheLysThrAlaMetLysValLeuAspLysGlyArgIleHisIleAlaLeu 250

931 GTGGCTGGGCTGCTCAAGAGATTGATTGAATGACTGCTGAGTACGCTGCACAAGGAAA 990

251 SerValGlyAlaAlaThrArgMetLeuGluAspSerLeuGlnTyrAlaValAlaArgLys 270

991 CAGTTTAAACAGAGGCTCAGTGAATTTGGATTGATTGAG-----GAGAAA 1035

271 GlnPheGlyGlnAlaIleAlaAsnPheGlnLeuIleGlnGlyMetLeuAlaAspSerLys 290

1036 TTTTGCACTGATGCTCAGAGGCTTACGTCATCGAGAGTATGACTACCTCACAGCAGGG 1095

291 AlaGluIleTyrAlaAlaLysCysMetValLeuAspAlaAlaArgLeuArgAspAlaGly 310

1096 ATGCTGGACCAACCTGGCTTTTCCGACTGCTCCATCGAGCAGCCAGTGTGAAGGTGTC 1155

311 Gln-----AsnValSerThrGluAlaSerCysAlaLysMetPhe 323

1156 AGCTCCGAGGCCCTGGCAGTGTGTGAGTGAGCGGCTGCAGATCTCTCGGGGCTGGGC 1215

324 AlaThrGluMetCysGlyArgValAlaAspArgGlyValGlnIleHisGlyGlyAlaGly 343

1216 TACAAGGAGCTATCCGTACGAGCGCATCTCGTGTGACACCGCGCATCTCTCATCTTC 1275

344 TyrIleSerGluTyrAlaIleGluArgPheTyrArgAspValArgLeuPheArgLeuTyr 363

US-10-272-419-6

754	Qy	GGTGGAGTCACTAATGGGAAACCGAGATAAAATTAGGCATTCTGGGGCTCCAAACACTTGT	813
191	Db	ProGlyIleSerLeuGlyIysArgApAlaHisIleThrCys	210
814	Qy	GAAGTCCATTTTCAAACACCAAGATACCTGTGAAAACATCTCTGAGAGGTC---GGA	870
211	Db	AspValIlePheGluAsnCysArgIleProAlaSerAlaLeuIleGlyValGluGly	230
871	Qy	GATGGGTTTAAGTGCCCATGAACATCTCTCAACAGCGCGGTTTCAGCATGGCGAGGTC	930
231	Db	ValGlyPheIysThrAlaMetIysValLeuAspIysGlyArgIleHisIleAlaLeu	250
931	Qy	GTGGCTGGGCTGCTCAAGAGATTGATTGAATCACTCTCAGTAGTCGCTGCACACAGAAA	990
251	Db	SerValGlyAlaAlaThrArgMetLeuGluAspSerLeuGlnTyrAlaValGluArgLys	270
991	Qy	CAGTTTAAACAGAGGCTCAGTGAATTTGGATTGATTTCAG-----GAGAAA	1035
271	Db	GlnPheGlyGlnAlaIleAlaAenPheGlnLeuIleGlnGlyMetLeuAlaAspSerLys	290
1036	Qy	TTTGCACTGATGCTCAGAGGCTTACGTTCATCGAGAGTATGACCTACCTACACAGCGGG	1095
291	Db	AlaGluIleTyrAlaAlaIysCysMetValLeuAspAlaAlaArgIleuArgApAlaGly	310
1096	Qy	ATGCTGGACCAACTGGCTTTTCCCGACTGTCTCATCGAGCGCCCATGTGTGAAGGTGTTTC	1155
311	Db	Gln-----AenValSerThrGluAlaSerCysAlaLysMetPhe	323
1156	Qy	AGTCTCGAGCGCCCTGGCGAGTGTGTGAGTGAGCGCTCGAGATCTCTCGGGGCTTGGGC	1215
324	Db	AlaThrGluMetCysGlyArgValAlaAspArgGlyValGlnIleHisGlyGlyAlaGly	343
1216	Qy	TACAAGGAGACTATCCGTACGAGCGCATCTCGTGTGACACCGCGCATCTCTCATCTTC	1275
344	Db	TyrIleSerGluTyrAlaIleGluArgPheTyrArgAspValArgLeuPheArgLeuTyr	363

US-09-945-326-3 (1-1863) x US-10-272-419-6 (1-384)

[illegible]


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Db      115  GluSerMetThrTyrProSerLeuAsnPheAlaLeuGlyGluThrIleAspMetLeuArg 34
      214  GGACCCGNGGAAAAATCTTCACTGAAGAGGTGGACTCCCA-----AAATTTGACGAG 267
      Db      35  AspGlnValArgGlyPheValAlaAlaGluLeuGlnProArgAlaAlaGlnIleAspGln 54
      268  GAAGGGAATCCAGATGAATCTTGGAGAAATGGAAGACCTAGGCTTTTGGGCTG 327
      Db      55  AspAsnGlnPheProMetAspMetTrpArgLysPheGlyGluMetGlyLeuLeuGlyIle 74
      328  CAAGTCCAGAGAATATGTGGCTGGCTTCTCCAACACCATGTACTCAAGACTAGGG 387
      Db      75  ThrValAspGluGluTyrGlyGlySerAlaLeuGlyTyrLeuAlaHisAlaValValMet 94
      388  GAGATCATCAGC---ATGATGGGTCCATCATCTGACCCCTGGCAGCGCACCGCTATT 444
      Db      95  GluGluIleSerArgAlaSerAlaSerValAlaLeuSerTyrGlyAlaHisSerAsnLeu 114
      445  GGCCTCAAGGGGATCATCTTGGCTGGCAGCTGAGGAGAGAAAGCAATATCTTCCTAAA 504
      Db      115  CysValAsnGlnIleLysArgAsnGlyAsnAlaGluGlnLysAlaArgTyrLeuProAla 134
      505  CTGGCTCCGGGAGCACATTTGAGCCTTCTGCTCAGGAGCCAGCCAGTGGAGCGAT 564
      Db      135  LeuValSerGlyGluHisIleGlyAlaLeuAlaMetSerGluProAsnAlaGlySerAsp 154
      565  CGAGCCTCAATCCGAGCAGCACACTAAGTGAAGCAAGAGCACTACATCCTCAAT 624
      Db      155  ValValSerMetLysLeuArgAlaAspArgValGlyAspArg-----PheValLeuAsn 172
      625  GGCTCCAAAGTCTCGATTACTTAATGGAGGACTGGCCAAATATTTTACTGTGTGGCAAAG 684
      Db      173  GlySerLysMetTrpIleThrAsnGlyProAspAlaHisThrTyrValIleTyrAlaLys 192
      685  ACTCAGTCTGTGATCTGTGATGATCATGATGAAGACAAA-----ATCACAGCA 732
      Db      193  ThrAspAla-----AspLysGlyAlaHisGlyIleThrAla 204
      733  TTCATAGTAGAAGAGACTTTTGGTGGAGTCACTAATGGGAAACCCGAAGATAAATAGGC 792
      Db      205  PheIleValGluArgAspTrpLysGlyPheSerArgGlyProLysLeuAspLysLeuGly 224
      793  ATTCCGGGCTCCAACTTGTGAAGTCCATTTTGAACCAACCAAGATACCTGTGGAAAC 852
      Db      225  MetArgGlySerAsnThrCysGluLeuIlePheGlnAspValGluValProGluGluAsn 244
      853  ATCCTTCGAGGCTCGGAGATGGTTTAAAGTGGCCATGAACATCTCAACACGCGCCGG 912
      Db      245  ValLeuGlyAlaValAsnGlyValLysValLeuMetSerGlyLeuAspTyrGluArg 264
      913  TTCAGCATGGCGACGCTGTGGCTGCTCAAGAGATTGATTGAATGACTGCTGAG 972
      Db      265  ValValLeuSerGlyGlyProValGlyIleMetGlnAlaCysMetAspValValPro 284
      973  TAGCCCTGCACAGGAACATTTAAACAGAGGCTCAGTGAATTTGGATTGATTCAGGAG 1032
      Db      285  TyrIleHisAspArgGlnPheGlyGlnSerIleGlyLysPheGlnLeuValGlnGly 304
      1033  AAATTT-----GCATGATGGCTCAGAGGCTTACGTGATGGAGATAG 1077
      Db      305  LysValAlaAspMetTyrThrAlaLeuAsnAlaSerArgAlaTyrLeu----- 320
      1078  ACCTACTCAGCAGGGAGTGTGGACCAACCTGGCTTTCCGACTGCTCCATCGAGGCA 1137
      Db      321  ---TyrAlaValAlaAlaAlaCysAspArgGly-----GluThrThrArgLysAspAla 337
      1138  GCATGGTGAAGTGTTCAGCTCCGAGGCGCTCGGAGTGTGTGAGTGAGGCGCTGCAG 1197
      Db      338  AlaglyValIleLeuTyrSerAlaGluArgAlaThrGlnMetAlaLeuAspAlaIleGln 357
      1198  ATCCTCGGGGCTTGGCTACACAAGGGACTATCCGTACGAGCGCATCTCGCTGACACC 1257
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Db      358  IleLeuGlyGlyAsnGlyTyrIleAsnGluPheProThrGlyArgLeuLeuArgAspAla 377
      1258  CGCATCTCTCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATC 1308
      Db      378  LysLeuTyrGluIleGlyAlaGlyThrSerGluIleArgArgMetLeuIle 394
      RESULT 10
      US-09-328-352-4850
      ; Sequence 4850, Application US/09328352
      ; Patent No. 6562958
      ; GENERAL INFORMATION:
      ; APPLICANT: Gary L. Breton et al.
      ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
      ; FILE REFERENCE: GTC99-03PA
      ; CURRENT APPLICATION NUMBER: US/09/328,352
      ; CURRENT FILING DATE: 1999-06-04
      ; NUMBER OF SEQ ID NOS: 8252
      ; SEQ ID NO 4850
      ; LENGTH: 382
      ; TYPE: PRT
      ; ORGANISM: Acinetobacter baumannii
      US-09-328-352-4850
      Alignment Scores:
      Pred. No.: 8,88e-48 Length: 382
      Score: 608.00 Matches: 142
      Percent Similarity: 56.20% Conservative: 71
      Best Local Similarity: 37.47% Mismatches: 154
      Query Match: 17.76% Indels: 12
      DB: 4 Gaps: 6
      US-09-945-326-3 (1-1863) x US-09-328-352-4850 (1-382)
      QY      187  GAACTTAATGAATCAATCATCTTCTGGGACCCGCGGAAAAATTTCTACTCAAGAG--- 243
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      QY      244  -----GTGACTCCCGAAAAATTTGACAGGAGGAAAAATCCAGATCAAACTTTGGAG 297
      Db      29  IleLysProAsnAlaSerAspTrpAspArgAspGlyThrPheProLysGluThrLeuThr 48
      QY      298  AAATTGAAGAGCTCAGGGCTTTTGGCTGCAAGTCCCAAGAAATATATGGTGGCTGGGC 357
      Db      49  GlnMetGlyGlnLeuGlyPheMetGlyMetLeuValSerGluGluTrpGlyGlySerAsp 68
      QY      358  TTCTCCAACACCATGTAC---TCAAGACTAGGGAGATCATCAGCATGGATGGTCCATC 414
      Db      69  ThrGlyAsnLeuAlaTyrValLeuAlaLeuGluGluValAlaAlaAlaAspGlyAlaThr 88
      QY      415  ACTGTGACCTCGCAGCGCACCGACTATTGGCTCAAGGGGATCATCTTGGCTGGCACT 474
      Db      89  SerThrIleMetSerValHisAsnSerValGlyCysValProIleLeuLysPheGlyThr 108
      QY      475  GAGGAGCAGAAAGCCAAATPACTTGCTAAACTGCGCTCCGGGGAGCACATTGCAGCCTTC 534
      Db      109  AspGluGlnLysGluArgPheLeuLysProLeuAlaGlnGlyGluMetIleGlyAlaPhe 128
      QY      535  TGCCTCAGGAGCCAGCCAGTGGGAGCGATGAGCCTCAATCCGAGGAGAGACCACTA 594
      Db      129  AlaLeuThrGluProHisThrGlySerAspAlaAlaIleLysThrArgAlaVal--- 147
      QY      595  AGTGAAGACAAAGACACTACATCTCAATGGCTCCAAGGTCTGATTACTAATGAGGA 654
      Db      148  ---LysAspGlyAspAspTyrIleLeuAsnGlyAlaLysGlnPheIleThrSerGlyAsn 166
      QY      655  CTGGCCAATATTTTCTGTTTCCAAAGACTGAGGTGCTGTGATTCTGATGGATCAGTG 714
      Db      167  AsnAlaGlyValIleIleValPheAlaValThrAsp-----ProSerAlaGly 182
      QY      715  AAAGACAAAATCACAGCATTCATAGTAAAGAGACTTTGGTGGAGTCACTAATCGGAAA 774
      Db      183  LysLysGlyIleSerAlaPheLeuValProArgGluThrProGlyTyrGluValIleArg 202
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QY 775 CCCGAAGATAAATTAGCATTCCGGGCTCCCAACACTTGTGAAGTCCATTTTGAACACACC 834
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 203 ValGluGluLysLeuGlyLeuHisAlaSerAspThrCysGlnIleAlaLeuThrAspVal 222
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 835 AAGTACTCTGGAAACATCTTGGAGAGTTCGGAGATCGGATGGTTTAAAGTGGCCATGAAC 894
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 223 ArgIleHisLysSerLeuMetLeuGlyGluGlyLeuLysIleAlaLeuAla 242
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 895 ATCTCAACAGCGCCGCTTCCAGCATCGGAGCGCTCGTGGCTGGCTCAAGAGATTG 954
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 AsnLeuGluGlyArgIleGlyIleAlaAlaGlnAlaValGlyLeuAlaArgAlaAla 262
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 955 ATTGAATAGTCTGTAGTACGCTGCACAAAGGAACAGTTTAAAGAGGCTCAGTGAA 1014
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 263 LeuGluAlaThrArgTyrAlaLysGluArgIleThrPheGlyLysProIlePheGlu 282
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1015 TTTGGATTGATTCAGGAGAATTGGCATGCTGCTCAGAGGCTTACGTCATGGAGATG 1074
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 283 HisGlnThrIleAlaPheArgLeuAlaSerMetAlaThrGluIleGluAlaAlaArgGln 302
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1075 ATGACCTACCTCACAGCAGGATGCTCGACCAACCTGGCTTCCCGACTGCTCCATCGAG 1134
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 LeuValHisTyr---AlaAlaArgLeuLysGluAlaGlyGlnPro---CysLeuAsnGlu 320
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1135 GCAGCCATGTTGAAGTGTTCAGCTCCGAGCGCCCTCGGAGTGTTGTAGTGAAGCGCTG 1194
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 321 AlaSerMetAlaLysLeuPheAlaSerGluMetThrGluArgValCysSerSerAlaLeu 340
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1195 CAGATCTCGGGCTTGGGCTACACAAAGGACTATCCGTACGAGCGCATCTCGCTGAC 1254
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 341 GlnValPheGlyGlyTyrGlyTyrLeuArgAspPheProIleGluArgIleTyrArgAsp 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1255 ACCGCATCTCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTATCGCC 1311
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 AlaArgIleCysGlnIleTyrGluGlyThrSerAspIleGlnArgLeuValIleAla 379
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RESULT 11

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US-09-949-016-6098
; Sequence 6098, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 6098
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6098
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Alignment Scores:
Pred. No.: 2,27e-47 Length: 432
Score: 604.00 Matches: 157
Percent Similarity: 54.46% Conservative: 81
Best Local Similarity: 35.93% Mismatches: 155
Query Match: 17.65% Indels: 44
DB: 4 Gaps: 14
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US-09-945-326-3 (1-1863) x US-09-949-016-6098 (1-432)

QY 55 GGTCTGGTGTCTCTTACCGGAAACCGCGGCTACTGCGCACCGCGCTGTACGAGCT 114

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Db 3 GlyLeuAlaVal |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 TTCCCAAGAGCTTTTCTAGCAAAATCAAGAAGAAAGATTTTCCCA---TTTCCA 171
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 17 ---ArgAsnPheLeuThrCysLeuSerSerTrpLysIleProHisValSer 33
QY 172 GAAGTTAGCAAGATGAA---CTTAATGAATCAATCAG-----TTCTTGGGACCC 219
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 34 LysSerSerGlnSerGluAlaLeuLeuAsnIleThrAsnAsnGlyIleHisPheAlaPro 53
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 GTGGAAAAATCTTCTACTGAAGAGTGGACTCCCGAAAA----- 258
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 54 LeuGlnThrPheThrAspGluMetMetIleLysSerSerValLysLysPheAlaGln 73
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 259 ---ATTGACCAGGAAGGAAATATCCAGATGAACT 291
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 GluGlnIleAlaProLeuValSerThrMetAspGluAsnSerLysMetGluLysSerVal 93
QY 292 TTGAGAAATTGAAGACCTTAGGCTTTTGGCTGCAAGTCCAGAGAAATATGTGGC 351
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 94 IleGlnGlyLeuPheGlnGlyLeuMetGlyIleGluValAspProGluTyrGlyGly 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 352 CTGGCC-----TTCTCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGAT 405
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 114 ThrGlyAlaSerPheLeuSerThrValLeuVal---IleGluGluLeuAlaLysValAsp 132
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 406 GGGTCCATCACTCTGACCTCGCGCAGCCAGCGCTATTGGCTCAAGGGGATCATCTTG 465
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 AlaSerValAlaValPheCysGluIleGlnAsnThrLeuIleAsnThrLeuIleArgLys 152
QY 466 GCTGGCACTGAGGAGCAAGAAACCAATATCTTCCCTAAACTGGCGTCCGGGAGCACATT 525
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 153 HisGlyThrGluGluGlnLysAlaThrTyrLeuProGlnLeuThrThr---GluLysVal 171
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 526 GCAGCCTTCTGCTCAGGAGCCAGCCAGTGGGAGCGATCCAGCTCAATCCCGGAGCAGA 585
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 GlySerPheCysLeuSerGluAlaGlyAlaGlySerAspSerPheAlaLeuLysThrArg 191
QY 586 GCCACACTAAGTGAAGCAAGAGACTACATCTCAATGGCTCCAAGGTCTGTGATTACT 645
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 192 AlaAspLysGluGlyAsp-----TyrTyrValLeuAsnGlySerLysMetTrpLysSer 209
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 646 AATGGAGAGCTGCCAATATTTTACTGTGTTTGCAGAGACTGAGGTCGTGATTCTGAT 705
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 210 SerAlaGluHisAlaGlyLeuPheLeuValMetAlaAsnVal-----Asp 224
QY 706 GGATCAGTGAAGACAAA---ATCAGCAGATTTCATAGTAGAAGAGACTTTGTGGAGTC 762
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 225 ProThrIleGlyTyrLysGlyIleThrSerPheLeuValAspArgAspThrProGlyLeu 244
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 763 ACTAATGGGAAACCCGAAGATAATTTAGGCATTCGGGGCTCCCAACACTCTGTAAGTCCAT 822
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 HisIleGlyLysProGluAsnLysLeuGlyLeuArgAlaSerSerThrCysProLeuThr 264
QY 823 TTTGAAAACACCAAGATACCTGTGAAAAACATCTTTGGAGAGTCCGAGATGGTTTAAAG 882
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 265 PheGluAsnValLysValProGluAlaAsnIleLeuGlyGlnIleGlyHisGlyTyrLys 284
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 883 GTGGCCATGAACATCTCTCAACAGCGCGCTTCCAGCATGGGAGCGCTGCTGGCTGGCTG 942
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 285 TyrAlaIleGlySerLeuAsnGluGlyArgIleGlyIleAlaAlaGlnMetLeuGlyLeu 304
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 943 CTCAGAGAGATTGATTCGAAATGACTGCTGAGTACGCTGCACCAAGGAAACAGTTTAAACAAG 1002
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 305 AlaGlnGlyCysPheAspTyrThrIleProTyrIleLysGluArgIleGlnPheGlyLys 324
QY 1003 AGGCTCAGTGAATTTGGATTTCAGGAGAAATTTGCACATGATGGCTCAGAAAGGCTTAC 1062
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 325 ArgLeuPheAspPheGlnGlyLeuGlnHisGlnValAlaHisValAlaThrGlnLeuGlu 344
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1063 GTCATGGAGAGTATGACCTTACCTCAAGCAGGAGGATCTGAGCAACACCTGCTTCCGAC 1122
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 345 AlaAlaArgLeuLeuThrTyrAsnAlaAlaArgLeuLeu---GluAlaGlyLysProPhe 363
 QY 1123 TGCTCATCGAGGAGCCATGGTGAAGTGTTCAGCTCCGAGGCGCTGCGCAGTGTGTG 1182
 Db 364 IleLys---GluAlaSerMetAlaLysTyrTyrAlaSerGluIleAlaGlyGlnThr 382
 QY 1183 AGTGAAGCGCTGCAGATCCTCGGGGGCTTGGGCTACACAAAGGACTATCCGTACGAGCGC 1242
 Db 383 SerLysCysIleGluTyrMetGlyGlyValGlyTyrThrLysAspTyrProValGluLys 402
 QY 1243 ATACTGCTGACACCGCATCTCTCTCATCTTCAGGGAACCAATGAGATT 1293
 Db 403 TyrPheArgAspAlaLysIleGlyThrIleTyrGluGlyAlaSerAsnIle 419

RESULT 12
 US-09-252-991A-31097
 ; Sequence 31097, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252.991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 31097
 ; LENGTH: 419
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-31097

Alignment Scores:
 Pred. No.: 2,48e-47 Length: 419
 Score: 603.50 Matches: 136
 Percent Similarity: 57.83% Conservative: 67
 Best Local Similarity: 38.75% Mismatches: 139
 Query Match: 17.63% Indels: 9
 DB: 4 Gaps: 6

US-09-945-326-3 (1-1863) x US-09-252-991A-31097 (1-419)

QY 262 GACACAGAGGAAATCCAGATGAACCTTGGAGAAATGAAGCCCTAGGCTTTT 321
 Db 74 AspArgGluHisArgPheProAlaGluAlaIleArgGluMetAlaAspLeuGlyPheLeu 93
 QY 322 GGGCTGCAAGTCCAGAAATATGGTGGCTGGCTTCTCCAAACACCATGTACTCA--- 378
 Db 94 GlyMetLeuValProGluGluTyrGlyGlyAlaGlnThrClyHisLeuAlaTyrAlaMet 113
 QY 379 AGACTGGGAGATCATCAGCATGGATGGGTCCATCACTGTGACCTGGCAGCGCACAG 438
 Db 114 AlaLeuGluGluIleAlaAlaGlyAspGlyAlaCysSerThrIleMetSerValHisAsn 133
 QY 439 GCTATTGGCTCAAGGGGATCATCTTGGCTGGCAGTGGAGCAGAGCAAGCAATACTTG 498
 Db 134 SerValGlyCysMetProIleHisLysPheGlySerAlaGluGlnLysGluArgPheLeu 153
 QY 499 CCTAACTGGCTCCGGGAGCACATTGTGACGCTTCTGCTCAGCGAGCGAGCAGTGGG 558
 Db 154 ArgProLeuAlaGlnGlySerMetLeuGlyAlaPheAlaLeuThrGluProGlnAlaGly 173
 QY 559 AGCATGACGCTCATCTCCGAGCAGCGCACACTAAGTGAAGCAAGAGCACTACATC 618
 Db 174 SerAspAlaSerPheLeuLysThrArgAla-----ArgArgAspGlyAspHisTyrVal 191
 QY 619 CTCAATGGCTCCAAAGTCTGGATTACTTAATGGAGGACTGGCCAATATTTTACTGTGTTT 678
 Db 192 LeuAsnGlyAlaLysGlnPheIleThrSerGlySerHisAlaGlyMetValIleValPhe 211

QY 679 GCAAAGCTCAGGTCGTTGATTCGTGATCAGTGAAGACAAATCA CAGCATTCATA 738
 Db 212 Ala-----ValThrAspProAspAlaGly---LysArgGlyIleSerAlaPheIle 227
 QY 739 GTAGAAAGACATTTGCTGGAGTCACATAATGGGAAACCCGAGCATAAATTAGGCAATTCGG 798
 Db 228 ValProThrAspThrProGlyTyrGluValValArgIleGluAspLysLeuGlyGlnHis 247
 QY 799 GGCTCCAAACACTTGTGAAGTCCATTTTGAACACCAAGATACCTGTGGAAAAACATCCTT 858
 Db 248 AlaSerAspThrCysGlnLeuAlaPheAsnAspLeuArgIleProAlaThrLeuArgLeu 267
 QY 859 GGAGAGTGGAGATGGGTTTAAGTGGCCATCAACATCTCTCAACAGCGCCCGTTCAGC 918
 Db 268 GlyGluGluGlyGlyTyrArgIleAlaLeuAlaAsnLeuGluGlyGlyArgIleGly 287
 QY 919 ATGGCAGCGCTCGTGGCTGGCTCAAGAGATTGATTGAAATGATGCTGCTGAGTACGCC 978
 Db 288 IleAlaAlaGlnAlaValGlyMetAlaArgAlaAlaPheGluAlaAlaArgAspTyrAla 307
 QY 979 TGCACAAGGAAACAGTTTAAACAGAGCTCAGTGAATTTGGATTGATTGAGGAGAAATTT 1038
 Db 308 HisGluArgGluThrPheGlyLysProIleIleGluHisGlnAlaValAlaPheArgLeu 327
 QY 1039 GCATCATGCTCAGAAAGCTTACGTCATGGAGAGTATGACCTACCTCAGCAGGGATG 1098
 Db 328 AlaAspMetAlaThrArgIleAlaValAlaArgGlnMetValHis---HisAlaAlaSer 346
 QY 1099 CTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGAGCCATGTTGAAGTGTTCAGC 1158
 Db 347 LeuArgGluAlaGlyLeuPro---CysLeuThrGluAlaSerMetAlaLysLeuPheAla 365
 QY 1159 TCGAGGCGCCCTGGCAGTGTGTGAGTGGGCTGCAGATCTCTCGGGGCTTGGGCTAC 1218
 Db 366 SerGluMetAlaGluGluValCysSerAlaAlaIleGlnThrLeuGlyGlyTyrGlyTyr 385
 QY 1219 ACAAGGAGCTATCCGTACGAGCGCTACTGCTGCAGCCGATCCCTCATCTTCGAG 1278
 Db 386 LeuLysAspPheProValGluArgIleTyrArgAspValArgValCysGlnIleTyrGlu 405

QY 1279 GGAACCAATGAGATTCTCCGATGTACATCGCC 1311
 Db 406 GlyThrSerAspValClnArgLeuValIleAla 416

RESULT 13
 US-09-328-352-6801
 ; Sequence 6801, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 6801
 ; LENGTH: 394
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-6801

Alignment Scores:
 Pred. No.: 1.19e-46 Length: 394
 Score: 596.00 Matches: 140
 Percent Similarity: 57.10% Conservative: 73
 Best Local Similarity: 37.53% Mismatches: 138
 Query Match: 17.41% Indels: 22
 DB: 4 Gaps: 9

US-09-945-326-3 (1-1863) x US-09-328-352-6801 (1-394)

QY 220 GTGGAATAATCTTCACTGAAGAGGTGGAC-----TCCCGAAAAATTCACCAGGAAGG 273
Db 25 ValAlaAlaPheCysAlaLysGluLeuAlaProIleAlaGlnValAspGlnAsn 44
QY 274 AAAATCCAGATGAATTTGGAGAAATGAAGAGCTAGGCTTTTGGCTGCAAGTC 333
Db 45 LysPheProAlaHisLeuTrpLysPheGlyAspMetGlyLeuLeuGlyMetThrVal 64
QY 334 CCAGAAGAATATGTGGCTGGCTTTCTCCCAACACCATGTACTCAAGACTAGGGAGATC 393
Db 65 SerGluGluTrpGlyGly-----AlaAsnMetGlyTyr-----LeuAlaHisIle 79
QY 394 ATCAGCATG-----GATGGTCCATCATCTGACCTGGAGCCGCAC 435
Db 80 IleAlaMetGlnGluIleSerArgAlaSerAlaAlaIleGlyLeuSerTyrGlyAlaHis 99
QY 436 CAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCCAAATAC 495
Db 100 SerAsnLeuCysValAsnGlnIleAsnArgAsnGlyAsnGlnGlnLysGlnLysTyr 119
QY 496 TTGCTTAATCTGGCTCCGGGAGCACATTCAGCCTTCTGCTCCACGGAGCCAGCCAGT 555
Db 120 LeuProLysLeuIleSerGlyGluTyrValGlyAlaLeuAlaMetSerGluProAsnAla 139
QY 556 GGGAGCGATGCGCTCAATCCGAGGAGCAGAGCCACACTAAGTGAAGACAGACCATC 615
Db 140 GlySerAspValValSerMetLysLeuArgAlaGluGlnLysGlyAsp-----HisPhe 157
QY 616 ATCTCAATCGCTCAAGGCTGCTGATTACTAATGAGGAGCTGGCCCAATATTTTACTGTG 675
Db 158 ValLeuAsnGlySerLysMetTrpIleThrAsnGlyGlyAspAlaAspValLeuVal 177
QY 676 TTTGCAAAAGACTGAGGTCGTGTGATTCTGATGGATCAGTGAAGACAAATAATCACAGATTC 735
Db 178 TyrAlaLysThr-----AspProGlnAlaGlyProLysGly---MetThrAlaPhe 193
QY 736 ATAGTGAAGAAGACTTTGTGGAGTCACTAATGGGAACCCGAAATATAATTAGGACTT 795
Db 194 LeuIleGluLysGlyMetLysGlyPheSerHisGlyAsnHisLeuAspLysLeuGlyMet 213
QY 796 CGGGCTCCACACTTGTGAAGTCCATTTTCAAAACACCAAGATACCTGTGGAAACATC 855
Db 214 ArgGlySerAsnThrTrpProLeuPhePheAspAsnValGluValProAlaGluAsnVal 233
QY 856 CTTGGAGAGTTCGAGATGGGTTTAAAGTGGCCATGAACATCTCTCAACAGCGCGCTTC 915
Db 234 LeuGlyGlyValGlyAsnGlyValLysValLeuMetSerGlyLeuAspTyrGluArgAla 253
QY 916 AGCATGGGAGCGTGTGGCTGCTCAAGAGATTGATTGAATGATGCTGCTGAGTAC 975
Db 254 ValLeuSerAlaGlyProLeuGlyIleMetAspAlaCysLeuAspValValIleProTyr 273
QY 976 GCCTGCACAGGAACAGTTTAAACAGAGCTCAGTGAATTTGATTGATTTCAGGAGAA 1035
Db 274 LeuHisGlnArgGluGlnPheGlyGlnAlaLeuGlyGluPheGlnLeuMetGlnGlyLys 293
QY 1036 TTTGCTACTGGCTCAGAAGGCTTACGTCATGAGAGATGATCACTTCACTCACAGCAGG 1095
Db 294 LeuAlaAspMetTyrSerThrTrpLeuAlaCysLysAlaLeuValTyrAlaValGlyAla 313
QY 1096 ATGCTGACCAACCTGGCTTTCCCGACTGCTCCATC-----GAGGAGCGCATGGTGAAG 1149
Db 314 AlaCysAspLysAlaAspHis---AspArgSerLeuArgLysAspAlaAlaSerAlaIle 332
QY 1150 GTGTTACGTCCTCGAGCGGCTGCGACTGTGTAGTGAGGCGTGCAGATCCTCGGGGCG 1209
Db 333 LeuTyrAlaAlaGluLysAlaThrTrpMetAlaGlyGluAlaIleGlnThrLeuGlyGly 352
QY 1210 TTGGGCTACCAAGGACTATCCCTACGAGCGCATCTGGCTGACCCCGCATCTCTCCTC 1269
Db 353 AsnGlyTyrIleAsnGluPheProAlaGlyArgLeuTrpArgAspAlaLysLeuTyrGlu 372
QY 1270 ATCTCGAGGGAACCAATGAGATTCTCCGGATGTACATC 1308

Db 373 IleGlyAlaGlyThrSerGluIleArgMetLeuIle 385
RESULT 14
US-09-364-230-30
; Sequence 30, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09364,230
; CURRENT FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,990
; EARLIER FILING DATE: July 31, 1998
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-364-230-30
Alignment Scores:
Pred. No.: 1,36e-46 Length: 409
Score: 595.50 Matches: 150
Percent Similarity: 54.87% Conservative: 64
Best Local Similarity: 38.46% Mismatches: 143
Query Match: 17.40% Indels: 33
DB: Gaps: 13
US-09-945-326-3 (1-1863) x US-09-364-230-30 (1-409)
QY 184 GATGAATTAATCAATCAATCAATGTTCTTGGGACCGCTGGAAAAATTTCTTCACTGAAGAG 243
Db 32 AspAspThrGlnGlu-----GlnPheLysGluSerValHisLysPheAlaGlnGluThr 49
QY 244 GTG-----GACTCCCGAAAAATTTGACCAGGAAGGAAAAATCCCA---GATGAAACTTTG 294
Db 50 IleAlaProHisAlaAlaIleAspAlaSerAsnHisPheProLysAspValAsnLeu 69
QY 295 GAGAAATTGAAG---AGCCTTAGGCTTTTGGCTGCAAGTCCCAAGAAATATGTGGC 351
Db 70 TrpLysLeuMetGlyAspPheAsnLeuHisGlyLeuThrAlaProGluGluTyrGly 89
QY 352 CTGGGCTTCTCCAACACCATGTACTCA-----AGACTAGGGGAGATCATCAGCATGAT 405
Db 90 MetGlyLeu---GlyTyrMetTyrHisCysIleAlaMetGluGluIleAsnArgAlaSer 108
QY 406 GGTCTCATCTACTGTGACCTCGGAGCGCACAGGCTATTGGCTCAAGGGGATCATCTTG 465
Db 109 GlySerValGlyLeuSerTyrSerAlaHisSerAsnLeuCysIleAsnGlnLeuValArg 128
QY 466 GCTGGCCTCAGGAGCAGAAAGCAATCTTGCCTAAACTGGCGTCCGGGAGCACAT 525
Db 129 HisGlySerProAlaGlnLysLeuLysTyrLeuProLysLeuIleThrGlyGluHisVal 148
QY 526 GCAGCCTTCTGCTCAGGAGCGCAGGCTGGGAGCGATGCGCTCAATCCGGAGCAGA 585
Db 149 GlyAlaLeuAlaMetSerGluProAsnSerGlySerAspValValSerMetLysCysLys 168
QY 586 GCCACACTAAGTGAACAGAGAGAC-----TACATCTCAATGCTCCAGGCTCGG 639
Db 169 Ala-----GluLysValTyrGlyTyrValIleAsnGlyLysMetTrp 184
QY 640 ATTACTAATGGAGGACTGGCCAAATATTTTACTGTGTGTTTCAAGAGCTGAGGTC---GTT 696
Db 185 CysThrAsnGlyProSerAlaGlnThrLeuGlyValTyrAlaLysThrAspIleThrAla 204
QY 697 GATTCTGTGATGATCAGTGAAGAGCAAAATACAGCATTTCTATAGTAAGAGACTTTGGT 756

205 GlySerLysGly-----IleThrAlaPheIleIleGluLysGlyMetAla 219
757 GGAGTCACATAATGGGAACCCAGAGATAAATAGGCATTTCGGGCTCCACACTTGTCAA 816
220 GlyPheSerThrAlaGlnLysLeuAspLysLeuGlyMetArgGlySerAspThrCysGlu 239
817 GTCCATTTTGAACACACCAAGATACCTGTGGAACACATCTTGGAGAGGTCCGAGATGGG 876
240 LeuValPheGluAsnCysPheValProHisGluAsnValLeuGluGlyLysGly 259
877 TTTAAGGTGGCCATGAACATCTCAACAGCCGCGTTCAGCATGGGAGCGTCGTGGCT 936
260 ValTyrValMetMetSerGlyLeuAsnLeuGluArgPheValLeuAlaAlaGlyProSer 279
937 GGGCTGCTCAAGAGATTGATTGAATGACTGCTGAGTACGCTCCACAGGMAACACTTT 996
280 AlaLeuMetGlnAlaCysLeuAspValAlaValLeuTyrValArgGlnArgGluInPhe 299
997 AACAGAGGCTCAGTGAATTTGGATTGATTCAGAGAAATTTGCACTGATGGCTCAGAAG 1056
300 GlyArgProIleGlyGluPheGlnPheIleArgGlyLysLeuAlaAspMetTyrThrSer 319
1057 GCTTACGTCATGGAGATGACCTACTCTACAGCA-----GGATGCTG 1101
320 LeuGlnSerSerArgSerPheValTyrSerValAlaArgAspCysAspAsnGlyLysVal 339
1102 GACCAACTGGCTTTCCCGACTGCTCCATCGAGCAGCCATGTTGAAGGTTCAGCTCC 1161
340 AspArg-----LysAspCys-----AlaGlyValIleLeuPheAlaAla 352
1162 GAGCCGCCCTGGCAGTGTGTAGTAGGCGCTGCAGATCTCCGGGGCTTGGGCTACACA 1221
353 GluArgAlaThrGlnValAlaLeuGlnAlaIleGlnCysLeuGlyGlyAsnGlyTyrIle 372
1222 AGGACTATCGTACGAGCCATCTACTCGGTGACACCCGCTCTCTCATCTTCGAGGGA 1281
373 AsnGluTyrProThrAlaArgLeuLeuArgAspAlaLysLeuPheGluIleGlyProGly 392
1282 ACCAATCAGATTCTCCGGATGTACATCGCC 1311
393 ThrSerGluLeuArgArgMetIleIleAla 402

RESULT 15
US-09-949-016-10443
; Sequence 10443, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10443
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10443
Alignment Scores:
Pred. No.: 3,11e-46 Length: 459
Score: 592.00 Matches: 161
Percent Similarity: 51.61% Conservative: 79
Best Local Similarity: 34.62% Mismatches: 179

Query Match: 17.29% Indels: 46
DB: 4 Gaps: 13
US-09-945-326-3 (1-1863) x US-09-949-016-10443 (1-459)
QY 8 GCTCGCGGCTCTTCCTCGCGCACCACCGCTCGCTCGCGGGTCTGTGTGTCT 67
DB SerAlaGlySerSerCysMetAlaGluMet--AlaThrAlaThrArgLeuLeuGlyTrpA 47
QY 68 CTACCCGGAACCGCGCGCTACTCGCGCACCACCGCGCTGTACGAGCTTTCCGCAAGAGC 127
DB rgValAlaSerTrpArgLeu-----ArgProProLeuAlaGlyPheValSerGln- 63
QY 128 TTTTCTAGCAAAATCAAGAAAGAAAGTTTCCCATTTTCCAGAGTTAGCCAAAGATG 187
DB 64 -----ArgAlaHisSerLeuLeuProValAspAlaIleAsnGlyL 78
QY 188 AACTTAATGAATCAATCAGTTCTTGGGACCCGTGGAAAAATTTCTTCACTGAAGAGTG- 246
DB euSerGluGluGlnArgGlnLeuArgGlnThrMetAlaLysPheLeuGlnGluHisLeuA 98
QY 247 -----GACTCCCGGAAAAATGACAGGAAGGAAAAATCCAGAT-----GAAACTTTGG 295
DB 98 laProLysAlaGlnGluIleAspArgSerAsnGluPheLysAsnLeuArgGluPheTrpL 118
QY 296 AGAAATGAAGAGCCCTAGGCTTTTGGGCTGCCAAGTCCCAGAGAATAATGTTGGGCTGG 355
DB 118 ysGlnLeuGlyAsnLeuGlyValLeuGlyIleThrAlaProValGlnTyrGlyIleGlySerG 138
QY 356 GCTTCTCCCAACCATGTACTCAAGACTAGGGAGATCATCAGC---ATGGATGGGTCCA 412
DB 138 lLeuGlyTyrLeuGluHisValLeuValMetGluIleIleSerArgAlaSerGlyAlav 158
QY 413 TCACTGTGACCTGGCAGCGCACCAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCA 472
DB 158 aGlyLeuSerTyrGlyAlaHisSerAsnLeuCysIleAsnGlnLeuValArgAsnGlyA 178
QY 473 CTGAGAGCAGAGAAGCAATACTTGCCTTAAATCTGGCGTCCGGGAGAGCACTTGCAGCCT 532
DB 178 enGluAlaGlnLysGluLysTyrLeuProLysLeuIleSerGlyGluTyrIleGlyAlaL 198
QY 533 TCTGCTCAAGAGCAGCGCAGTGGAGGATGCGACCTCAATCCGAGAGCAGGACACAC 592
DB 198 euAlaMetSerGluProAsnAlaGlySerAspValValSerMetLysLeuLysAla--- 216
QY 593 TAAGTGAACACAGAAG-----CACTACATCTCAATGGCTCCCAAGGCTCGATTACTA 646
DB 217 -----GluLysLysGlyAsnHisTyrIleLeuAsnGlyAsnLysPheTrpIleThra 234
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DB 234 enGlyProAspAlaAspValLeuIleValTyrAlaLysThrAspLeuAlaAlaValProA 254
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DB 254 laSer-----ArgGlyIleThrAlaPheIleValGluLysGlyMetProGlyPheSerT 272
QY 767 ATGGGAACCCGGAAGATAAATTTAGGCATTTCGGGCTCCCAACACTTGTGAAGTCCATT 826
DB 272 hrSerLysLysLeuAspLysLeuGlyMetArgGlySerAsnThrCysGluLeuIlePheG 292
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QY 887 CCATGAACATCTCAACAGCGCCCGTTCAGCATGGGAGCGCTCGTGGCTGGCTGCTCA 946
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DB 332 InAlaValLeuAspHisThrIleProTyrLeuHisValArgGluAlaPheGlyGlnLysI 352

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GenCore version 5.1.6
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Run on: May 2, 2005, 14:49:52 ; Search time 206.808 Seconds
(without alignments)
6001.474 Million cell updates/sec

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Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 2852064

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	3153	92.1	621	9	US-09-945-326-2	Sequence 2, Appli
2	3153	92.1	621	14	US-10-168-274-24	Sequence 24, Appl
3	3153	92.1	621	15	US-10-112-944-420	Sequence 420, App
4	3153	92.1	621	16	US-10-408-765A-1059	Sequence 1059, Ap
5	3153	92.1	621	16	US-10-408-765A-2053	Sequence 2053, Ap
6	3129	91.4	628	15	US-10-112-944-869	Sequence 869, App
7	1360	39.7	655	15	US-10-362-537-10	Sequence 9, Appli
8	1356.5	39.6	653	15	US-10-362-537-9	Sequence 10, Appli
9	1345	39.3	655	15	US-10-362-537-11	Sequence 11, Appli
10	1308	38.2	655	15	US-10-362-537-1	Sequence 1, Appli
11	1308	38.2	655	16	US-10-408-765A-534	Sequence 534, App
12	1299	37.9	655	16	US-10-408-765A-320	Sequence 320, App
13	1210.5	35.4	613	15	US-10-369-493-5444	Sequence 5444, Ap
14	954	27.9	188	16	US-10-408-765A-1442	Sequence 1442, Ap
15	954	27.9	188	16	US-10-408-765A-2052	Sequence 2052, Ap
16	844.5	24.7	594	15	US-10-369-493-16704	Sequence 16704, A
17	821	24.0	594	15	US-10-369-493-17429	Sequence 17429, A
18	816	23.8	581	15	US-10-369-493-19424	Sequence 19424, A
19	815.5	23.8	594	15	US-10-369-493-23285	Sequence 23285, A
20	799	23.3	585	15	US-10-369-493-9765	Sequence 9765, Ap
21	795.5	23.2	583	15	US-10-369-493-9771	Sequence 9771, Ap
22	765	22.3	583	15	US-10-369-493-10383	Sequence 10383, A
23	704	20.6	373	15	US-10-369-493-16614	Sequence 16614, A
24	699	20.4	382	15	US-10-369-493-16795	Sequence 16795, A
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27	682	19.9	378	15	US-10-369-493-23196	Sequence 23196, A
28	678	19.8	381	15	US-10-369-493-16818	Sequence 16818, A
29	675.5	19.7	379	15	US-10-369-493-16613	Sequence 16613, A
30	663	19.4	646	14	US-10-156-761-10104	Sequence 10104, A
31	658	19.2	380	15	US-10-369-493-17459	Sequence 17459, A
32	652.5	19.1	379	15	US-10-369-493-23337	Sequence 23337, A
33	652	19.0	387	15	US-10-369-493-577	Sequence 577, App
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36	641	18.7	375	15	US-10-369-493-8807	Sequence 8807, A
37	640	18.7	378	15	US-10-369-493-16449	Sequence 16449, A
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39	630.5	18.4	387	15	US-10-369-493-13698	Sequence 13698, A
40	629.5	18.4	381	15	US-10-369-493-546	Sequence 546, App
41	629	18.4	374	15	US-10-369-493-9830	Sequence 9830, App
42	626	18.3	373	15	US-10-369-493-11638	Sequence 11638, A
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45	624	18.2	378	15	US-10-369-493-9086	Sequence 9086, Ap

ALIGNMENTS

RESULT 1
US-09-945-326-2
; Sequence 2, Application US/09945326
; Patent No. US20020127680A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Hunter, John Joseph
; TITLE OF INVENTION: 62112, A NOVEL HUMAN DEHYDROGENASE AND
; FILE REFERENCE: MNI-187
; CURRENT APPLICATION NUMBER: US/09/945,326
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,831
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-326-2

APPLICANT: TANG, Y. Tom
APPLICANT: HILLMAN, Jennifer
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda
APPLICANT: LU, Dyoung Aina M.
TITLE OF INVENTION: HUMAN OXIDOREDUCTASE PROTEINS
FILE REFERENCE: PF-0754 PCT
CURRENT APPLICATION NUMBER: US/10/168, 274
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 60/172,367
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PERL Program
SEQ ID NO 24
LENGTH: 621
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030124106A1 5540437CD1
US-10-168-274-24

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US-09-945-326-3 (1-1863) x US-10-168-274-24 (1-621)

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Db	21	ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla	40
Qy	121	AAAGAGCTTTCTAGGCAAAATCAAGAAAGAGTTCCTCCATTTCCAGAGTTAGC	180
Db	41	LysGluLeuPheLeuGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys	60
Qy	181	CAAGATGAATTAATGAAATCAATCAGTCTTGGGACCGCTGGGAAATTTCTTCACTGAA	240
Db	61	GlnAspGluLeuLeuGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLys	80
Qy	241	GAGGTGAGCTCCGAAAAATTTGACAGGAGGAGGAAATCCAGATGAAATTTGGAGAAA	300
Db	81	GluValAspSerArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys	100
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Qy	361	TCCAAACCACTGACTCAAGACTAGGAGGAGATCATCAGCATGGATGGGTCCATCAGCTGTG	420
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Qy	481	CAGAAAGCCAAATCTTGCCTAACTGGCTCCGGGAGGAGCAGATTCAGGCTTCGCTC	540
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RESULT 3

US-10-112-944-420
; Sequence 420, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: Pf_Fl_genes Version 5.0
; SEQ ID NO 420
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-944-420

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.11% Indels: 0
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US-09-945-326-3 (1-1863) x US-10-112-944-420 (1-621)

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QY 1021 TTGATTCCAGGAGAAATTTGCACCTGATGGCTCAGAGGCTTACGTATGAGAGATGACC 1080
Db 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
QY 1081 TACCTCACAGCAGGAGTGTGGACCAACTGGCTTTCCGACTGTCTCAATCCAGGAGCAGC 1140
Db 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAla 380

```
QY 1141 ATGGTGAAGCTGTTCAGCTCCGAGCGCGCTGGAGTGTGTGAGTGAGGCGCTGCAGATC 1200
Db 381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400
QY 1201 CTCGGGGCTTGGCTACACAGGGACTATCCGTACGAGCGCATCTGCGTGACACCCGC 1260
Db 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
QY 1261 ATCTCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1320
Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY 1321 CTCGAGCATCCCGCCCATCTGACTACAGATCCATGAGCTTAACAGGCCAAGTG 1380
Db 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY 1381 AGCACAGTCAATGATACCGTTGGCCGAGGCTTCGGGACTCCCTGGGCCGAACTGTGGAC 1440
Db 461 SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 480
QY 1441 CTCGGGCTGACAGCCACCATGAGTTGTCCACCCAGTCTTCGGGACAGTCCCAACAAG 1500
Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY 1501 TTTGAGGAGAACACTACTCTCTCCGCGCCGACCGTGGAGACACTGTCTCCGCTTTGGC 1560
Db 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
QY 1561 AAGACCATCATGAGGAGCAGCTGGTACTCAAGCGGTGGCCCAACATCTCATCAACCTG 1620
Db 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
QY 1621 TATGGCATGACGGCGCTGTCTGCGGGCCAGCGCTCCCATCGCATTTGGGCTCCGCAAC 1680
Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY 1681 CAGCACACAGGTTCTCTTGGCCCAACACTCTGCGTGGAGCTTACTTGCAGATCTC 1740
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
QY 1741 TTCAGCTCTCTCAGCTGGACAAGTAGTCTCCAGAAACCTAGATGACGAGATTAAAGAA 1800
Db 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
QY 1801 GTGTCCAGCAGATCTCTGAGAGCGAGCCTATATCTGTGCCACCTCTCGACAGGACA 1860
Db 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
QY 1861 TGC 1863
Db 621 Cys 621
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RESULT 4

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US-10-408-765A-1059
; Sequence 1059, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1059
; LENGTH: 621
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1059
Alignment Scores:
Pred. No.: 1,296-251 Length: 621
Score: 3153.00 Matches: 621
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.11% Indels: 0
DB: 16 Gaps: 0
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US-09-945-326-3 (1-1863) x US-10-408-765A-1059 (1-621)

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QY 1 ATGAGCGGCTCGGGCTCTTCCTGCGGCACACAGCGCTCGGCTCGTGCCTCGCGGGTCTG 60
Db 1 MetSerGlyCysGlyLeuPheLeuArgThrAlaAlaAlaArgAlaCysArgGlyLeu 20
QY 61 GTGGTCTCTACCGCAACCGCGGCTACTGCGCACACAGCCCGCTGTACGAGCTTTCCGCC 120
Db 21 ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProProValArgAlaPheAla 40
QY 121 AAAGAGCTTTCTTAGCGCAAAATCAAGAGAAAGAGCTTTTCCCATTTCCAGAGATTAGC 180
Db 41 LysGluLeuPheLeuGlyLysIleLysLysLysLysValPheProPheProGluValSer 60
QY 181 CAAGATGAATTAATCAAAATCAATCAGTCTTGGGACCCCTGGAGAAATATCTTCACCTGAA 240
Db 61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPhePheThrGlu 80
QY 241 GAGGTGACTCCCGAAAAATTGACCAGGAGGAGGAAAAATCCAGATGAACTTTGGAGAAA 300
Db 81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100
QY 301 TTCAAGAGCTCAGGGCTTTTGGGCTGCAAGTCCCAAGAACAAATATGCTGGCTGGGCTTC 360
Db 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyLeuGlyPhe 120
QY 361 TCCAACACCATGTAATCAAGACTAGGGAGATCATCAGCATGGATGGGTCCATCAGCTGTG 420
Db 121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
QY 421 ACCTGGCAGCGCACAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCAGCTGAGGAG 480
Db 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160
QY 481 CAGAAAGCCAAATACTTGCCTAACTGGCTCCGGGAGCACATTGTCAGGCTTCTGCCTC 540
Db 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeu 180
QY 541 ACGGAGCCAGCCAGTGGGAGCGATGCAGGCTCAATCCGGAGCAGAGCCACACTAAGTGAA 600
Db 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
QY 601 GACAGAGCAGCTACATCTCAATGGCTCAAGGCTCTGGATTACTTAATGAGGAGCTGGCC 660
Db 201 AspLysLysHisTyrIleLeuAsnGlySerLysValTyrIleThrAsnGlyGlyLeuAla 220
QY 661 AATATTTTACTGTGTTTGCAGAGACTGAGTCTGTGATTCTGATGATCAGTCAAGAGAC 720
Db 221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
QY 721 AAAATCACAGCATTCATAGTAGAAAGAGACTTTGGTGAGTCACTAATGGGAAACCCGAA 780
Db 241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260
QY 781 GATAAATTAGGCATTCGGGGCTCCAACTTGTGAAGTCCATTTTGAACACCAAGATA 840
Db 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
QY 841 CCTGTGAAAAACATCTCTGGAGAGGTCGGAGATGGGTTTAAGTGGCCATGAACATCCTC 900
Db 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
```

```
QY 901 AACAGCGCGGTTTCAGCATGGGCAGCGTCGTGGCTGGCTCAAGAGATTGATTGAA 960
Db |||||
QY 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuYsArgLeuIleGlu 320
Db |||||
QY 961 ATGACTGCTGAGTACGCTCCACAGGAACAGTTTAAACAGAGGCTCAGTGAATTGGA 1020
Db |||||
QY 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
Db |||||
QY 1021 TTGATTTCAGAGAAATTTGGCACTGATGCTCAGAGGCTTACGTCATCGAGAGATATGACC 1080
Db |||||
QY 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
Db |||||
QY 1081 TACCTCACAGCGGATGCTGGACCAACCTGGCTTCCCGACTGCTCCATCGAGGAGGCC 1140
Db |||||
QY 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaA 380
Db |||||
QY 1141 ATGCTGAAGGTGTTTCAGCTCCGAGGCGCTGGCAGTGTGTGAGTAGGCGCTGCAGATC 1200
Db |||||
QY 381 MetValLysValPheSerSerGluAlaAlaTyrGlnCysValSerGluAlaLeuGlnIle 400
Db |||||
QY 1201 CTGGGGCTGGGCTACACAGGGACTATCCGTACGAGCGCATCTGCGTGACACCCGC 1260
Db |||||
QY 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
Db |||||
QY 1261 ATCTCCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1320
Db |||||
QY 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
Db |||||
QY 1321 CTGAGCATCCGCGCGCATCTGACTACAGGATCCATGAGCTTAAACAGGCCAACAGTG 1380
Db |||||
QY 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
Db |||||
QY 1381 AGCACAGTCATGATACCGTTGGCCGAGGCTTCGGGACTCCCTGGGCCCAACTGTGGAC 1440
Db |||||
QY 461 SerThrValMetAspThrValGlyArgLeuArgLeuArgAspSerLeuGlyArgThrValAsp 480
Db |||||
QY 1441 CTGGGCTGACAGGCAACCATGAGTTGTGCACCCAGTCTTGGGACAGTGCACCAACAG 1500
Db |||||
QY 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
Db |||||
QY 1501 TTTGAGGAGAACACTACTCTTCGCGCGGACCGTGGAGACATGTGCTGCCCTTTGGC 1560
Db |||||
QY 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuA-gPheGly 520
Db |||||
QY 1561 AAGACCATCATGNGGAGCAGCTGGTACTGACGGGTGGCCACATCTCTCATCAACCTG 1620
Db |||||
QY 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
Db |||||
QY 1621 TATGGCATGACGGCGGTGCTGTCGGGGCCAGCGCTCCATCCGCAATTGGGCTCCGCAAC 1680
Db |||||
QY 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
Db |||||
QY 1681 CAGACACAGAGTTCTCTTTGGCAACACTCTTCGCTGGAAGCTTACTTGCAGATCTC 1740
Db |||||
QY 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
Db |||||
QY 1741 TTGAGCTCTCTAGCTGGACAGTATGCTCCAGAAAACCTAGATGAGCAGATTAGAAA 1800
Db |||||
QY 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
Db |||||
QY 1801 GTGTCCAGCAGATCTCTTGAAGACGAGCTATATCTGTGCCACCTCTGGACAGGACA 1860
Db |||||
QY 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
Db |||||
QY 1861 TGC 1863
Db |||
QY 621 Cys 621
```

RESULT 5

US-10-408-765A-2053

; Sequence 2053, Application US/10408765A

; Publication No. US20040101874A1

```
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
```

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; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2053
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-2053
```

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Alignment Scores:
Pred. No.: 1,29e-251 Length: 621
Score: 3153.00 Matches: 621
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.11% Indels: 0
DB: 16 Gaps: 0
```

US-09-945-326-3 (1-1863) x US-10-408-765A-2053 (1-621)

```
QY 1 ATGAGCGGCTGGCGGCTCTTCTGCGCACACAGCGCTGCGGCTGCTGCTGCGGGGTCTG 60
Db |||||
QY 1 MetSerGlyCysGlyLeuPheLeuArgThrThrAlaAlaAlaArgAlaCysArgGlyLeu 20
Db |||||
QY 61 GTGGTCTCTACCGCGAACCGGGGCTACTGCGCACCGCCGCTGTACGAGCTTTGCGCC 120
Db |||||
QY 21 ValValSerThrAlaAsnArgLeuLeuArgThrSerProProValArgAlaPheAla 40
Db |||||
QY 121 AAGAGCTTTTCTAGCGCAAAATCAAGAGAAGAAAGTTTCCCATTTCCAGAAAGTTAGC 180
Db |||||
QY 41 LysGluLeuPheLeuGlyLysIleLysLysLysLysLysLysLysLysLysLysLys 60
Db |||||
QY 181 CAAGATGAACCTTAATGAAATCAATCAGTCTTTGGGACCGCTGGAAAAATTTCTTCACTGAA 240
Db |||||
QY 61 GlnAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPheThrGlu 80
Db |||||
QY 241 GAGGTGAGCTCCCGAAAAATTCACAGGAAGGAAAAATCCAGATGAAATTTGGAGAAA 300
Db |||||
QY 81 GluValAspSerArgLysIleAspGlnGluGlyLysIleProAspGluThrLeuGluLys 100
Db |||||
QY 301 TTGAAGAGCTAGGGCTTTTGGGCTGCAAGTCCAGAGAAAGATATGCTGGCTGGGCTTC 360
Db |||||
QY 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluTyrGlyLeuGlyPhe 120
Db |||||
QY 361 TCCAAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCCATCACTGTG 420
Db |||||
QY 121 SerAsnThrMetTyrSerArgLeuGlyGluIleSerMetAspGlySerIleThrVal 140
Db |||||
QY 421 ACCTGGCAGCGCACCGAGCTATTGGCTCAAGGGGATCATCTTGGCTGGCAGCTAGGAG 480
Db |||||
QY 141 ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleLeuAlaGlyThrGluGlu 160
Db |||||
QY 481 CAGAAAGCCAAATACATTGCTTAACTGGGCTCCGGGGAGCACATTGAGGCTTCTGCCTC 540
Db |||||
QY 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaPheCysLeu 180
Db |||||
QY 541 ACGGAGCCAGCCAGTGGGAGCGATGCGAGCTCAATCCGAGCAGAGCCACACATAAGTGAA 600
Db |||||
QY 181 ThrGluProAlaSerGlySerAspAlaAlaSerIleArgSerArgAlaThrLeuSerGlu 200
Db |||||
QY 601 GACAAGACACTTACATCTCATGCTCCAGGCTCGAGTTACTTAATGAGAGCTGGCC 660
Db |||||
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Db 201 AspLysLysHisTyrIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
Qy 661 AATATTCTTACTGTGTTGCAAAAGACTGAGGTGGTTGATTCGTGATGATCAGTGAAGAC 720
Db 221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
Qy 721 AAAATCAGCAGCATTCATAGTAGAAAGAGACTTGGTGGAGTCACTAATGGGAACCCGAA 780
Db 241 LysIleThrAlaPheIleValGluArgAspPheGlyValThrAsnGlyLysProGlu 260
Qy 781 GATAAATTAGGCATTCGGGCTCCACACCTTGGAAGTCCATTTGAAAAACACCAAGATA 840
Db 261 AspLysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
Qy 841 CCTGTGGAACACATCTCTGAGAGGTCGGAGATGGGTTTAAAGTGGCCATGAACATCCTC 900
Db 281 ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
Qy 901 AACAGCGCCGGTTCAGCATGGCAGCGTCTGGCTGGCTGCTCAAGAGATTGATTGAA 960
Db 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
Qy 961 ATGACTGCTGAGTACCCCTGCAAGGAAACAGTCTTAAAGAGGCTCAAGTGAATTGGA 1020
Db 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
Qy 1021 TTGATTTCAGAGAAATTTGACATGGCTCAGAGGCTTACGTCATGAGAGATATGACC 1080
Db 341 LeuIleGlnLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
Qy 1081 TACCTCACAGCAGGATGTGGACCAACCTGGCTTTCCGACTGCTCCATCGAGGAGGCC 1140
Db 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
Qy 1141 ATGGTGAAGTGTTCAGCTCCGAGGCGCTCGCAGTGTGTGAGTGGCGCTGCAGATC 1200
Db 381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400
Qy 1201 CTCGGGGCTTGGCTTACACAAGGGATATCCGTACGAGGCGTACTGCGTGACACCCGC 1260
Db 401 LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
Qy 1261 ATCCCTCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGT 1320
Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
Qy 1321 CTCGAGATCCCGCGCATCTGACTACAGATTCATGAGTCTTAAACAGGCCAAAGTC 1380
Db 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
Qy 1381 AGCACAGTCATGATACCGTGGCGGAGGCTTCGGGACTTCCTGGGCGCGAACTGTGGAC 1440
Db 461 SerThrValMetAspThrValGlyArgGluArgAspSerLeuGlyArgThrValAsp 480
Qy 1441 CTGGGGCTGACAGGCAACCATGGAGTTGTGCACCCCGCTTCGGGACAGTGCACCAAG 1500
Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
Qy 1501 TTTGAGAGAACACTTACTGCTTCGGCGGCGAGCGCTGAGACATGCTGCTCCCGCTTGGC 1560
Db 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
Qy 1561 AAGACCATCATGAGGAGCAGCTGGTACTGAAGCGGTGGCCCAACATCTTCATCAACCTG 1620
Db 521 LysThrIleMetGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
Qy 1621 TATGGCATGACGCGCTGTGTCGCGGCGCAGCGCTCCATCCGCATTTGGCTCCGCAAC 1680
Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
Qy 1681 CAGACACAGAGGTTCTCTTGGCCCAACACTCTTGGTGGGAAGCTTACTTGCAGATCTC 1740
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580

Qy 1741 TTCAGCCTCTCTCAGCTCGACAGTATGCTCCAGAAAAACCTAGATGAGCAGATTAGAAA 1800
Db 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
Qy 1801 GTGTCCACAGACCTCTTCAGAGCGAGCTATATCTGTGCCACCTCTCTGGACAGGACA 1860
Db 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
Qy 1861 TGC 1863
Db 621 Cys 621
RESULT 6
US-10-112-944-869
; Sequence 869, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Kui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 869
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(628)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set fort
; OTHER INFORMATION: in Example 2
US-10-112-944-869
Alignment Scores:
Pred. No.: 1,25e-249 Length: 628
Score: 3129.00 Matches: 616
Percent Similarity: 99.52% Conservative: 2
Best Local Similarity: 99.19% Mismatches: 3
Query Match: 91.41% Indels: 0
DB: 15 Gaps: 0
US-09-945-326-3 (1-1863) x US-10-112-944-869 (1-628)

```
QY 1 ATGAGCGGCTGCGGGCTCTTCTCGGCACCAACCGGCTCGGCTCGTCTGCGGGGTCG 60
Db MetSerGlyCysGlyLeuPheLeuArgThrThralaalaalargAlaCysArgGlyLeu 27
QY 61 GTGTCCTCTACCGGAAACCGCGGCTACTGCGCACCGCGGCTGTACAGCTTTGCGC 120
Db ValValSerThrAlaAsnArgArgLeuLeuArgThrSerProValArgAlaPheAla 47
QY 121 AAAGAGCTTTTCTAGCAAAATCAAGAAGAAAGTTCCTTCCATTTCAGAGTTAGC 180
Db LysGluLeuPheLeuGlyLysIleLysLysGluValPheProPheProGluValSer 67
QY 181 CAAGATGAATTAATGAATCAATCACTTCTTGGGACCCGTGGAAAATTTCTTCACTGA 240
Db GluAspGluLeuAsnGluIleAsnGlnPheLeuGlyProValGluLysPheThrGlu 87
QY 241 GAGGTGACTCCCGAAAATTTGACAGGAAGGAAATCCAGATGAATCTTTGGAGAA 300
Db GluValAspSerArgLysIleAspGlnGluLysIleProAspGluThrLeuGluLys 107
QY 301 TTGAAGAGCCTAGGGCTTTTGGCTGCAAGTCCAGAGAATATGTCGCTGGCTTC 360
Db LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluThrGlyGlyLeuGlyPhe 127
QY 361 TCCAACACCATGTACTCAAGACTAGGGAGATCATCAGCATGGATGGTCCATCACTGTG 420
Db SerAsnThrMetTyrSerArgLeuGlyGluThrIleSerMetAspGlySerIleThrVal 147
QY 421 ACCCTGGCAGCGCACCGGCTATTGGCTCAAGGGATCATCTTGGCTGGCATGAGGAG 480
Db ThrLeuAlaAlaHisGlnAlaIleGlyLeuLysGlyIleLeuAlaGlyThrGluGlu 167
QY 481 CAGAAAGCCAAATACTTGCCTAAACTGGCTCGGGGAGCACATTTCAGCCTTCTGCCTC 540
Db GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluAlaLeuAlaPheCysLeu 187
QY 541 ACGAGCCAGCCAGTGGGAGCATGTAGCTTCAATCCGGAGCAGAGCCACACTAAGTGAA 600
Db ThrGluProAlaAsnGlySerAspAlaAla**IleArgSerArgAlaThrLeuSerGlu 207
QY 601 GACAAGACGACTACATCTCTCAATGGCTCCAAGTCTGGATCTGAATCTAATGAGACTGGCC 660
Db AspLysHisTyrIleLeuAsnGlySerLysValTrrpIleThrAsnGlyGlyLeuAla 227
QY 661 AATATTTTACTGTGTTGCAAGACTGAGTCTGATTCTGATCGATCAGTGAAGAC 720
Db AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 247
QY 721 AATATCAGCATTCATAGTAGAAGAGACTTTGGTGGAGTCACCTAATCGGAACCCGAA 780
Db LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 267
QY 781 GATAAATTAGGCATTCGGGCTCCACACTGTGTAGTCCATTTTGAAACACCAAGATA 840
Db AspLysLeuGlyLysArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 287
QY 841 CCTGTGGAACCAATCTCTGGAGAGTGGGAGTGGGTTTAAAGTGGCCATGAACATCTCTC 900
Db ProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 307
QY 901 AACAGGCGCGTTCAGCATGGCAGCGCTGGTGGCTGCTCAAGAGCTCAGTGAATTGGA 960
Db AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 327
QY 961 ATGACTGCTGAGTACCGCTGCAAGAAACAGTTTAAACAGGCTCAGTGAATTGGA 1020
Db MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 347
QY 1021 TTGATTCAAGAGAAATTTGCATGTAGTGGCTCAGAAGCTTACCTCATGGAGATGACC 1080
Db LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 367
```

```
QY 1081 TACCTCACAGCAGGATGCTGGACCAACCTGGCTTTCCGACTGCTCCATCCTGAGGCGAC 1140
Db TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 387
QY 1141 ATGGTCAAGGTGTTACGCTCCGAGCGCGCTCGAGTGTGTGAGTGGCGCTGCAGATC 1200
Db MetValLysValPheSerSerGluAlaAlaIatrpGlnCysValSerGluAlaLeuGlnIle 407
QY 1201 CTCGGGGCTTGGCTACACAGGAGTACTCGTAGCAGCGCATACTGGTGTGACCCCGC 1260
Db LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 427
QY 1261 ATCCTCCTCATCTTCCAGGAAACCAATGAGATTCTCCGATGTACATCGCCCTGACGGGT 1320
Db IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 447
QY 1321 CTGACGATGCGCGCGCATCTGACTACAGGATCCATGAGCTTAAACAGGCCAAAGTG 1380
Db LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 467
QY 1381 AGCACAGTCATGATACCGTTGGCGGAGCTTCCGGACTCCCTGGCGCACTGGAC 1440
Db SerThrValMetAspThrValGlyArgArgLeuArgAspSerLeuGlyArgThrValAsp 487
QY 1441 CTGGGGCTGACAGCAACCATGAGTTGTGCACCCCGAGTCTTCCGACAGTGCACAAAG 1500
Db LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 507
QY 1501 TTTGAGGAGAACACCTACTGTCTTGGCGGAGACCGTGGAGACACTGCTGCTCCGCTTTGGC 1560
Db PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 527
QY 1561 AAGACCATCATGCGAGCAGCTGTACTGAAGCGGGTGGCCAAACATCTCATCAACCTG 1620
Db LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 547
QY 1621 TATGCATGACGCGCGTGTCTGTCGGCGGCGAGCCCTCCATCCGATTTGGGCTCCGCAAC 1680
Db TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 567
QY 1681 CAGACACGAGGTCTCTTGGCCAAACCTTCTCGGTGGAAAGCTTACTTGAGATCTC 1740
Db HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 587
QY 1741 TTCACCTCTCTCAGCTGACCAAGTATGCTCCAGAAAACCTAGATGAGCAGATTAAAGAA 1800
Db PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 607
QY 1801 GTGTCCCGCAGATCCTTGAAGCGAGCCCTATATCTGTGCCACCCTCTGGACAGGACA 1860
Db ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 627
QY 1861 TGC 1863
Db 628 Cys 628
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RESULT 7

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US-10-362-537-10
; Sequence 10, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 US0P
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 655
```

TYPE: PRT
ORGANISM: Mouse
US-10-362-537-10

Alignment Scores:

Pred. No.: 2,8e-103 Length: 655
Score: 1360.00 Matches: 287
Percent Similarity: 66.05% Conservative: 106
Best Local Similarity: 48.24% Mismatches: 184
Query Match: 39.73% Indels: 18
DB: 15 Gaps: 9

US-09-945-326-3 (1-1863) x US-10-362-537-10 (1-655)

QY 103 CTGTACGAGCT-----TTCCGCAAGAGAGCTTTTCTTCCAGCAAAATCAAGAAG 150
DB 66 ProAlaArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrIle 85
QY 151 AAGNAGTTTCCCATTTCCAGAGTT---AGCCAAGATGAATTAATGAATCAATCAG 207
DB 86 AspGlnValPheProtyrProSerValLeuSerGluGluGlnAlaGlnPheLeuLysGlu 105
QY 208 TTCTTGGGACCCGCGGAAATCTTCACTGAAGAGGTGGACTCCCGAAATTTGACCAG 267
DB 106 LeuValGlyProValAlaArgPhePheGluGluValAlaSerProAlaLysAsnAspAla 125
QY 268 GAAGGGAAATCCAGATGAATCTTTGGAGAAATTTGAAGAGCCCTAGGGCTTTTGGGCTG 327
DB 126 LeuGluLysValGluAspThrLeuGlnGlyLeuLysGluLeuGlyAlaPheGlyLeu 145
QY 328 CAAGTCCGAGAAATATGTGGCTTCTTCAACACCATGATGTAATCAAGACTAGGG 387
DB 146 GlnValProSerGluLeuGlyGlyLeuGlyLeuSerAsnThrGlnTyAlaArgLeuAla 165
QY 388 GAGATCATCAGCATG---GATGGTCCATCACTGTGACCTGGCAGCGCACCCAGGCTATT 444
DB 166 GluIleValGlyMetHisAspLeuGlyValSerValThrLeuGlyAlaHisGlnSerile 185
QY 445 GGCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCAATATCTTGCCTAAA 504
DB 186 GlyPheLysGlyIleLeuLeuTyThrLysAlaGlnArgGluLysTyThrLeuAsn 205
QY 505 CTGGCTCCGGGAGCATTGAGCCCTTCTGCTCAGGAGCCAGCCAGTGGGAGGAT 564
DB 206 ValAlaSerGlyGlnAlaLeuAlaPheCysLeuThrGluProSerSerGlySerAsp 225
QY 565 GCAGCTCAATCCGAGCAGACCCACACTAAGTGAAGACAGCAAGCACTACCTCAAT 624
DB 226 ValAlaSerIleArgSerAlaIleProSerProCysGlyLysTyThrLeuAsn 245
QY 625 GGCTCAAGGTCTCGATTACTAATGGAGGACTGGCCCAATATTTTACTGTGTGTTGCAAAG 684
DB 246 GlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLys 265
QY 685 ACTGAGTCTTGTAT---TCTGATGATCAGTGAAGACAAATCAACAGCATTCATAGTA 741
DB 266 ThrProIleLysAspAlaAlaThrGlyAlaValLysGluLysIleThrAlaPheValVal 285
QY 742 GAAGAGACTTTCGTGAGTCACTAATGGGAAACCCGCAAGATTAATTAGGCATTCGGGG 801
DB 286 GluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGlyIleLysAla 305
QY 802 TCCAACTTGTGAAGTCCATTTTGAACACCAAGATACCTGTGGAAACATCTTGGGA 861
DB 306 SerAsnThrSerGluValTyPheAspGlyValLysValProSerGluLysValLeuGly 325
QY 862 GAGGTCCGAGATGGTTTAAGTGGCCATGAACATCTCAACAGCCGCGGTTTCAGCATG 921
DB 326 GluValGlyAspGlyPheLysValAlaValAsnIleLeuAsnGlyArgPheGlyMet 345
QY 922 GCGAGCGTCTGGCTGGCTCCTCAAGAGATTGATGAATGATGCTGCTGAGTACGCTGC 981
DB 346 AlaAlaThrLeuAlaGlyThrMetLysSerLeuIleAlaLysAlaValAspHisAlaThr 365

QY 982 ACAAGGAAACAGTTTAAACAAGAGCGCTCAGTGAAATTTTGGATGTATTCAGGAGAAATTTGCA 1041
DB 366 AsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLysLeuAla 385
QY 1042 CTGATCGCTCAGAAGGCTTACGTTCATGGAGAGTATGACCTACCTCAGCAGAGGGATGCTG 1101
DB 386 ArgMetAlaIleLeuGlnTyValThrGluSerMetAlaTyMetLeuSerAlaAsnMet 405
QY 1102 GACCAACCTGGCTTCCCGACTCTCCATCGAGCAGCCATGTGTGAAGTGTTCAGCTCC 1161
DB 406 AspGln---GlyPheLysAspPheGlnIleGluAlaAlaIleSerLysIlePheCysSer 424
QY 1162 GAGCGCCCTGGCAGTGTGTGATGAGGCGCTCGAGATCTCTCGGGGCTTGGGCTACACA 1221
DB 425 GluAlaAlaTrpLysValAlaAspGluCysIleGlnIleMetGlyGlyMetGlyPheMet 444
QY 1222 AGGACTATCTCGTACGAGCGCATCTCGTGACACCCGATCTCTCTCTCATCTCTTCAGGGA 1281
DB 445 LysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePheGluGly 464
QY 1282 ACCAATGAGATCTCTCGGATGTATCATCGGCTGACGGGTCTGCAGCATGCGCGCCGATC 1341
DB 465 AlaAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysGlyLysGlu 484
QY 1342 CTGACTACCAAGATCCATGAGCTTAAACAG-----GCCAAGTGAAGCAGCAGTATGGAT 1395
DB 485 LeuThrGlyLeuGlyAsnAlaLeuLysAsnProPheGlyAsnValGlyLeuLeuMetGly 504
QY 1396 ACCTTGGCGGAGGCTTCGGGACTCCCTGGGCGGAACTGTGGACCTGGGGCTGACAGGC 1455
DB 505 GluAlaGlyLysGlnLeuArgArgThrGlyIleGlySerGlyLeuSerLeuSer--- 523
QY 1456 AACCATGGAGTGTGCAACCCAGCTTTCGGGACAGCTGCCAACAAAGTTTGAAGGAGAACACC 1515
DB 524 -----GlyIleValHisProGluLeuSerArgSerGlyGluLeuAlaValGlnAlaLeu 541
QY 1516 TACTGTCTCGCGCGGACCGTGGAGACACTGCTCTCGCTTTCGGCAAGACCATCATGGAG 1575
DB 542 AspGlnPheAlaThrValGluAlaLysLeuValLysHisLysLysGlyIleValAsn 561
QY 1576 GAGCAGCTGTACTGAAGCGGTGGCCAACTCTCATCAACCTGTATGATGATGATGATGATGATG 1635
DB 562 GluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyAlaMetValVal 581
QY 1636 GTCTGTGCGGGCGGACCGCTCCATCCGATTTGGGCTCCGCCAACCAACGACGAGGTT 1695
DB 582 ValLeuSerArgAlaSerArgSerLeuSerGluGlyTyProThrAlaGlnHisGluLys 601
QY 1696 CTCTTGGCCCAACCTTCTGCGTGAAGCT-----TACTTGCAGATCTCTTTCAGC 1746
DB 602 MetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMetAlaSer 621
QY 1747 CTCTCTCAGTGACAAAGTATGCTCCAGAAACCTAGATGACGAGCATTAAGAAGTCTCC 1806
DB 622 LeuGlnSerSerProGlnHis-----GlnGluLeuPheArgAsnPheArgSerIleSer 639
QY 1807 CACGAGATCTTCAGAAAGCGAGCGCTATATCTGTGCCACCCCTCTG 1851
DB 640 LysAlaMetValGluAsnGlyGlyLeuValThrGlyAsnProLeu 654

RESULT 8

US-10-362-537-9
; Sequence 9, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21

RESULT 9

US-10-362-537-11
; Sequence 11, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 11
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Bovine
US-10-362-537-11

Alignment Scores:
Pred. No.: 4,88e-102 Length: 655
Score: 1345.00 Matches: 285
Percent Similarity: 65.51% Conservative: 110
Best Local Similarity: 47.26% Mismatches: 194
Query Match: 39.29% Indels: 14
DB: 15 Gaps: 9

US-09-945-326-3 (1-1863) x US-10-362-537-11 (1-655)

QY	67	TCTACCGCGAAGCGCGCTACTGCGCAGCAGCGCGCTGTACGAGCTTTCGCCAAGAG	126
DB	57	SerGluAlaSerThrArgGluLysArgAlaAsnSerValSerLysSerPheAlaValGly	76
QY	127	CTTTTCCTAGCGAAATCAAGAGAAAGATTTTCCATTTCCAGAGTT---AGCCAA	183
DB	77	ThrPheLysGlyGlnLeuThrAspGlnValPheProTyrProSerValLeuAsnGlu	96
QY	184	GATGAATTAATGAATCAATCAGTTCTTGGGACCGTGGAAATTTCTTCACTGAAG	243
DB	97	AspGlnThrGlnPheLeuLysGluLeuValGlyProValThrArgPhePheGluGluVal	116
QY	244	GTGACTCCCGAAAAATTGACCGAGGAGGAAATCCAGATGAATCTTGGAGAAATTG	303
DB	117	AsnAspAlaAlaLysAsnAspMetLeuGluArgValGluGluThrMetGlnGlyLeu	136
QY	304	AAGAGCCTAGGCTTTTGGGCTTCAAGTCCCGAAGAAATATGGTGGCTTGGCTTCTCC	363
DB	137	LysGluLeuGlyAlaPheGlyLeuGlnValProAsnGluLeuGlyGlyValGlyLeuCys	156
QY	364	AACACATGACTCAAGACTAGGGAGATCATCAGCATG---GATGGTCCATCAGTGTG	420
DB	157	AsnThrGlnTyrAlaArgLeuValGluLeuValGlyMetTyrAspLeuGlyValGlyLeu	176
QY	421	ACCTTGGCAGCGACCAAGCTATTGGCTCAAGGGATCATCTTGGCTGGCAGTGGAG	480
DB	177	ValLeuGlyAlaHisGlnSerIleGlyPheLysGlyLeuLeuPheGlyThrLysAla	196
QY	481	CAGAAACCCAAATCTTGCCTAACTGGCTGCGGGAGCAGCATTTGAGCCTTCTGCTC	540
DB	197	GlnLysGluLysTyrLeuProLysLeuAlaSerGlyGluThrIleAlaPheCysLeu	216
QY	541	ACGGAGCCACCATGAGGAGATGAGCCTCAATCCGGAGCAGAGCCACACTAAGTGAA	600
DB	217	ThrGluProSerSerGlySerAspAlaAlaSerIleArgSerSerAlaValProSerPro	236
QY	601	GACAAGAGCACTACATCTCAATGGCTCCAGGTCTGGATTACTAATGAGGAGTGGCC	660
DB	237	CysGlyLysTyrTyrThrLeuAsnGlySerLysIleTyrIleSerAsnGlyGlyLeuAla	256
QY	661	AATATTTTACTGTGTTTGCAGAACTGAGTGTGAT---TCTGATGGATCAGTGAAA	717

Db	257	AspIlePheThrValPheAlaLysThrProValThrAspThrAlaThrGlyAlaValLys	276
QY	718	GACAAAATCACAGCATTCATAGTAGAAGAGACTTTTGGTGGAGTCACTAATGGGAAACCC	777
DB	277	GluLysIleThrAlaPheValValGluArgSerPheGlyGlyValThrHisGlyProPro	296
QY	778	GAGATATAATAGGCATTCCGGGCTCCAAACACTTGTGAAGTCCATTTTGAACACCAAG	837
DB	297	GluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheAspGlyValArg	316
QY	838	ATACCTGTGAAACATCCCTTGGAGAGTGGGCTTAAAGTGGCCATCAACATC	897
DB	317	ValProAlaGluAsnValLeuGlyGlyValGlyGlyPheLysValAlaMetHisIle	336
QY	898	CTCAACAGCGCGCTTTCAGCATGGGCGCTGTGGCTGGCTGTCTCAAGAGATGATT	957
DB	337	LeuAsnAsnGlyArgPheGlyMetAlaAlaAlaLeuAlaGlyThrMetLysGlyIle	356
QY	958	GAAATGACTCTGAGTACGCTGCACAAAGAAACAGTTTAAACAGAGCTCAGTGAATTT	1017
DB	357	AlaLysAlaValAspHisAlaAlaAsnArgThrGlnPheGlyGluLysIleHisAsnPhe	376
QY	1018	GGATTGATTCAGAGAAATTTGCACGTGCTCAGAGGCTTACGTCACTCAGAGATG	1077
DB	377	GlyLeuIleGlnGluLysLeuAlaArgMetAlaMetLeuGlnTyrValThrGluSerMet	396
QY	1078	ACCTACCTCACAGCAGGATCTGGACCAACCTTGGCTTCCCGAGCTGTCTCCATCAGGCA	1137
DB	397	AlaTyrMetValSerAlaAsnMetAspGln---GlySerThrAspPheGlnIleGluAla	415
QY	1138	GCCATGTGTAAGTGTTCAGCTCCGAGCGCGCTGCGCAGTGTGTGAGTGGAGCGCTGAC	1197
DB	416	AlaIleSerLysIlePheGlySerGluAlaAlaTyrLysValThrAspGluCysIleGln	435
QY	1198	ATCTCGGGGCTTGGCTACACAGGACTATCCGTACGAGCGCATCTCGCGTACAC	1257
DB	436	IleMetGlyGlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeu	455
QY	1258	CGCATCTCTCATCTTCGAGGGAACCAATGAGATCTCCGGATGTACATCGCCCTCAGC	1317
DB	456	ArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGln	475
QY	1318	GGTCTGCAGCATCCCGCCGCTCTGACTACCAAGGATCCATGAGTTAAACAG-----	1371
DB	476	GlyCysMetAspLysGlyLysGluLeuSerGlyLeuGlyAsnAlaLeuLysAsnProPhe	495
QY	1372	GCCAAAGTAGCACATCATGGATACCGTTGGCGGAGGCTTCGGGACTCCTCGGCGCA	1431
DB	496	GlyAsnAlaGlyLeuLeuGlyGluAlaGlyLysGlnLeuArgArgAlaGlyLeu	515
QY	1432	ACTGTGACCTGGGCTGACAGGCAACCATGGAGTTGTGCACCCAGCTTTCGCGACAGT	1491
DB	516	GlySerGlyLeuSerLeuSer-----GlyIleValHisGlnGluLeuSerArgSer	532
QY	1492	GCCAAAGTTTCAGGAGAAACACCTACTGCTTCGGCGGAGCCGCTGGAGACACTCTGCTC	1551
DB	533	GlyGluLeuAlaValGlnAlaLeuGluGlnPheAlaThrValValAlaLysLeuIle	552
QY	1552	CGCTTGGCAAGACCATCATGGAGGAGCAGCTGTGTACTGAAGCGGTGGCCAACTCCTC	1611
DB	553	LysHisLysLysAspIleIleAsnGluGlnPheLeuLeuGlnArgLeuAlaAspSerAla	572
QY	1612	ATCAACTGTATGGCAGCGGCTGTCTGCGGGCCAGCGCTCCATCCGATTTGGG	1671
DB	573	IleAspLeuTyrAlaMetValValLeuSerArgAlaSerArgSerLeuSerGluGly	592
QY	1672	CTCGCAACACACACGAGGTTTCTTGGCCAAACACCTTCTCGTGGAGCT-----	1725
DB	593	HisProThrAlaGlnHisGluLysMetLeuCysAspSerTyrCysIleGluAlaAla	612
QY	1726	---TACTTTCGAGAACTCTTTCAGCTCTCTCAGCTGGCAGAGTATGCTCCGAAAACCTA	1782

Db 613 ArgileArgGluAenMetThraLeu---GlnSerAspProGlnGlnGlu---Leu 630
QY 1783 GATGAGCAGATTAGAAGTGTCCACAGATCCTTTCAGAGCAGAGCCTATATCTGTGCC 1842
Db 631 PheArgAsnPhelysSerIleSerLysAlaLeuValGluAargGlyGlyValValThrSer 650
QY 1843 CACCCTCTG 1851
Db 651 AsnProLeu 653
RESULT 10
US-10-362-537-1
; Sequence 1, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 1
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Human
; US-10-362-537-1
Alignment Scores:
Pred. No.: 5,61e-99 Length: 655
Score: 1308.00 Matches: 276
Percent Similarity: 64.97% Conservative: 106
Best Local Similarity: 46.94% Mismatches: 194
Query Match: 38.21% Indels: 12
DB: 15 Gaps: 8
US-09-945-326-3 (1-1863) x US-10-362-537-1 (1-655)
QY 109 CGAGCTTTCGCCAAGAGCTTTCTTAGGCAAAATCAAGAAAGAAAGATTTTCCCATTTT 168
Db 71 LysSerPheAlaValAlGlyMetPheLysGlyGlnLeuThrThrAspGlnValPheProTyr 90
QY 169 CCAGAACTTAGCCAGATGACTTAATGAA--ATCAATCAGTCTTGGGACCGGTGAA 225
Db 91 ProSerValLeuAenGluGluGlnThrGlnPheLeuLysGluLeuValGluProValSer 110
QY 226 AAATTTCTTCACTGAAGAGGTGGACTCCCGAAAAAATTGACCAGGAAGGAAATCCAGAT 285
Db 111 ArgPhePheGluGluValAlaAsnAspProAlaLysAsnAspAlaLeuGluMetValGluGlu 130
QY 286 GAAACTTTGAGAAATTAAGAGCCTTAGGCTTTTGGCTGCAAGTCCAGAGCAAGATAT 345
Db 131 ThrTrpGlnGlyLeuLysGluLeuGlyAlaPheGlyLeuGlnValProSerGluLeu 150
QY 346 GGTGGCTGGCTTCTCCACACCATGTACTCAAGACTAGGGAGATCATCAGCATG--- 402
Db 151 GlyValValGlyLeuCysAsnThrGlnTyrAlaArgLeuValGluIleValGlyMetHis 170
QY 403 GATGGGTTCCTACTGTGACCCTGGCAGCGCACAGGCTATTGGCCCTCAAGGGGATCATC 462
Db 171 AspLeuGlyValGlyIleThrLeuGlyAlaHisGlnSerIleGlyPheLysGlyIleLeu 190
QY 463 TTGCTGGCACTGAGGAGCAGAAAGCCAAATACTTGCCTAAATCGGCGTCCGGGAGCAC 522
Db 191 LeuPheGlyThrLysAlaGlnLysGluLysGlyIleThrLeuProLysLeuAlaSerGlyGluThr 210
QY 523 ATTGCAGCTTCTGCCTCAGGAGCCAGCGAGTGGAGCCATCAGCCTCAATCCGGAGC 582
Db 211 ValAlaAlaPheCysLeuThrGluProSerSerGlySerAspAlaAlaSerIleArgThr 230

QY 583 AGAGCCACACTAAGTGAAGACAAAGACACTACATCCTCAATGGCTCCAAAGTCTGGATT 642
Db 231 SerAlaValProSerProCysGlyLysTyrThrLeuAsnGlySerLysLeuTriple 250
QY 643 ACTAATGGAGGACTGGCCAAATATTTTACTGTGTTTGCAAAAGACTGAGGTCTGTGAT--- 699
Db 251 SerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLysThrProValThrAspPro 270
QY 700 TCTGATGGATCAGTGAAGACAAATACAGCAGCATTCATAGTAGAAAGAGACTTTGGTGA 759
Db 271 AlaThrGlyAlaValLysGluLysIleThrAlaPheValValGluArgGlyPheGlyGly 290
QY 760 GTCACATAATGGGAAACCCGAAAGATAAATTAGGCATTTCGGGGCTCCAACTTGTGAAGTC 819
Db 291 IleThrHisGlyProProGluLysLysMetGlyIleLysAlaSerAsnThrAlaGluVal 310
QY 820 CATTTTGAAAACACCAAGATACCTGTGGAAAAACATCCTTGGAGAGGTGCGAGATGGTTT 879
Db 311 PhePheAspGlyValArgValProSerGluAsnValLeuGlyGluValGlySerGlyPhe 330
QY 880 AAGGTGGCCATGAACATCCTCAACAGCGCGCTTCAGCATGGCGAGCGTCTGGCTGGG 939
Db 331 LysValAlaMethHisIleLeuAsnGlyArgPheGlyMetAlaAlaLeuAlaGly 350
QY 940 CTGCTCAAGAGATTGATTGAAATGACTGTGACTACGCTGCAAGGAAACAGTTTAAAC 999
Db 351 ThrMetArgGlyIleIleAlaLysAlaValAspHisAlaThrAsnArgThrGlnPheGly 370
QY 1000 AAGAGCTCAGTGAATTTGGATTGATTTCAGGAGAAATTTCCACTGATGGCTCAGAAGCT 1059
Db 371 GluLysIleHisAsnPheGlyLeuIleGlnGlyLysLeuAlaArgMetValMetLeuGln 390
QY 1060 TAGCTCATGGAGAGTATGACCTACCTCACAGCAGGATGTGACCAACCTGGCTTTCCC 1119
Db 391 TyrValThrGlnSerMetAlaTyrMetValSerAlaAsnMetAspGln---GlyAlaThr 409
QY 1120 GACTGTCTCCATCAGGAGCAGCATGTGTAAGGTGTTTCAGTCTCCAGGCGCGCTGGCAGTGT 1179
Db 410 AspPheGlnIleGluAlaIleSerLysIlePheGlySerGluAlaIleTyrLysVal 429
QY 1180 GTGAGTGAGCGCTGAGATCCTCGGGGCTTGGCTACACAAGGAGACTATCGTAGCAG 1239
Db 430 ThrAspGluCysIleGlnIleMetGlyMetGlyPheMetLysGluProGlyValGlu 449
QY 1240 CGCATACTGGTCACACCCGATCCTCCTCATCTTCGAGGAAACCAATGAGATTCTCCGG 1299
Db 450 ArgValLeuArgAspLeuArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArg 469
QY 1300 ATGTACATCCCTGAGCGGTCTGACAGCATGCCGCGCGCATCCTGACTACAGGATCCAT 1359
Db 470 LeuPheValAlaLeuGlnGlyCysMetAspLysGlyLysGluLeuSerGlyLeuGlySer 489
QY 1360 GAGCTTAAACAG-----GCCAAAGTGAGCACAGTATGATACCGTTGGCCGGAGGCTT 1413
Db 490 AlaLeuLysAsnProPheGlyAsnAlaGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeu 509
QY 1414 CGGGACTCCCTGGCGCGAACTGTGGACCTGGGCTGCAGGCGCAACCATGAGTGTGTCCAC 1473
Db 510 ArgArgAlaGlyLeuGlySerGlyLeuSerLeuSer-----GlyLeuValHis 526
QY 1474 CCAGCTTTGCGGACAGTGCCAAAGATTTGAGGAGAAACCTACTGCTTTCGGCCGGAGCC 1533
Db 527 ProGluLeuSerArgSerGlyGluLeuAlaValArgAlaLeuGluGlnPheAlaThrVal 546
QY 1534 GTGAGACACTGCTGCTCGCTTGGCCAGACCATCATGGAGGAGGAGCTGTACTGAAG 1593
Db 547 ValGluAlaLysLeuIleLysHisLysGlyIleValAsnGluGlnPheLeuLeuGln 566
QY 1594 CGGGTGGCAACATCCTCATCAACCTGTATGGATGACCGCGCTGTGTCTCGCGGCGCAGC 1653
Db 567 ArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetValValLeuSerArgAlaSer 586
QY 1654 CGTCCATCCGCAATGGGCTTCGCAACACGACGACAGAGTTCTCTTGGCCCAACACCTTC 1713

```
Db 587 ArgSerLeuSerGluGlyHisProThrAlaGlnHisGluLysMetLeuCysAspThrTirp 606
Qy 1714 TGGGTGAA-----GCTTACTTGCAGAACTCTCTCAGCTCTCTCAGCTGGCAAGTAT 1767
Db 607 CysAlaGluAlaAlaAlaAlaArgGluGlyMetAlaAlaLeuGlnSerAspProTirp 626
Qy 1768 GCTCCAGAAACCTAGATGACGAGATTAGAAAGTGTCCGACGAGATCCTTTGAGAACCGA 1827
Db 627 GlnGlnGlu---LeuTyrArgAsnPheLysSerIleSerLysAlaLeuValGluArgGly 645
Qy 1828 GCCTATATCTGTGCCACCTCTG 1851
Db 646 GlyValValThrSerAsnProLeu 653

RESULT 11
US-10-408-765A-534
; Sequence 534, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Zhang, Bing
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 534
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-534

Alignment Scores:
Pred. No.: 5,61e-99 Length: 655
Score: 1308.00 Matches: 276
Percent Similarity: 64.97% Conservative: 106
Best Local Similarity: 46.94% Mismatches: 194
Query Match: 38.21% Indels: 12
DB: 16 Gaps: 8

US-09-945-326-3 (1-1863) x US-10-408-765A-534 (1-655)
Qy 109 CGAGCTTTCGCAAGAGCTTTTCTAGGCAAAATCAAGAAGAAAGTATTTCCCATTT 168
Db 71 LysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGlnValPheProTyr 90
Qy 169 CCAGAACTTAGCCAGATGAATTAATGAA---ATCAATCAGTCTTTGGGACCCGCGTAA 225
Db 91 ProSerValLeuAsnGluGlnThrGlnPheLeuLysGluLeuValGluProValSer 110
Qy 226 AATATCTTCTACTGAGAGTGGACTCCGAAATATGACCAAGGAGGAAATCCCATAT 285
Db 111 ArgPhePheGluGluValAsnAspProAlaLysAsnAlaLeuGluMetValGluGlu 130
Qy 286 GAAACTTTGAGAAATTAAGAGAGCTAGGGCTTTTGGCTGCAAGTCCCAAGAGATAT 345
Db 131 ThrThrTrpGlnGlyLeuLysGluLeuGlyAlaPheGlyLeuGlnValProSerGluLeu 150
Qy 346 GGTGGCTGGGCTTCTCCACACCATGATCTAAGACTAGGGAGATCATCAGCATG--- 402
Db 151 GlyGlyValGlyLeuCysAsnThrGlnTyrAlaArgLeuValGluIleValGlyMetHis 170
Qy 403 GATGGGTCCATCTACTGTGACCTGGGACGCGACCGACCATATTTGGCTCAAGGGATCATC 462
Db 171 AsnLeuGlyValGlyIleThrLeuGlyAlaHisGlnSerIleGlyPheLysGlyIleLeu 190
```

```
Qy 463 TTGGCTGGCACTGAGGAGCGAGAAAGCCAAATATCTTGCTTAAACTGGCGTCCGGGAGCAC 522
Db 191 LeuPheGlyThrLysAlaGlnLysGluLysTyrLeuProLysLeuAlaSerGlyGluThr 210
Qy 523 ATTGACAGCTTCTGCTCAGCGAGCCAGGAGCGATCGAGCTCAATCCGAGC 582
Db 211 ValAlaAlaPheCysLeuThrGluProSerGlySerAspAlaAlaSerIleArgThr 230
Qy 583 AGAGCCACACTAAGTGAAGACAAAGACACTACATCTCAATGGCTCCAAGTCTGGATT 642
Db 231 SerAlaValProSerProCysGlyLysTyrThrLeuAsnGlySerLysLeuTirpile 250
Qy 643 ACTAATGGAGGACTGCCCAATATTTTACTGTGTGTTTGCAGAGTGAAGTCTGTGAT--- 699
Db 251 SerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLysThrProValThrAspPro 270
Qy 700 TCTGATGATCAGTGAAGACAAATACACAGCATTTCATAGTAAAGAGACTTTGGTGA 759
Db 271 AlaThrGlyAlaValLysGluLysIleThrAlaPheValValGluArgGlyPheGlyGly 290
Qy 760 GTCACTAATGGGAAACCCGAAAGATAAATTAGGCATTGGGGCTCCAACTTGTGAATC 819
Db 291 IleThrHisGlyProGluLysLysMetGlyIleLysAlaSerAsnThrAlaGluVal 310
Qy 820 CATTTTGAACACCAAGATACCTGTGGAAACATCTCTGGAGAGTTCGGAGATGGTTT 879
Db 311 PhePheAspGlyValArgValProSerGluAsnValLeuGlyGluValGlySerGlyPhe 330
Qy 880 AGGTGGCCATGAACATCTCAACAGCGCGCTTCAGCATGGCAGCGCTGGCTGGG 939
Db 331 LysValAlaMethHisIleLeuAsnAsnGlyArgPheGlyMetAlaAlaLeuAlaGly 350
Qy 940 CTGCTCAAGAGATTGATGAATGACTGTGCTAGCTACGCTGCACAGGAACAGTTTAA 999
Db 351 ThrMetArgGlyIleIleAlaLysAlaValAspHisAlaThrAsnArgThrGlnPheGly 370
Qy 1000 AAGAGCTCAGTGAATTTGGATTGATTGAGGAAATTTTCACACTGATGGCTCAGAGCT 1059
Db 371 GluLysIleHisAsnPheGlyLeuIleGlnGluLysLeuAlaArgMetValMetLeuGln 390
Qy 1060 TAGCTCATGAGAGTATGACCTACCTCACAGAGGATGCTGGACCAACCTGGCTTCCC 1119
Db 391 TyrValThrGluSerMetAlaTyrMetValSerAlaAsnMetAspGln---GlyAlaThr 409
Qy 1120 GACTGTCTCCATCAGGCGAGCATGTTGAGGTGTTTCAGCTCCGAGGCGCTGCGACTGT 1179
Db 410 AspPheGlnIleGluAlaIleSerLysIlePheGlySerGluAlaAlaTirpLysVal 429
Qy 1180 GTGAGTGGAGCGCTGAGATCTCTCGGGGCTTGGGCTACAAAGGAGACTATCCGTACG 1239
Db 430 ThrAspGluCysIleGlnIleMetGlyGlyMetGlyPheMetLysGluProGlyValGlu 449
Qy 1240 CGCATACTGGTGACACCCGCTCTCTCTCATCTTCGAGGGAACCAATGAGATTCCTCGG 1299
Db 450 ArgValLeuArgAspLeuArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArg 469
Qy 1300 ATGTACATCCCTGAGCGGTCTGACGATCGCCGCGCATCTCTGACTACACGAGATCCAT 1359
Db 470 LeuPheValAlaLeuGlnGlyCysMetAspLysGlyIleGluLeuSerGlyLeuGlySer 489
Qy 1360 GAGCTTTAAACAG-----GCCAAAGTGAGCACATCATGTGATACCGTTGGCCGAGGCTT 1413
Db 490 AlaLeuLysAsnProPheGlyAsnAlaGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeu 509
Qy 1414 CGGAGCTCCCTGGCGCAACTGTGGACCTGGGCTGCACAGGCAACCATGAGTTGTGCAC 1473
Db 510 ArgArgAlaGlyLeuGlySerGlyLeuSerLeuSer-----GlyLeuValHis 526
Qy 1474 CCCAGTCTTGGGACAGTGCACAAAGTTTGAAGAGAACACCTACTGCTTCCGCGGAGC 1533
Db 527 ProGluLeuSerArgSerGlyGluLeuAlaValArgAlaLeuGluGlnPheAlaThrVal 546
```


Qy	1414	CGGAGCTCCCTGGGCGCAACCTGTGTGGACCTGGGGCTGTACAGAGCAACCAATGTGGAGTTGTGTGCAC	1473
Db	510	ArgArgArgAlaGluLeuGlySerGlyLeuSerLeuSer-----GlyLeuValHis	526
Qy	1474	CCCAGTCTTGGGAGAGTGCCCAACAAGTTTGGAGGAGAACCCTACTGCTTCGCGCGCGGACC	1533
Db	527	ProGluLeuSerArgSerGlyLeuLeuAlaValArgAlaLeuGluGlnPheAlaThrVal	546
Qy	1534	GTGGAGACACTGCTGCTCCGCTTTGGCAAGACCATCATGGAGGAGCAGCTGTGTTACTGAAG	1593
Db	547	ValGluAlaIysLeuIleLysHisLysIysGlyIleValAsnGluGlnPheLeuLeuGln	566
Qy	1594	CGGTGGCCCAACATCCTCATCAACCTGTATGGCATGACGGCCGCTGCTGCGCGGGCCGACG	1653
Db	567	ArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetValValValLeuSerArgAlaSer	586
Qy	1654	CGCTCCATCCGCAATGGGCTCCGCAACCAACACACGAGGTTCCTCTGGCCAAACACCTTC	1713
Db	587	ArgSerLeuSerGluGlyHisProThrAlaGlnHisGluLysMetLeuCysAspThrTrp	606
Qy	1714	TGCGTGGAA-----GCTTACTTCAGAACTCTTTCAGCCCTCTCTCAGCTGGGACAAGTAT	1767
Db	607	CysIleGluAlaAlaIleArgIleArgGluGlyMetAlaLaLeuGlnSerAspProTrp	626
Qy	1768	GCTCCAGAAAACCTTAGATGAGCAGATTAAAGAAAGTGTCACAGAGATCCTTTGAGAAGCGA	1827
Db	627	GlnGlnGlu---LeuTyrArgAsnPheLysSerIleSerLysAlaLeuValGluArgGly	645
Qy	1828	GCCTATATCTGTGCCCAACCTCTGT	1851
Db	646	GlyValValThrSerAsnProLeu	653

RESULT 13

```

US-10-369-493-5444
; Sequence 5444, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO. 5444
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5444

```

Alignment Scores:		
Pred. No.:	6,35e-91	Length:
Score:	1210.50	Matches:
Percent Similarity:	61.16%	Conservative:
Best Local Similarity:	43.66%	Mismatches:
Query Match:	35.36%	Indels:
DB:	15	Gaps:
		14
		613

US-09-945-326-3 (1-1863) X US-10-369-493-5444 (1-613)

[illegible]

```
QY 1213 GGCTACACAGGAGGATATCCGTACGAGCGCATACTGGTGACACCGGCATCTCTCTCATC 1272
Db 409 GlyPheMetArgGluThrGlyLeuGluArgValLeuArgAspLeuArgIlePheArgIle 428
QY 1273 TTCGAGGAAACCAATGAGATTCTCCGATGTATACCTGCGGCTGCGAGCATGCC 1332
Db 429 PheGluGlyAlaAsnAspValLeuArgLeuPheIleAlaLeuThrGlyAlaGlnHisAla 448
QY 1333 GGCCGCATCTGACTACAGGATCCATGACTTAACAGGCCAAAGTGAGCAGCATG 1392
Db 449 GlyLys-----HisLeuAlaGluGlnAla-----SerGlyValGly 460
QY 1393 GATACCGTTCGGCGGAGCTTCGGGACTCCTCGCGCGAACTGTGGACCTGGCGGTGACA 1452
Db 461 GlyLeuIleGlyLeuAlaValSerArgValThrGly-----GlyAsnThr 475
QY 1453 GGC---AACCATGGA---GTTGTGCACCCCGAGTCTTCGGGACAGTCCCAACAGTTTGAG 1506
Db 476 GlySerAsnPheGlyGlnValValAspAlaSerLeuGlnAspSerAlaLysValLeuAsp 495
QY 1507 GAGAACACCTACTGCTTCGGCGGACCGGTGGAGACACTGCTGCTCGCTTGGCAAGACC 1566
Db 496 GlnGlnIleAlaLeuPheGlyGlnThrValGlnGlyLeuLeuMetLysHisLysGly 515
QY 1567 ATCATGAGGAGGAGCTGGTACTGAAGCGGTGGCCCAACATCTCTCAACCTGTATGGC 1626
Db 516 IleIleAspArgGlnThrGluMetHisArgValAlaAspAlaIleAlaIleThrSer 535
QY 1627 ATGACGCGCTGCTGTCGCGGCGCAGCGCTCCATCGCATGCGCTTCCGCAACACGAC 1686
Db 536 SerAlaAlaValLeuSerArgAlaThrTyrAlaIleLysAsnLysSerSerAlaAsp 555
QY 1687 CAGAGTTCTCTGGCCACACCTCTGCTGCTGGAGCTTACTTGAGATCTCTTCAGC 1746
Db 556 PheGluArgLysValAla---ThrTyrTyrValAspLysAlaMetLys-----Ser 571
QY 1747 CTCTCTCAGCTGGCAGATGATGTCTCCAGAAAACCTAGATGAGCAGATTAAGAAAGTGTC 1806
Db 572 SerAsnArgPheLeuLysAspAlaGlySerGlyValGluAsnAlaSerLysValAlaThr 591
QY 1807 CAGCAGATCTTGAGAGCGAGCGCTATATCTGTGCC-----CAC 1845
Db 592 IleGluSerLeuAlaLysGlu-----ValCysGlyAsnGlyGlyLeuThrLeuGlnHis 609
QY 1846 CCTCTGGAC 1854
Db 610 ProValGlu 612
```

```
RESULT 14
US-10-408-765A-1442
; Sequence 1442, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1442
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1442
```

```
Alignment Scores:
Pred. No.: 6,38e-70 Length: 188
Score: 954.00 Matches: 188
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.87% Indels: 0
DB: 16 Gaps: 0

US-09-945-326-3 (1-1863) x US-10-408-765A-1442 (1-188)
QY 1300 ATGTACATCGCCTGACGGGTCTGAGCATGTCGGCGCATCTCTGACTACAGGATCCAT 1359
Db 1 MetTyrIleAlaLeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHis 20
QY 1360 GAGCTTAAACACGGCCAAAGTGAGCAGTCATGGATACCGTTGGCCGGAGGCTTCGGGAC 1419
Db 21 GluLeuLysGlnAlaLysValSerThrValMetAspThrValGlyArgArgLeuArgAsp 40
QY 1420 TCCTCGGCGCGAACTGTGGACCTGGGCGCTGACAGGCAACCATGGAGTTGTGCACCCAGT 1479
Db 41 SerLeuGlyArgThrValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSer 60
QY 1480 CTTCGGGACAGTCCCAACAAAGTTTGAGGAGAACACCTACTGCTTCGCGCGGACCGTGGAG 1539
Db 61 LeuAlaAspSerAlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGlu 80
QY 1540 ACACCTGCTCTCGCTTCGGCAAGCACCATCATGGAGGAGCAGCTGCTACTGAAGCGGGTG 1599
Db 81 ThrLeuLeuLeuArgPheGlyLysThrIleMetGluGluGlnLeuValLeuLysArgVal 100
QY 1600 GCCAACATCTCATCAACCTGTATGGCATGACGGCGCTGCTGTCGGCGGCGCAGCCCTCC 1659
Db 101 AlaAsnIleLeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSer 120
QY 1660 ATCCGATTTGGGCTCGGCAACACAGCACGAGGTTCTCTTGGCCCAACACCTTCTCGGTG 1719
Db 121 IleArgIleGlyLeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysVal 140
QY 1720 GAAGCTTACTTGAGAAATCTTTCAGCCCTCTCTCAGCTGGACAAGTATGCTCCAGAAAAC 1779
Db 141 GluAlaTyrLeuGlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsn 160
QY 1780 CTAGATGAGCAGATTAAAGAAAGTGTCCAGCAGATCTTTGAGAGGAGCCTATATCTGT 1839
Db 161 LeuAspGluGlnIleLysLysValSerGlnIleLeuGluLysArgAlaTyrIleCys 180
QY 1840 GCCCACCCTCTGGACAGGACATGC 1863
Db 181 AlaHisProLeuAspArgThrCys 188

RESULT 15
US-10-408-765A-2052
; Sequence 2052, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2052
; LENGTH: 188
; TYPE: PRT
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ORGANISM: Homo sapiens
US-10-408-765A-2052

Alignment Scores: 6.38e-70 Length: 188
Pred. No.: 954.00 Matches: 188
Score: 954.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.87% Indels: 0
DB: 16 Caps: 0

US-09-945-326-3 (1-1863) x US-10-408-765A-2052 (1-188)

QY	1300	ATGTACATCCCTGACGGTCTGCAGCATGCCGGCGCATCTCTGACTACAGATCCAT	1359
DB	1	MetTyrIleAlaLeuThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHis	20
QY	1360	GACCTTAACAGCCCAAGTGACACAGTCATCGATACCGTTGCCGGAGCTTCGGAC	1419
DB	21	GluLeuLysGlnAlaLysValSerThrValMetAspThrValGlyArgArgLeuArgasp	40
QY	1420	TCCTGGCGCGAACTGTGGACCTGGGGCTGACAGGCAACCATGGAGTTGTCAACCCAGT	1479
DB	41	SerLeuGlyArgThrValaspLeuGlyLeuThrGlyAsnHisGlyValValHisProSer	60
QY	1480	CTTGGCGACAGTCCCAACAAAGTTTGAGGAGAACACCTACTCTTCGGCCGGACCGTGGAG	1539
DB	61	LeuAlaAspSerAlaAsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGlu	80
QY	1540	ACACTGCTGCTCCGCTTTGGCAAGACCATCATGGAGGAGCAGCTGGTACTGAAGCGGGTG	1599
DB	81	ThrLeuLeuLeuArgPheGlyLysThrIleMetGluGlnLeuValLeuLysArgVal	100
QY	1600	GCCAACTCTCATCAACCTGTATGGCATGACGCGCTGTCTCGGGGCGACGCGCTCC	1659
DB	101	AlaAsnIleLeuIleAsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSer	120
QY	1660	ATCCGATTGGGCTCCGCAACCAACGACACAGAGTTCTCTTGGCCCAACACCTTCTGCGTG	1719
DB	121	IleArgIleGlyLeuArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysVal	140
QY	1720	GAAGCTTACTTGCAGAACTCTTTCAGGCTCTCTCAGCTGGACAAAGTATGCTCCAGAAAAC	1779
DB	141	GluAlaTyrLeuGlnAsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsn	160
QY	1780	CTAGATGAGCAGATTAAAGAAAGTGTCACGACATCCTTCAGAAAGCGAGCTATATCTGT	1839
DB	161	LeuAspGluGlnIleLysLysValSerGlnGlnIleLeuGlnLysArgAlaTyrIleCys	180
QY	1840	GCCCACCTCTGGACAGGACATGC	1863
DB	181	AlaHisProLeuAspArgThrCys	188

Search completed: May 2, 2005, 15:57:38
Job time : 256.808 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 2, 2005, 14:27:05 ; Search time 60.2291 Seconds
(without alignments)
5952.335 Million cell updates/sec

Title: US-09-945-326-3
Perfect score: 3423
Sequence: 1 atgagcggtcgcggtctt.....acctctggacaggacatgc 1863

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPto_spool_p/US09945326/runat_02052005_135411_22364/app_query.fasta_1.4686
-DB=PIR -QPMT=fastcan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCHI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09945326 @CGN 1.1 225 @runat_02052005_135411_22364 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3149	92.0	621	2 JC7892	acyl-CoA dehydroge
2	1356.5	39.6	655	2 A54872	acyl-CoA dehydroge
3	1308	38.2	655	2 S54183	acyl-CoA dehydroge
4	1210.5	35.4	613	2 T15905	hypothetical prote
5	821	24.0	594	2 F84085	butyryl-CoA dehydr
6	815.5	23.8	594	2 C70021	butyryl-CoA dehydr
7	711	20.8	650	2 A70817	probable fadE10 pr
8	699	20.4	382	2 B87302	acyl-CoA dehydroge
9	691.5	20.2	384	2 B83443	probable acyl-CoA
10	690	20.2	379	2 G84124	acyl-CoA dehydroge
11	682	19.9	378	2 D69658	acyl-CoA dehydroge
12	682	19.9	381	2 AC3536	butyryl-CoA dehydr
13	678	19.8	381	2 B87472	acyl-CoA dehydroge
14	658	19.2	380	2 F84124	acyl-CoA dehydroge

15	652.5	19.1	379	1 S55421	acyl-CoA dehydroge
16	652	19.0	387	2 D75417	acyl-CoA dehydroge
17	648	18.9	379	2 T45286	butyryl-CoA dehydr
18	644	18.8	456	2 AF3637	butyryl-CoA dehydr
19	630	18.4	389	2 C70979	probable fadE25 pr
20	629.5	18.4	381	2 E75458	acyl-CoA dehydroge
21	626	18.3	380	2 F98299	probable acyl-CoA
22	626	18.3	380	2 A12983	acyl-CoA dehydroge
23	625.5	18.3	379	2 T47262	butyryl-CoA dehydr
24	625.5	18.3	379	2 F97233	butyryl-CoA dehydr
25	617.5	18.0	387	2 A83393	probable acyl-CoA
26	615	18.0	419	2 T15088	hypothetical prote
27	613	17.9	380	2 T44811	acyl-CoA dehydroge
28	611.5	17.9	402	2 D69530	probable acyl-CoA
29	610.5	17.8	381	2 B83791	butyryl-CoA dehydr
30	609	17.8	389	2 B87001	probable acyl-CoA
31	606	17.7	380	2 G69893	butyryl-CoA dehydr
32	604	17.6	432	1 A55680	acyl-CoA dehydroge
33	603.5	17.6	375	2 F83326	probable acyl-CoA
34	594.5	17.4	422	2 H75382	acyl-CoA dehydroge
35	593	17.3	397	2 B69378	probable acyl-CoA
36	588.5	17.2	398	2 B75411	acyl-CoA dehydroge
37	587.5	17.2	423	2 A37033	isovaleryl-CoA deh
38	586	17.1	397	2 H84225	acyl-CoA dehydroge
39	585.5	17.1	382	2 AE3492	isovaleryl-CoA deh
40	585.5	17.1	424	1 C34252	isovaleryl-CoA deh
41	583	17.0	412	2 A30605	acyl-CoA dehydroge
42	579	16.9	412	2 B30605	acyl-CoA dehydroge
43	579	16.9	412	2 T16568	hypothetical prote
44	576.5	16.8	421	2 AD2384	acyl-CoA dehydroge
45	576.5	16.8	421	2 C98299	probable acyl-CoA

ALIGNMENTS

RESULT 1

JC7892
acyl-CoA dehydrogenase (EC 1.3.99.3) - 9 - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 09-Jul-2004
C;Accession: JC7892
R;Zhang, J.; Zhang, W.; Zou, D.; Chen, G.; Wan, T.; Zhang, M.; Cao, X.
Biochem. Biophys. Res. Commun. 297, 1033-1042, 2002
A;Title: Cloning and functional characterization of ACAD-9, a novel member of human acyl-
A;Reference number: JC7892; MUID:22246103; PMID:12359260
A;Accession: JC7892
A;Molecule type: mRNA
A;Residues: 1-621 <ZHA>
A;Cross-references: UNIPROT:Q9H845; GB:AF327351
A;Experimental source: Dendritic cells
C;Comment: This enzyme, which belongs to a family of mitochondrial enzymes that catalyze
-long-chain acyl-CoA and has specific activity toward palmitoyl-CoA (C16:0).
C;Genetics:
A;Gene: acad-9
A;Map position: 3q26
C;Keywords: oxidoreductase

Alignment Scores:	5e-200	Length:	621
Pred. No.:	3149.00	Matches:	620
Score:	99.84%	Conservative:	0
Percent Similarity:	99.84%	Mismatches:	1
Best Local Similarity:	92.00%	Indels:	0
Query Match:	92.00%	Gaps:	0
DB:	2		

US-09-945-326-3 (1-1863) x JC7892 (1-621)

Qy	1	ATGAGCGGCTGCGGCTCTTCCTCGCACACGCGCTGCGCTGCTGCTCCCGGGCTG 60
Db	1	MetSerGlyCysGlyLeuPheLeuArgThrAlaAlaAlaArgGlyLeu 20
Qy	61	GTGGTCTTACCGGCAACCGCGGCTACTCGGCACACGCGGCTGTACAGCTTCGCC 120

Db 21 ValValSerThrAlaAanArgArgLeuLeuArgThrSerProValArgAlaPheAla 40
QY 121 AAGAGCTTTTCTAGGCAAAATCAAGAAAGAGTTTCCCATTTCCAGAGTTAGC 180
Db 41 LysGluLeuPheLeuGlyLysIleLysLysLysGluValPheProGluValSer 60
QY 181 CAAGATCAACTTAATGAAATCAATCAGTCTCTGGGACCCGTGGAAAATTTCTTCACTGAA 240
Db 61 GlnAspGluLeuAanGluIleAanGlnPheLeuGlyProValGluLysPhePheThrGlu 80
QY 241 GAGGTGACCTCCGAAAATTTGACAGAGAGGAAAATCCAGATGAAATCTTTGGAGAAA 300
Db 81 GluValAspSerArgLysIleAspGlnGluLysIleProAspGluThrLeuGluLys 100
QY 301 TTGAGAGCTAGGGCTTTTGGCTTCAAGTCCAGAGAAATATGGTGGCTTGGCTTC 360
Db 101 LeuLysSerLeuGlyLeuPheGlyLeuGlnValProGluGluThrGlyGlyLeuGlyPhe 120
QY 361 TCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATGGATGGTCCATCACTGTG 420
Db 121 SerAsnThrMetTyrSerArgLeuGlyGluIleIleSerMetAspGlySerIleThrVal 140
QY 421 ACCTGCAGCGCACCGAGCTATTGGCTCAAGGGATCATCTTGGCTGCACTGAGGAG 480
Db 141 ThrLeuAlaIleHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGlu 160
QY 481 CAGAAAGCCAAATCTTGCCTTAACCTGGCTCCGGGAGCACATTCAGGCTTCTGCCTC 540
Db 161 GlnLysAlaLysTyrLeuProLysLeuAlaSerGlyGluHisIleAlaPheCysLeu 180
QY 541 ACGGAGCCAGCTAGTGGGAGCGATGACGCTCAATCCGGAGCAGAGCCACATAAGTGAA 600
Db 181 ThrGluProAlaSerGlySerAspAlaIleSerIleArgSerArgAlaThrLeuSerGlu 200
QY 601 GACAAGAGCACTACATCTCAATGGCTCCAGGTCTGGATTACTAATGAGGAGCTGGCC 660
Db 201 AsplysLysHisTyrIleLeuAanGlySerLysValTrpIleThrAsnGlyGlyLeuAla 220
QY 661 AATATTTTACTGTGTGCAAGACTGAGTGGTTCGATCTGATGATCAGTGAAGAGAC 720
Db 221 AsnIlePheThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAsp 240
QY 721 AAAATCACAGCATTCATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGGAACCCGAA 780
Db 241 LysIleThrAlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGlu 260
QY 781 GATAAATTAGGCATTCGGGGCTCAACACTGTGTGAAGTCCATTTGAAAACACCAAGATA 840
Db 261 AsplysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAanThrLysIle 280
QY 841 CCTGTGAAAACATCTTTGGAGAGGTCGAGATGGGTAAAGTGGCCATGAACATCCTC 900
Db 281 ProValGluAanIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
QY 901 AACAGCGCGGGTTTACGATGGGCGAGCGTCTGGCTGGCTGCTCAAGAGATGATGAA 960
Db 301 AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
QY 961 ATGACTGCTGATGAGCTGCAAGAGAAACAGTTTAAACAGAGGCTCAGTGAATTTGGA 1020
Db 321 MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
QY 1021 TTGATTTCAGGAGAAATTTGGCACTCATGGCTCAGAGGCTTACGTCATGGAGAGTATGACC 1080
Db 341 LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
QY 1081 TACCTTCAGCAGGAGTCTGGACCAACCTGGCTTTCCCGACTGCTCCATCGAGGCGACC 1140
Db 361 TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
QY 1141 ATGTTGAAGGTTCAGCTCCGAGCGCCCTGGCAGTGTGTGAGTGGCGCTCGACATC 1200
Db 381 MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluValLeuGlnIle 400
pb

QY 1201 CTCGGGGCTTGGCTACACAAGGGACTATCCGTACGAGCGCATACTGCTGTGACCCCGC 1260
Db 401 LeuGlyLysLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
QY 1261 ATCTCTCTCATCTTCGAGGGAACCAATAGATTCTCCGATGTACATCGCCCTGACGGGT 1320
Db 421 IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
QY 1321 CTGCAGCATGCCGCGCGCATCTGACTACAGAGTCCATGAGCTTAAACAGGCGCAAGTG 1380
Db 441 LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
QY 1381 AGCACAGTTCATGATACCTTGGCCGAGGCTTCCGGACTCCCTGGCGCGAACTGTGGAC 1440
Db 461 SerThrValMetAspThrValGlyArgGluArgAspSerLeuGlyArgThrValAsp 480
QY 1441 CTGGGGCTCAGAGGCAACCATGGAGTTGTGCACCCAGTCTTTGCGGACAGTGCCACAAG 1500
Db 481 LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
QY 1501 TTTGAGGAGAACACCTACTGCTTCGCGCGAGCGTGGAGACACTGCTGCTCGCTTTGGC 1560
Db 501 PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
QY 1561 AAGACCATCATGGAGGAGCAGCTGTGTAAGAGCGGGTGGCCAAACATCTCTCAATCAACCTG 1620
Db 521 LysThrIleMetGluGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
QY 1621 TATGGCATCAGCGCCCTGTGTGCGGGCAGCGCTCCATCCGCATTTGGCTCCCGAAC 1680
Db 541 TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
QY 1681 CAGGACCAAGGTTCTCTTGGCCACACCTTCTGCTGGAGCTTACTTGCAGATCTC 1740
Db 561 HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
QY 1741 TTCAGCTCTCTCAGCTGGACAGTATGTCTCAGAAAAACCTAGATGACGACAGATTAAGAAA 1800
Db 581 PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
QY 1801 GTGTCCAGCAGATCTCTTGAAGCGAGGCTATATCTGTGCCACCTCTTGGACAGGACA 1860
Db 601 ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
QY 1861 TGC 1863
Db 621 Cys 621

RESULT 2

A54872

acyl-CoA dehydrogenase (EC 1.3.99.-) very-long-chain-specific precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004

C;Accession: A54872

R;Aoyama, T.; Ueno, I.; Kamiyo, T.; Hashimoto, T.

J. Biol. Chem. 269, 19088-19094, 1994

A;Title: Rat very-long-chain acyl-CoA dehydrogenase, a novel mitochondrial acyl-CoA dehy-

ced amino acid sequence and distinct specificities of the cDNA-expressed protein.

A;Reference number: A54872; MUID:94308174; PMID:8034667

A;Accession: A54872

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-655 <AOY>

A;Cross-references: UNIPROT:P45953; GB:D30647; NID:95333356; PIDN:BAA06331.1; PID:d1006895

C;Keywords: oxidoreductase

F;1-40/Domain: signal sequence #status predicted <SIG>

Alignment Scores:			
Pred. No.:	1,18e-81	Length:	655
Score:	1356.50	Matches:	295
Percent Similarity:	63.36%	Conservative:	108
Best Local Similarity:	46.38%	Mismatches:	192

QY 979 TGCACAAGAAAAGTTTAACAAGAGCGCTCAGTGAATTTGGATTGATTACAGGAGAAATTT 1038

Db 364 ThrAsnArgThrGlnPheGlyAspLeuIleHisAsnPheGlyValIleGlnGluLeu 383

QY 1039 GCACCTGATGCTCAGAAAGGCTTAGCTCATCGAGAGTAGTACCTACCTCAGACAGGAGGATG 1098

Db 384 AlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAlaAsn 403

QY 1099 CTGGACCAACTGGCTTTTCCCGACTGCTCCATCGAGCAGCCCATGGTGAAGGTGTTTCAGC 1158

Db 404 MetAspGln--GlyPheLysAspPheGlnIleGluAlaIleSerLysAlaPheGly 422

QY 1159 TCCAGAGCCGCTGGCGAGTGTGTGAGTAGGCGCTGCAGATCCTCGGGGGCTTGGGGTAC 1218

Db 423 SerGluAlaAlaTrpLysValThrAspGluCysIleGlnIleMetGlyGlyMetGlyPhe 442

QY 1219 ACAAGGACTATCCGTACGAGCGCATACTCGGTGACACCCGCACTCCTCCTCATCTTCGAG 1278

Db 443 MetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePheGlu 462

QY 1279 GGAACCAATCAGATTTCCCGGATGTACATCGCCCTCAGCGGCTTCGACGATCGCGGCCG 1338

Db 463 GlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysGlyLys 482

QY 1339 ATCCTGACTACCAAGATCCATGAGCTTAAACAG-----GCCAAAGTGCACAGCATCATG 1392

Db 483 GluLeuThrGlyLeuGlyAsnAlaLeuLysAsnProLeuGlyAsnValGlyLeuLeuIle 502

QY 1393 GATACCGTTGGCGGAGGCTTCGGGACTCCTCGGCGCACTGTGGACCTGGGGCTGACACA 1452

Db 503 GlyGluAlaSerLysGlnLeuArgArgThrGlyIleGlySerGlyLeuSerLeuSer 522

QY 1453 GGCAACCATCGAGTTGTGCACCCAGCTTTCGGCACAGTCCCAACAAGTTTGAGGAGAAC 1512

Db 523 -----GlyIleValHisProGluLeuSerArgSerGlyGluLeuAlaValGlnAla 539

QY 1513 ACCTACTGCTTCGGCGGACCGTGGAGACACTGCTGCTCGCTTTGGCAAGACCATCATG 1572

Db 540 LeuGluGlnPheAlaThrValValGluAlaLysLeuMetLysHisLysGlyIleVal 559

QY 1573 GAGGAGCAGCTGGTACTGAAGCGGTGGCCAAATCTCTCATCACTGTATGCATGACG 1632

Db 560 AsnGluGlnPheLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetVal 579

QY 1633 GCGTGTCTGTCGGCGCACCGCTCCATCCGCTATGGGCTCCGCCAACACGACCCACGAG 1692

Db 580 ValValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHisGlu 599

QY 1693 GTTCTCTGCCAACACCTTCTCGCTGGAGCT-----TACTTGCAGATCTCTTC 1743

Db 600 LysMetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGlnAsnMetAla 619

QY 1744 AGCTCTCTCAGCTGACAGATGTATGCTCCGAAACCTAGATGACGAGATTAGAAGTG 1803

Db 620 SerLeuGlnSerAsnProGln-----GlnGlnGluLeuPheArgAsnPheArgSerIle 637

QY 1804 TCCAGCAGATCCTTCAGAGCGAGCGCTATATCTGTGCCACCCCTCTG 1851

Db 638 SerLysAlaMetValGluAsnGlyLeuValThrSerAsnProLeu 653

RESULT 3

S54183

acyl-CoA dehydrogenase (EC 1.3.99.-) very-long-chain specific - human

C/Species: Homo sapiens (man)

C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C/Accession: S54183

R/Andresen, B.S.

submitted to the EMBL Data Library, April 1995

A/Reference number: S54183

A/Accession: S54183

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-655 <AND>

REDDI
S54183

acyl-CoA

C;Specie

C; Date:

C; Access

·R;Andres

A. Raftery

A;Release
A:Access

A: Status

A; Molecu

A;Cross-references: UNIPROT:P49748; EMBL:X86556; NID:g790446; PID:g790447
C;Genetics:
A;Gene: GDB:ACADVL; VLCAD
A;Cross-references: GDB:I248185; OMIM:201475
A;Map position: 17p11.2-17p11.1
C;Keywords: oxidoreductase

Alignment Scores:
Pred. No.: 1.89e-78 Length: 655
Score: 1308.00 Matches: 276
Percent Similarity: 64.97% Conservative: 106
Best Local Similarity: 46.94% Mismatches: 194
Query Match: 38.21% Indels: 12
DB: 2 Gaps: 8

US-09-945-326-3 (1-1863) x S54183 (1-655)

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QY 109 CGAGCTTTGCCAAAGAGCTTTCTAGGCAAAATCAAGAAAGAAAGATTTTCCCATTT 168
DB 71 LysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGlnValPheProTyr 90
QY 169 CGAAGTTAGCCAGATGAATTAATGAA---ATCAATCAGTTCTTGGGACCCGCTGGA 225
DB 91 ProSerValLeuAsnGluGlnThrGlnPheLeuLysGluLeuValGluProValSer 110
QY 226 AATTTCTTCACTGAAGAGTGGACTCCCGAAATAATGACCAGGAAGGAAATCCCCAGAT 285
DB 111 ArgPheGluGluValAsnAspProAlaLysAsnAspAlaLeuGluMetValGluGlu 130
QY 286 GAAACTTTGGAGAAATTAAGAGCCTAGGCTTTTGGGCTGCAAGTCCAGAGAAATAT 345
DB 131 ThrTrpGlnGlyLeuLysGluLeuGlyAlaPheGlyLeuGlnValProSerGluLeu 150
QY 346 GTGGCTGGGCTTCTCAACACCATGACTCAAGACTAGGGGAGATCATCAGCATG--- 402
DB 151 GlyGlyValGlyLeuCysAsnThrGlnTyrAlaArgLeuValGluIleValGlyMethis 170
QY 403 GATGGTCCACTGACCTGGACCTGGCAGCGCAGCAGGCTATTGGCTTCAAGGGGATCATC 462
DB 171 AspLeuGlyValGlyIleThrLeuGlyAlaHisGlnSerIleGlyPheLysGlyIleLeu 190
QY 463 TTGGCTGGCTAGGAGCAGAAAGCCAAATACCTTGGCTTAACTGGCGTCCGGGAGCAC 522
DB 191 LeuPheGlyThrLysAlaGlnLysGluLysTyrLeuProLysLeuAlaSerGlyGluThr 210
QY 523 ATTCCAGCTTCTCCTCAGCGACCCAGCCAGTGGGAGCGATCAGCCTCAATCCGAGC 582
DB 211 ValAlaAlaPheCysLeuThrGluProSerSerGlySerAspAlaAlaSerIleArgThr 230
QY 583 AGGCCACACTAAGTGAAGACAAAGCACTACATCTCAATGGCTCCAAGGCTCGGATT 642
DB 231 SerAlaValProSerProCysGlyLysTyrTyrThrLeuAsnGlySerLysLeuTrpIle 250
QY 643 ACTAATCGAGACTGGCCAAATATTTTACGTGTGTTTCAAGACTGAGGTCTGTGAT--- 699
DB 251 SerAsnGlyGlyLeuAlaAspIlePheThrValPheAlaLysThrProValThrAspPro 270
QY 700 TCTGATGATCAGTGAAGCAAAATCAGCATTACTAGTAGAAGAGACTTTGGTGA 759
DB 271 AlaThrGlyAlaValLysGluLysIleThrAlaPheValGluAlaArgGlyPheGlyGly 290
QY 760 GTCACTAATGGGAAACCGGAGATAATTAGGCATTCGGGCTCCAACTTGTGAAGTC 819
DB 291 IleThrHisGlyProProGluLysLysMetGlyIleLysAlaSerAsnThrAlaGluVal 310
QY 820 CATTTTGAACACCAAGATACCTGTGGAAACATCTTGGAGAGTCCGAGATGGGTTT 879
DB 311 PhePheAspGlyValAsgValProSerGluAsnValLeuGlyGluValGlySerGlyPhe 330
QY 880 AAGTGGCCATGACATCTTCAACAGCGCGGTTCAGCATGGGCAGCGCTGTGGCTGGG 939
DB 331 LysValAlaMetHisIleLeuAsnAsnGlyArgPheGlyMetAlaAlaLeuAlaGly 350
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QY 940 CTGCTCAAGAGATTGATTGAAATGACTGCTGAGTAGCGCTGCACAAAGAAACAGTTTAAAC 999
DB 351 ThrMetArgGlyIleIleAlaLysAlaValAspHisAlaThrAsnArgThrGlnPheGly 370
QY 1000 AAGAGCTCAGTGAATTTGGATTGATTGAGGAAATTTGCACTGATGCTCAGAAGGCT 1059
DB 371 GluLysIleHisAsnPheGlyLeuIleGlnGluLysLeuAlaArgMetValMetLeuGln 390
QY 1060 TAGCTCATGGAGATGATGACCTACCTACAGCAGGATGCTGCACCAACCTGCTTCC 1119
DB 391 TyrValThrGluSerMetAlaTyrMetValSerAlaAsnMetAspGln---GlyAlaThr 409
QY 1120 GACTGCTCCATCAGAGCAGCCATGTGAAGTGTTCAGCTCCGAGGCCCTGGCAGTGT 1179
DB 410 AspPheGlnIleGluAlaIleSerLysIlePheGlySerGluAlaAlaTrpLysVal 429
QY 1180 GTGAGTGAGCGCTGCAGATCTCCGGGGCTTGGGCTACACAAGGACTATCCGTACGAG 1239
DB 430 ThrAspGluCysIleGlnIleMetGlyGlyMetGlyPheMethLysGluProGlyValGlu 449
QY 1240 CGCATACTCGCTGACACCCCGCATCTCTCTCATCTTCGAGGGAACCAATGAGATTCTCCGG 1299
DB 450 ArgValLeuArgAspLeuArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArg 469
QY 1300 ATGTACATCCCTGACGGTCTGACGATGCGCGCCGATCTCTGACTACCAAGATCCAT 1359
DB 470 LeuPheValAlaLeuGlnGlyCysMetAspLysGlyLysGluLeuSerGlyLeuGlySer 489
QY 1360 GAGCTTAAACAG-----GCCAAAGTGACACAGTATCATGATACCTTGGCCGAGGCTT 1413
DB 490 AlaLeuLysAsnProPheGlyAsnAlaGlyLeuLeuLeuGlyGluAlaGlyLysGlnLeu 509
QY 1414 CGGAGCTCTCCGGCCGAACTGTGGACCTGGGGCTGCACAGGCAACCATCTGAGTTGTCAC 1473
DB 510 ArgArgAlaGlyLeuGlySerGlyLeuSerLeuSer-----GlyLeuValHis 526
QY 1474 CCAGTCTTGGCAGCAGTGCACCAAGATTTGAGGAGAAACACTTACTGCTTGGCCCGGACC 1533
DB 527 ProGluLeuSerArgSerGlyGluLeuAlaValArgAlaLeuGluGlnPheAlaThrVal 546
QY 1534 GTGGACACACTGCTGCTCGCTTGGCAAGACCATCATCGAGGAGCAGCTGGTACTGAAG 1593
DB 547 ValGluAlaLysLeuIleLysHisLysLysGlyIleValAsnGluGlnPheLeuGln 566
QY 1594 CGGCTGCCCAACATCTCATCAACCTGTATGGCATGACGCGCTGTGCTCGCGGGCAGC 1653
DB 567 ArgLeuAlaAspGlyAlaIleAspLeuTyrAlaMetValValLeuSerArgAlaSer 586
QY 1654 CGTCCATCCGCAATTTGGCTCCGCAACCCAGCAGCAGGATCTCTTGGCCACACCTTC 1713
DB 587 ArgSerLeuSerGlyGlyHisProThrAlaGlnHisGluLysMetLeuCysAspThrTrp 606
QY 1714 TGCGTGGAA-----CCTTACTTGCAGAAATCTCTTCAGCTCTCTCAGCTGGCAAGTAT 1767
DB 607 CysIleGluAlaAlaAlaArgIleArgGluGlyMetAlaLeuGlnSerAspProTrp 626
QY 1768 GCTCCAGAAACCTAGATGACGAGATTAAAGAAAGTGTCCGAGCAGATCTCTTGAAGACGA 1827
DB 627 GlnGlnGlu---LeuTyrArgAsnPheLysSerIleSerLysAlaLeuValGluArgGly 645
QY 1828 GCCTATATCTGTGCCACCTCTG 1851
DB 646 GlyValValThrSerAsnProLeu 653
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RESULT 4

T15905
hypothetical protein E04F6.5 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15905
R;Pauley, A.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of *C. elegans* cosmid E04F6.

Qy	793	ATTCGGGGCTCCACACCTTGTTGAGTGCATTTTGAARAACACCAAGATACCTCTGGAAAC	85
Db	270	IleYsGlySerAsnThrThrGluValHisPheAsnLeuLysIleProValGluAsn	289
Qy	853	ATCCTCGAGAGAGTTCGGAGATGGGTTTAAAGTGGCCATGAACATCCTCAACAGCGCCGG	912
Db	290	LeuLeuGlyLysGluGlyGluGlyPheLysValAlaMetAsnIleLeuAsnAenGlyAArg	309
Qy	913	TTACAGCATGGCAGCGTCTGGTGGCTGCTCCTCAAGAGATTGATTGAATAGTCTGCTGAG	972
Db	310	PheGlyIleProAlaAlaCysThrGlyAlaMetLysHisCysIleGlnLysThrValAsp	329
Qy	973	TACGCTTCGCAACGAAGAAGCTTTAAACAGAGGCTCAGTGAATTTGGATTGATTCAGGAG	103
Db	330	HisIleThrThrArgValGlnPheGlyLysLysLeuGlnGluPheGlyAsnIleGlnGlu	349
Qy	1033	AAATTTGCACCTGATGGCTCAGAAGCTTACCTCATGGAGAGTATGACCTTACCTCACAGCA	109
Db	350	LysLeuValGluMetIleSerLysLeuTyrAlaThrGluSerIleValTyrMetLeuSer	369
Qy	1093	GGGATCTGGACCAACCTGGCTTTCCGAGCTCTCCATCGAGCGACCCATGTGTAAGGTG	115
Db	370	SerAsnMetAspAArg--GlyIleLysGluTyrGlnLeuGluAlaAlaIleGlyLysVal	388
Qy	1153	TTACGCTCCGAGGGCGCTGCGCAGTGTGTAGTAGGCGCTGCACATCTCTCGGGGCTTG	121
Db	389	LeuAlaSerGluAenAlaTrpLeuValCysAspAlaIleGlnValHisGlyGlyMet	408
Qy	1213	GGCTACACAGGGACTATCCGTACGAGCGCATCTGCGTGACACCCGCATCTCCTCATC	127
Db	409	GlyPheMetArgGluThrGlyLeuGluArgValLeuArgAspLeuArgIlePheArgIle	428
Qy	1273	TTCCAGGGAAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTGCAGCATGCC	133
Db	429	PheGluGlyAlaAsnAspValLeuArgLeuPheIleAlaLeuThrGlyAlaGlnHisAla	448
Qy	1333	GGCCGCATCTGACTACACAGATCATGAGCTTAAACAGGCCAAAGTAGGACACAGTCATG	139
Db	449	GlyLys-----HisLeuAlaGluGlnAla-----SerGlyValGly	460
Qy	1393	GATACCTGTGGCCGGAGGCTTCGGGACTCCCTGGGCCGAACCTGTGAGACCTGGGGCTGACA	145
Db	461	GlyLeuIleGlyLeuAlaValSerArgValThrGly-----GlyAsnThr	475
Qy	1453	GGC---AACCATTGA--GTTGTGCACCCAGTCTTTCGGGACAGTGCCCAACAGTTTGAG	150
Db	476	GlySerAsnPheGlyGlnValValAspAlaSerLeuGlnAspSerAlaLysValLeuAsp	495
Qy	1507	GAGAACACCTACTCTCTCGGCCGGACCGGTGGAGACATCTGCTCTCGCTTGGCAAGACC	156
Db	496	GlnGlnIleAlaLeuPheGlyGlnThrValGlnGlyLeuLeuMetLysHisLysLysGly	515
Qy	1567	ATCATGAGGAGCAGCTGGTACTGAAGCGGTGGCCACATCTCTCATCAACCTGTATGGC	162
Db	516	IleIleAspArgGlnTyrGluMetHisArgValAlaAspAlaAlaIleAsnIleTyrSer	535
Qy	1627	ATGACGGCGTGTCTCGGGCCAGCGCTCCATCCGCTATTCGGGTCTCGCAACACACGAC	168
Db	536	SerAlaAlaValLeuSerArgAlaThrTyrAlaIleLysAsnLysSerSerAlaAsp	555
Qy	1687	CACGAGGTCTCTTTGGCCCAACACCTTCTCGGTGGAAAGCTTACTTCGCAAGATCTCTTCAGC	174
Db	556	PheGluArgLysValAlaA--ThrTyrTyrValAspLysAlaMetLys-----Ser	571
Qy	1747	CTCTCTCAGTGGACATAGTATGCTCCAGAAAACCTAGATGACGACATTAAGAAAGTGTCC	180
Db	572	SerAsnArgPheLeuLysAspAlaGlySerGlyValGluAenAlaSerLysValAlaThr	591
Qy	1807	CACGAGATCTCTGAGAAGCGCCTATATCTGTGCC-----ValCysGlyAsnGlyLeuThrLeuGlnHis	184
Db	592	IleGluSerLeuAlaLysGlu-----ValCysGlyAsnGlyLeuThrLeuGlnHis	609
Qy	1846	CCTCTGGAC	1854

Qy	793	ATTCGGGGCTCCACACCTTGTTGAGTGCATTTTGAARAACACCAAGATACCTCTGGAAAC	85
Db	270	IleYsGlySerAsnThrThrGluValHisPheAsnLeuLysIleProValGluAsn	289
Qy	853	ATCCTCGAGAGAGTTCGGAGATGGGTTTAAAGTGGCCATGAACATCCTCAACAGCGCCGG	912
Db	290	LeuLeuGlyLysGluGlyGluGlyPheLysValAlaMetAsnIleLeuAsnAenGlyAArg	309
Qy	913	TTACAGCATGGCAGCGTCTGGTGGCTGCTCCTCAAGAGATTGATTGAATAGTCTGCTGAG	972
Db	310	PheGlyIleProAlaAlaCysThrGlyAlaMetLysHisCysIleGlnLysThrValAsp	329
Qy	973	TACGCTTCGCAACGAAGAAGCTTTAAACAGAGGCTCAGTGAATTTGGATTGATTCAGGAG	103
Db	330	HisIleThrThrArgValGlnPheGlyLysLysLeuGlnGluPheGlyAsnIleGlnGlu	349
Qy	1033	AAATTTGCACCTGATGGCTCAGAAGCTTACCTCATGGAGAGTATCACTTACCTCACAGCA	109
Db	350	LysLeuValGluMetIleSerLysLeuTyrAlaThrGluSerIleValTyrMetLeuSer	369
Qy	1093	GGGATGTGGACCAACCTGGCTTTCCGAGCTCTCCATCGAGCAGCCCATGTGTAAGGTG	115
Db	370	SerAsnMetAspAArg--GlyIleLysGluTyrGlnLeuGluAlaAlaIleGlyLysVal	388
Qy	1153	TTACGCTCCGAGGGCGCTGCGCAGTGTGTAGTAGGCGCTCCAGATCTCTCGGGGCTTG	121
Db	389	LeuAlaSerGluAenAlaTrpLeuValCysAspAlaIleGlnValHisGlyGlyMet	408
Qy	1213	GGCTACACAGGGACTACCGTACGAGCGCATCTGCGTGACACCCGCATCTCCTCATC	127
Db	409	GlyPheMetArgGluThrGlyLeuGluArgValLeuArgAspLeuArgIlePheArgIle	428
Qy	1273	TTCCAGGGAAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGTCTGCAGCATGCC	133
Db	429	PheGluGlyAlaAenAspValLeuArgLeuPheIleAlaLeuThrGlyAlaGlnHisAla	448
Qy	1333	GGCCGCATCTGACTACACAGATCATGAGCTTAAACAGGCCAAAGTAGGACACAGTCATG	139
Db	449	GlyLys-----HisLeuAlaGluGlnAla-----SerGlyValGly	460
Qy	1393	GATACCTGTGGCCGGAGGCTTCGGGACTCCCTGGGCCGAACCTGTGAGACCTGGGGCTGACA	145
Db	461	GlyLeuIleGlyLeuAlaValSerArgValThrGly-----GlyAsnThr	475
Qy	1453	GGC---AACCATGGA--GTTGTGCACCCAGTCTTTCGGGACAGTGCCCAACAGTTTGAG	150
Db	476	GlySerAsnPheGlyGlnValValAspAlaSerLeuGlnAspSerAlaLysValLeuAsp	495
Qy	1507	GAGAACACCTACTCTGCTCGGCCGGACCGTGGAGACACTGTGCTCTCGCTTTGGCAAGACC	156
Db	496	GlnGlnIleAlaLeuPheGlyGlnThrValGlnGlyLeuLeuMetLysHisLysLysGly	515
Qy	1567	ATCATGAGGAGCAGCTGGTACTGAGGGGGTGGCCACATCTCTCATCAACCTGTATGGC	162
Db	516	IleIleAspArgGlnTyrGluMetHisArgValAlaAspAlaAlaIleAsnIleTyrSer	535
Qy	1627	ATGACGGCGTGTCTGCGGGCCAGCGCTCCATCCGCTATTCGGGCTCCGCAACACACGAC	168
Db	536	SerAlaAlaValLeuSerArgAlaThrTyrAlaIleLysAsnLysSerSerAlaAsp	555
Qy	1687	CACGAGGTCTCTTTGGCCCAACACCTTCTCGTGGAAAGCTTACTTCGACGAATCTCTTCAGC	174
Db	556	PheGluArgLysValAlaA--ThrTyrTyrValAspLysAlaMetLys-----Ser	571
Qy	1747	CTCTCTCAGTGGACATGATGCTCCAGAAAACCTAGATGACGACATTAAGAAAGTGTCC	180
Db	572	SerAsnArgPheLeuLysAspAlaGlySerGlyValGluAenAlaSerLysValAlaThr	591
Qy	1807	CACGAGATCTCTGAGAAGCGCCTATATCTGTGCC-----ValCysGlyAsnGlyLeuThrLeuGlnHis	184
Db	592	IleGluSerLeuAlaLysGlu-----ValCysGlyAsnGlyLeuThrLeuGlnHis	609
Qy	1846	CCTCTGGAC	1854

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Db      610 ProValGlu 612
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RESULT 5
F84085
butyryl-CoA dehydrogenase BH3486 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84085
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84085
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-594 <STO>
A;Cross-references: UNIPROT:Q9K784; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BA0072
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3486

Alignment Scores:
Pred. No.:      2,64e-46      Length:      594
Score:          821.00      Matches:    207
Percent Similarity: 50.00%      Conservative: 105
Best Local Similarity: 33.17%      Mismatches: 210
Query Match:     23.98%      Indels:     102
DB:              2          Gaps:         13

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Db      16 LeuAspGluLeuAspAlaAspLysValPhe-----ThrProGluAspPhe 30
QY      193 AATGAATCAATCAGTTCTTGGGACCGCTGGAAAAATCTTCACT----- 237
Db      31 ThrGluGluHisGluMetIleGlyLysThrGluGluPheValValAsnGluValVal 50
QY      238 -----GAAGAGTGGACTCCCGAAAAATGACACGAGGAGGAAAAATCCCGATGAA 288
Db      51 ProValLeuAspGluIleGluAsnHisGlnPheAsp-----IleSerArgArg 66
QY      289 ACTTTGAGAAATTAAGAGAGCTAGGCTTTTGGGCTGCAAGTCCACAGAGAAATATGGT 348
Db      67 LeuLeuThrGlnAlaGlyGluLeuGlyLeuLeuGlyAlaAspValProGluGluTyrGly 86
QY      349 GGCCTGGGCTTCTCCAAACACCATGTACTCAAGACTAGGGAGAGATCATCAGCATGGATGGG 408
Db      87 GlyLeuGlyLeuAspLysIleSerSerSerIleIleThrGluLysPheSerArgAlaGly 106
QY      409 TCATCATCTGTGACCTCGGACGCGCACAGGCTATTGGCTCTCAAGGGAGATCATCTTGGCT 468
Db      107 GlyPheSerLeuSerTyrGlyAlaHisValClyIleGlySerLeuProIleValPhePhe 126
QY      469 GGCCTAGGAGGAGAGCAATATCTTCGCTAAACTGGCGTCCGGGAGGACACATTGCA 528
Db      127 GlyAsnGluAspGlnLysLysLysTyrLeuProAspLeuAlaThrGlyAlaArgIleAla 146
QY      529 GCCTTCCTGCTCCAGGACCGACGAGTGGGAGCGCATCGACCTCAATCCGGAGCAGAGCC 588
Db      147 AlaTyrAlaLeuThrGluProSerSerGlySerAspAlaLeuGlyAlaLysThrAla 166
QY      589 ACATAGTAGAACAAGACATACATCTCAATGCTCCCAAGTCTGGATTACTAAT 648
Db      167 ValLeuAsnGluAlaGlyThrHisTyrValLeuAsnGlyGluLysGlnTrpIleThrAsn 186
QY      649 GGAGGACTGGCCATATTTTACTGTCTTGCAGAAAGTCAAGGTCGTGTGATTCTTGATGGA 708
Db      187 SerAlaPheAlaAspValPheIleValTyrAlaLysIle-----AspGly 201
QY      709 TCAGTGAAGACAAAAATCACAGCATTCATAGTAGAAGAGACTTTTGGTGGAGTCACTAAT 768
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Db      202 -----GluHisPheSerAlaPheIleValGluLysAspPheGluGlyValSerThr 218
QY      769 GCGAAACCCCAAGATAAATTAGGCATTTCGGGGCTCCAAACACTTGTGAAGTCCATTTTGAA 828
Db      219 GlyProGluGluLysMetGlyIleLysGlySerSerThrArgThrLeuLeuGlu 238
QY      829 AACACCAAGATACCTGTGGAACACATCTTGGAGAGTCCGAGATGGTTTAAGTGCGCC 888
Db      239 AspAlaLeuValProLysGluAsnLeuLeuGlyValGlyLysGlyHisValIleAla 258
QY      889 ATGAACATCTCAACAGCGCCGTTTCAGCATCGGACAGCGTCTGGTGGTGGCTGCTCAAG 948
Db      259 PheAsnIleLeuAsnValGlyArgTyrLysLeuGlyValGlyCysIleGlyGlySerLys 278
QY      949 AGATTGATTGAATGACTCTGTAGTAGCGCTGCACAGGAACAGAGTTTACACAGAGCGTC 1008
Db      279 ArgGlyIleGluLeuAlaLysTyrAlaAsnGluArgLysGlnPheLysGlnProIle 298
QY      1009 AGTGAATTTGGATTGATTTCAGGAGAAATTTGCATGTATGGCTCAGAAGGCTTACGTCTG 1068
Db      299 AlaLysPheThrLeuIleGlnGluLysLeuAlaAsnMetAlaValThrThrTyrAlaAla 318
QY      1069 GAGAGTATGACCTACCTCACAGCAGGAGTCTCGAACCA----- 1107
Db      319 GluSerSerIleTyrArgThrGlyLysLeuPheGluAspArgLeuGlyGlyLeuSerGlu 338
QY      1108 -----CCTGGCTTTCCGACTGCTCCATCGAGGCA 1137
Db      339 GluGlnGlnLysAspGlyArgGluValAlaLysAlaIleAlaGluTyrAlaIleGluCys 358
QY      1138 GCCATGGTGAAGGTGTTTCAGCTCCGAGGCGCGCTGTCAGTGTGTGAGTAGGGGCTCGAG 1197
Db      359 SerLeuAsnLysValValGlySerGluAlaLeuAspPheValAlaAspGluAlaValGln 378
QY      1198 ATCCTCGGGGGCTTGGGCTACACAGGGACTATCCGTACAGGCGCATCTGCGTGACACC 1257
Db      379 IleHisGlyGlyTyrGlyPheMetAlaGluTyrGluValGluArgMetTyrArgAspSer 398
QY      1258 CGCATCTCTCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTATACGCGCTCAGC 1317
Db      399 ArgIleAsnArgIlePheGluGlyThrAsnGluIleAsnArgLeuLeuValProGlyThr 418
QY      1318 GGTCTGCAGCATGCC-----GGCGGCATC---CTGACTACCAAGGATCCATGAGCTTAAA 1368
Db      419 IleLeuArgLysAlaMetLysGlyGluLeuProPheLeuGluLysAlaThrAlaLeuGln 438
QY      1369 CAGGCCAAAGTAGACACAGTCATGGATACCGTTGGCGGAGGCTTCGGGACTCCCTGGGC 1428
Db      439 GluGluLeuMetMetLeuMetProGlnGluValGly----- 450
QY      1429 CGAACTGTGGACCTGGGGCTGCACAGGCAACCATGGAGTTGTGCACCCAGTCTTTCGGAC 1488
Db      450 ----- 450
QY      1489 AGTGCCAAACAAGTTTGAGGAGAACACCTACTGTCTCGCGCGGACCGCTGGAGACACTGCT 1548
Db      451 ---AspGluProLeuGluGlnGluLysTyrLeuLeuSerMetAlaLysLysValPheLeu 469
QY      1549 CTC-----CGCTTTGGCAAGACCATCATCTATGGCATGACGGCGGCTGTCTCGCGG 1587
Db      470 MetIleAlaGlyThrGlyAlaGlnThrTyrGlyLysLeuGlnGlnGluGlnLeu 489
QY      1588 CTGAAGCGGTGGCCAAACATCTCATCACTGTATGGCATGACGGCGGCTGTCTCGCGG 1647
Db      490 LeuAlaAsnValAlaAspIleValSerAspIlePheSerMetGluSerValIleLeuArg 509
QY      1648 GCCAGCGCTCCATC---CGCATTTGGGCTCCGCAACCCACACACAGGAGTCTCTTGGCC 1704
Db      510 ThrGluLysAlaIleArgArgAsnGlyLeuGluLysAlaGluGlnLysLeuAlaLeuThr 529
QY      1705 AACACCTTCTGCTGGAGAGCTTAC----- 1728
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Db 530 GlnValPheCysGlnGluAlaPheAsnArgIleGluAlaHisAlaLysGluSerLeuVal 549
 Qy 1729 -----TTGCAGAAATCTCTTCAGC---CTCTCTCAGCTCGACAAG 1764
 Db 550 AlaMetGlnSerGlyAspThrLeuArgThrMetThrSerIleLeuArgLysLeuThrArg 569
 Qy 1765 TATGCTCCAGAAACCTAGATGACGATTAAAGAAATGTCCCGAGCAGATCTTGAGAAG 1824
 Db 570 HisThrProIleAnValIleAlaLysArgGluIleAlaGlyArgIleLeuGluAla 589
 Qy 1825 CGAGCCTATATC 1836
 Db 590 GluArgTyrVal 593

RESULT 6
 C70021
 butyryl-CoA dehydrogenase homolog yusJ - Bacillus subtilis
 C/Species: Bacillus subtilis
 C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C/Accession: C70021
 R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brouillette, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Wintere, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A.; Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A/Reference number: A69580; MUID:98044033; PMID:9384377
 A/Accession: C70021
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-594 <KUN>
 A/Cross-references: UNIPROT:O32176; GB:Z39120; GB:AL009126; NID:G2635613; PIDN:CAB15271.
 A/Experimental source: strain 168
 C/Genetics:
 A/Gene: yusJ

Alignment Scores:
 Pred. No.: 6,1e-46 Length: 594
 Score: 815.50 Matches: 201
 Percent Similarity: 49.58% Conservative: 97
 Best Local Similarity: 33.44% Mismatches: 202
 Query Match: 23.82% Indels: 101
 DB: 2 Gaps: 12

US-09-945-326-3 (1-1863) x C70021 (1-594)

Qy 175 GTTAGCCAGATGAACCTTAATGAATCAATCAGTCTTTGGGACCCGTGGAAATTTCTTC 234
 Db 45 IleGluGlnAspValLeuProHisIle----- 53
 Qy 235 ACTGAAGAGGTGAGCTCCGAAATTTGACAGAGAGGAAATCCAGATGAACCTTTG 294
 Db 54 ---AspAspIleGluAnHisGlnPheGluHisSerValArgLeu-----Leu 68
 Qy 295 GAGAAATTGAAGAGCTTAGGCTTTTGGCTGCACTCCAGAGAAATATGTTGGCTG 354
 Db 69 LysLysAlaGlyGluLeuGlyLeuLeuGlyAlaAspValProGluGluTyrGlyGlyLeu 88
 Qy 355 GGCTTCTCCAAACACCATGTACTCAAGATAGGGGAGATCATCAGCATGGATGGTCCATC 414
 Db 89 GluLeuAspLysIleSerSerAlaLeuIleThrGluLysPheSerArgAlaGlySerPhe 108
 Qy 415 ACTGTGACCTGGCAGCGCACCGAGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACT 474
 Db 415 -----SerGlyValLeu----- 454

Db 109 SerLeuSerTyrGlyAlaHisValGlyIleGlySerLeuProIleValPhePheGlySer 128
 Qy 475 GAGGAGCAGAAAGCCAAATACTTGCCTAAACTTGGCGTCCGGGGAGCACATTTGACGCCTTC 534
 Db 129 GluGluGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 148
 Qy 535 TGCTCTACGAGCAGCCAGCTGGAGCGATGCGAGCCTCAATCCGGAGCAGAGCCACACATY 594
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 Qy 595 AGTGAGAGACAAGAAGCAGCTACATCTCAATGGCTCCCAAGTCTCGATTACTTAATGGAGGA 654
 Db 169 AsnGluAlaGlyThrHisLysValLeuThrGlyLysGlnThrIleThrAsnSerAla 188
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 Qy 715 AAAGACAAATACAGCATTCATAGTAAAGAGACTTTTGGTGGAGTCACCTAATGGGAA 774
 Db 202 ---AspLysPheSerAlaPheIleValGluLysGluPheProGlyValSerThrGlyPro 220
 Qy 775 CCGAAGATAAATTAGGCATTTCGGGGCTCCCAACACTTGTGAAGTCCATTTTGAACACACC 834
 Db 221 GluGluLysLysMetGlyLysLysGlySerSerThrArgThrLeuIleLeuAspGlnAla 240
 Qy 835 AAGATACCTCTGGAAACATCTTGGAGAGCTCGAGATCGGTTTAAGTGGCCATGAAC 894
 Db 241 GluValProLysGluAsnLeuLeuGlyGluIleGlyLysGlyHisValIleAlaPheAsn 260
 Qy 895 ATCTCTACAGCGCGCGTTCAGCATGGGCGAGCGTCTGGCTGGCTGGCTGGCTGGCTGGCT 954
 Db 261 IleLeuAsnIleGlyArgTyrLysLeuAlaValGlyThrIleGlyAlaSerLysArgVal 280
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 Db 281 IleLeuLeuSerAlaAlaTyrAlaAsnGlnArgGlnPheLysThrProIleAlaGly 300
 Qy 1015 TTTGGATTGATTTCAGGAAATTTTGCACATGGCTCAGAGGCTTACGTCTGAGAGAGT 1074
 Db 301 PheSerLeuThrGlnGluLysIleGlyThrMetAlaSerArgLeuTyrAlaMetGluSer 320
 Qy 1075 ATGACCTACCTCAGCAGCGGATCTGGACCAA----- 1107
 Db 321 SerValTyrArgThrValGlyLeuPheGluAspAsnMetSerGlnPheThrAlaGluAsp 340
 Qy 1108 -----CTGGGCTTTCCGACTGCTCCATCGAGGAGCCATG 1143
 Db 341 LeuLysAspGlyArgGlnIleAlaLysSerIleAlaGluTyrAlaIleGluCysSerLeu 360
 Qy 1144 GTGAAGGTGTTTACGCTCCGAGCGCGCTGCGCAGTGTGTGAGTGGAGCGCTGCGAGATCCTC 1203
 Db 361 AsnLysValPheGlySerGluThrLeuAspTyrIleValAspGluGlyValGlnIleHis 380
 Qy 1204 GGGGGCTTGGGCTACACAGGAGCTATCCGTACAGAGCGCATCTGCTGACACCCGCTATC 1263
 Db 381 GlyGlyTyrGlyPheMetGlnGluTyrGluValGluAlaTyrArgAspSerArgIle 400
 Qy 1264 CTCTCATCTTCAGAGGAACCAATGAGATTCTCCGGATGTACATCGCCCTGACGGGCTG 1323
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 Db 421 LysLysAlaLeuLysGlyGluLeuProLeuPheGluLysAlaGlnSerLeuGlnGlu 440
 Qy 1375 AAAGTGAGCACATCATGATACCGTTGGCGGAGCGCTTCGGGACTCCCTGGGCCCGAAGT 1434
 Db 441 LeuMetMetLeuMetProGluGluProGly----- 450
 Qy 1435 GTGACCTGGGCTGACAGCGCAACCATGAGTGTGTGACCCAGTCTTGGGACAGTGCC 1494
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Score: 690.00 Matches: 147
Percent Similarity: 61.39% Conservative: 74
Best Local Similarity: 40.83% Mismatches: 125
Query Match: 20.16% Indels: 14
DB: 2 Gaps: 6

US-09-945-326-3 (1-1863) x G84124 (1-379)

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Qy	292	TTGGAAGAAATTGAAGAGCCTTAGCGCTTTTGGCGTCGCAAGTCCCGCAGAGAATAATGGTGGC	351
Db	42	ValysGluMetGlyGluLeuGlyLeuMetGlyIleProIleProGluAlaIleValGlyGly	61
Qy	352	CTGGGCTTCTCCAACACCATGTAC---TCAGACTAGGGGAGATCATCAGCATCGATGGG	408
Db	62	AlaGluMetAspPheThrSerTyrIleIleAlaIleHisGluLeuSerLysValSerAla	81
Qy	409	TCCATCTACTGTGACCCCTGGCAGCCGACCCAGGCTATTGGCCCTCAAGGGGATCATCTTGGCT	468
Db	82	ThrValGlyValIleLeuSerValHisThrSerValGlyThrAsnProIleLeuPhePhe	101
Qy	469	GGCACTGAGGAGCAAGAACCAATACTTGCCTAACTGGCGTCCGGGGAGCACATTGCA	528
Db	102	GlyThrGluGluGlnLysSerArgPheIleProLysLeuAlaIleGlyGlyTyrLeuGly	121
Qy	529	GCCTTCGCTCAGCGAGCCAGCGAGTGGAGCGCATCAGCGCTCAATCCGAGCAGAGACC	588
Db	122	AlaPheGlyLeuThrGluProSerAlaGlySerAspAlaAlaAsnLeuLysThrThrAla	141
Qy	589	ACATAAGTGAAGACAAGACACTACATCTCTCAATGGCTCCAAAGTCTCGGATTAATAAT	648
Db	142	LeuLysGlnGlyAsp-----HisTyrArgLeuAsnGlySerLysValPheIleThrAsn	159
Qy	649	GGAGACTGGCCAAATATTTTACTGTGTGTGCAAGAGCTAGGTCGTGTGATCTGATGGA	708
Db	160	GlyGlyAlaAlaAspThrTyrValValPheAlaSerThr-----AsnProSer	175
Qy	709	TCAGTGAAGACAAATAACACAGCATTCATAGTACAAAGAGACTTTGGTGAGTCACATAAT	768
Db	176	AlaGlyArgLysGlyIleSerAlaPheIleValGluLysGluThrProGlyPheThrVal	195
Qy	769	GGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAAACACTTGTGAAGTCAATTTTCAA	828
Db	196	GlyLysLysGluLysLysMetGlyLeuHisGlySerAsnThrThrGluLeuIlePheGlu	215
Qy	829	AACACCAAGATACCTGTGGAAAAATCCTCTGGAGAGGTTCGAGATGGTTTAAAGTGGCC	888
Db	216	AspAlaLeuValProLysGluAsnLeuGlyValGluGlyAspGlyTyrLysIleAla	235
Qy	889	ATGAACATCTCAACAGGCGCGGTTTCAGCATGGCAGCGCTCGTGGCTGGGCTCCTCAAG	948
Db	236	MetAlaAsnLeuGluAlaGlyArgIleGlyIleAlaAlaGlnSerLeuGlyIleAlaGlu	255
Qy	949	AGATTGATTGAATGACTGCTGACTAGCGCTGCACAAAGGAAACAGTTTAAACAGAGCGCT	1008
Db	256	AlaAlaLeuGluAlaAlaThrSerTyrAlaLysGluArgLysGlnPheGlyLysSerIle	275
Qy	1009	AGTGAATTTGGATTGATTCAGGAGAAATTTGACTGATGGCTCAGAAGGCTTACGTCATG	1068
Db	276	GlyGlnGlnGlnAlaIleAlaPheLysLeuAlaAspLeuAlaThrGlnValGluAlaAla	295
Qy	1069	GAGAGTATGACTTACCTTCACAGCAGGAGTGTCTGACCAACCTGGCTTCCGACTGCTCC	1128
Db	296	LysLeuLeuThrTyr---ArgAlaAlaGlnLeuLysGlnGlnGlyIle---SerCysAla	313
Qy	1129	ATCAGGCGAGCAGTGGTGAAGGTGTTCAGCTCCGAGGCGCGCTGGCAGTGTTGAGTGAG	1188
Db	314	LysGluSerMetAlaLysLeuPheAlaSerLysThrLamMetLysAlaAlaIleGlu	333
Qy	1189	CGCTGTCAGATCTCTCGGGGGCTTGGGCTTACACAAGGAGACTATCCGTACGAGCGCATCTG	1248

Db 334 AlavalGlnllePheGlyGlyTyrrGlyrThryrsGlutyrProValGluatrgTyrPhe 353
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RESULT 11

D6958 acyl-CoA dehydrogenase mmgC - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: D6958
 E:Kunst, F.; Ogasawara, N.; Moezer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.
 C.: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter,
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferri,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.R.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.;
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holteappel, S.; Hosono, S.; Hu,
 Koester, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Li,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohll, T.M.; P
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadai, Y.; Sato, T;
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska,
 akeuchi, M.; Tamakoehi, A.; Tanaka, T.; Terpstka, P.; Tognoni, A.; Tosato, V.;
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Y
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshioka, H.; Danchin, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus s
 A:Reference number: A69580; PMID:98044033; PMID:9384377
 A:Accession: D6958
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-378 <KUN>
 A:Cross-references: UNIPROT:P45857; GB:Z99116; GB:AL009126; MID:g2634723; PIDN:
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: mmgC
 C:Superfamily: acyl-CoA dehydrogenase

Alignment Scores:	
Pred. No.:	3,49e-37 Length: 378
Score:	682.00 Matches: 157
Percent Similarity:	56.33% Conservative: 70
Best Local Similarity:	38.96% Mismatches: 130
Query Match:	19.92% Indels: 46
DB:	2 Gaps: 8

US-09-945-326-3 (1-1863) x D6958 (1-378)

Qy 106 GTACGACTTTGCCAAGAAGCTTTTCTTAGGCAAAATCAAGRAAGAAGTTTTCCCCA 165
 Db 14 ValargaspPheaLa-----ArglysGluileAlapro 24
 Qy 166 TTTCACAAGGTAGCCAAGATAAATGAATCAAATCAATCAGTTCTTGCGACCCTGGAA 225
 Db 25 AlaalaGluile----- 28
 Qy 226 AAATTCTTCTACTGAAGAGGTGGACTCCGAAAAAATTCACCAAGGAAGAAATCCCAGAT 285
 Db 29 -----MetGluIysThrAspGluPhePropHe 37
 Qy 286 GAACACTTTGAGAAATTGAGAGCCTAGGCTTTTGGCGTGCAGGTCCACGAGAGAATAT 345
 Db 38 GlmleuilelylsMetGlyHisGlyLeuMetGlylleProvalProgluginfiry 57
 Qy 346 GGTCGCTGGGCTTCTCAACACCATGTAC---TCAAGACTAGGGGAGATCATCAGCATG 402
 Db 58 GlyGlyAladylaapValserTyrlleleualaalleHISGluileSerArgile 77
 Qy 403 GATGGGTCCATCACTGTGACCCCTGGCAGCGCAGCAGGCTATTGTGCCTCAAGGGGATCATC 462
 Db 78 SerAlaalavAlglylalleLeuSerValHisThrSerValGlyThrAanProilleu 97

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QY 463 TTGGCTGGCACTGAGGAGCAGAAAGCAATACTTGCCTAAACTGGCGTCCGGGAGCAC 522
Db 98 Ty-PheGlyAsnGluGluGlnLysMetLysTyIleProAsnLeuAlaSerGlyAspHis 117
QY 523 ATTGCAGCCTTTCCTCAGGAGCCAGCAGTGGGAGCGATCAGCCTCAATCCGGAGC 582
Db 118 LeuGlyAlaPheAlaLeuThrGluProHisSerGlySerAspAlaGlySerLeuA-gthr 137
QY 583 AGAGCACACCTAAGTGAAGCAAGAACACTACATCTCAATGGCTCCAAAGGCTCGGATT 642
Db 138 ThrAlaIleLysLysAsnGlyLys-----TyrlLeuLeuAsnGlySerLysIlePheIle 155
QY 643 ACTAATGGAGACTGGCAATATTTTACTGTGTGTTCGAAAGACTGAGGTCGTGATTCT 702
Db 156 ThrAsnGlyGlyAlaAlaAspIleTyIleThrPheAlaLeuThr-----Ala 171
QY 703 GATGGATCACTGAAGCAAAATCACAGCATTCATAGTAGAAGAGACTTTGGTGGAGTC 762
Db 172 ProAspGlnGlyArgHisGlyIleSerAlaPheIleValGluLysAsnThrProGlyPhe 191
QY 763 ACTAATGGGAAACCCGAAGATAAATTAGGCATTCGGGGCTCCAAACACTTGTGAAGTCCAT 822
Db 192 ThrValGlyLysLysGluArgLysLeuGlyLeuTyrlGlySerAsnThrThrGluLeuIle 211
QY 823 TTTGAAACACCAAGATACCTCTGTGGAACATCCTTGGAGAGTCGCGAGATGGTTTAAG 882
Db 212 PheAspAsnAlaGluValProGluAlaAsnLeuLeuGlyLysGluGlyAspGlyPheHis 231
QY 883 GTGGCCTGAACATCTCCACAGCGCGGCTTCAGCATGGCGAGCTCGTGGCTGGGCTG 942
Db 232 IleAlaMetAlaAsnLeuAsnValGlyArgIleGlyIleAlaAlaGlnAlaLeuGlyIle 251
QY 943 CTAAGAGATTGATTGAATGACTGTCTGAGTAGCTGAGCTGCACAAAGGAAACAGTTTAAACAG 1002
Db 252 AlaGluAlaAlaLeuGluHisAlaValAspTyrlAlaLysGlnArgValGlnPheGlyArg 271
QY 1003 AGGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCACTGATGTGCTCAGAGCTTAC 1062
Db 272 ProIleAlaAlaAsnGlnGlyIleSerPheLysLeuAlaAspMetAlaThrArgAlaGlu 291
QY 1063 GTACGAGAGATGACCTACCTCAGCAGGAGGATGCTGGACCAACCTGCTTCCCGAC 1122
Db 292 AlaAlaArgHisLeuValTyrlHisAlaAlaAsp---LeuHisAsnArgGlyLeu---Asn 309
QY 1123 TGCTCCATCAGGAGCAGCATCGTGAAGTGTCTCAGCTCCGAGCGCGCTCGCAGTGTGTG 1182
Db 310 CysGlyLysGluAlaSerMetAlaLysGlnPheAlaSerAspAlaAlaValLysAlaLeu 329
QY 1183 AGTGAGCGCTGAGATCCCTCGGGGCTTGGGCTTACACAAGGAGCTATCCGTACGAGCGC 1242
Db 330 ---AspAlaValGlnIleTyrlGlyTyrlGlyTyrlMetLysAspTyrlProValGluArg 348
QY 1243 ATACTGGGTACACCCGCATCCTCCTCATCTTCGAGGGAACCAATGAGATTCCTCGGATG 1302
Db 349 LeuLeuArgAspAlaLysValThrGlnIleTyrlGluGlyThrAsnGluIleGlnArgLeu 368
QY 1303 TACATGCC 1311
Db 369 IleIleSer 371
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RESULT 12

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AC3536
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3536
R;DelVecchio, V.G.; Kapratl, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AC3536
A;Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-381 <UNP>
A;Cross-references: UNIPROT:Q8YDG3; GB:AE008918; PIDN:AAL53454.1; PID:g17984354; GSPDB:G1
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME110213
A;Map position: II
C;Superfamily: acyl-CoA dehydrogenase
C;Keywords: oxidoreductase

Alignment Scores: 3.5e-37 Length: 381
Pred. No.: 682.00 Matches: 151
Score: 60.70% Conservative: 73
Percent Similarity: 40.92% Mismatches: 131
Best Local Similarity: 19.92% Indels: 14
Query Match: 2 Gaps: 7
DB: 7

US-09-945-326-3 (1-1863) x AC3536 (1-381)
QY 220 GTGCAAAATTTCTCACTGAAGAGGTG-----GACTCCGAAAAAATTGACCAGGAA 270
Db 16 ValArgArgPheValArgGluArgLeuValProAlaGluSerArg---ValGluGluThr 34
QY 271 GGGAAATCCAGATGAACCTTTGGAGAAATTTGAAGAGCCTAGGGCTTTTGGGCTGCAA 330
Db 35 AsnArgIleProAspAspIleIleGluGluMetArgAlaMetGlyLeuPheGlyLeuSer 54
QY 331 GTCCCAAGAAATATGGTGGCTGGCTTCTCCACACCATGTACTCAAGACTAGGG--- 387
Db 55 IleProGluGluTyrlGlyLeuGlyLeuThrMetGluGluValArgValGlyPhe 74
QY 388 GAGATCATCAGCATGATGGTCTCATCTGTGACCTGTGCAGCCAGCCAGGCTATTGGC 447
Db 75 GluLeuGlyTyrlThrSerProAlaPheArgSerValIleGlyThrAsnAsnGlyIleGly 94
QY 448 CTCAGGGGATCATCTTGGCTGCACTGAGAGCAGAAAGCAAAATACTTGCCTAAACTG 507
Db 95 SerGlnGlyIleIleAlaAspGlyThrAspAspGlnLysLysTyrlTrpLeuProArgLeu 114
QY 508 GGGTCCGGGAGCACATTCAGCCTTCTGCTCAGCAGGAGCCAGCCAGTGGGAGCGATGCA 567
Db 115 AlaSerGlyGlyIleIleAlaSerPheAlaLeuThrGluProAspValGlySerAspAla 134
QY 568 GCCTCAATCCGAGCAGAGCCACTTAAGTGAAGACAAAGCAAGCACTACATCTCAATGGC 627
Db 135 GlyAlaValArgThr-----ThrAlaGluArgAspGlyAspSerTyrlIleIleAsnGly 152
QY 628 TCCAAGCTCTGGATTACTAATGGAGGACTGGCCCAATATTTTACTGTGTGTTGCAAGACT 687
Db 153 ThrLysArgPheIleThrAsnAlaProValAlaGlyValPheThrLeuMetAlaArg--- 171
QY 688 GAGTCTGTTGATCTCATGATGATGAGTGAAGACAAATCACAGCATTCATAGTAGAAGA 747
Db 172 -----MetGlyGlySerGlyProSerGlyIleSerAlaPheLeuAlaGluArg 187
QY 748 GACTTTGTGGAGTCACTAATGGGAAACCCGAAGATAAAATTAGGCATTCGGGCTCCAAAC 807
Db 188 AspLeuProGlyLeuThrValGlyThrProAspHisLysMetGlyGlnArgGlyThrGln 207
QY 808 ACTTGTGAAGTCCATTTTGAAGAACACCAAGATACCTGTGTGGAAGAACATCTCTTGAGAGGTC 867
Db 208 ThrCysAspValTyrlLeuGluAsnValArgValProAlaThrSerIleIleGlyIleVal 227
QY 868 ---GGAGATGGTTTAAGTGGCCATGAACATCTCTCAAGCGCGCGGTTTCAGCATGGGC 924
Db 228 GluGlyArgGlyPheLysThrAlaMetLysValLeuAsnArgGlyArgLeuHisIleSer 247
QY 925 AGCGTCTGGCTGGGCTGTCTCAAGAGATTGATTGAAATGACTGCTGAGTACGCTGCAC 984
Db 248 SerValCysAlaGlyThrAlaGluArgProIleGluGluSerValGlyPheAlaGlySer 267
QY 985 AGGAAACAGTTTAAACAGAGGCTCAGTGAATTTGGATTGATTTCAGGAGAAATTTGCAC 1044
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A;Molecule type: DNA

A;Residues: 1-380 <STO>

A;Cross-references: UNIPROT:Q9K6D1; GB:AF001520; NID:gl0176401; PIDN:BA079

A;Experimental source: strain C-125

C;Genetics:

A;Gene: acdA

C;Superfamily: acyl-CoA dehydrogenase

Alignment Scores:

Pred. No.:	1-34e-35	Length:	380
Score:	658.00	Matches:	156
Percent Similarity:	57.96%	Conservative:	66
Best Local Similarity:	40.73%	Mismatches:	139
Query Match:	19.22%	Indels:	22
DB:		Gaps:	8

US-09-945-326-3 (1-1863) x F84124 (1-380)

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DB	7	AspGluGlnMetIleLysLysMet-----ValArgAspPheAlaGluAsnGlu	23
QY	244	GTG-----GACTCCGAAAAATTCACAGAGGGAATCCAGATGAATCTTGGAG	297
DB	24	ValAlaProThrAlaGluGluArgAspGluGluArgPheAspArgGluIlePheAsp	43
QY	298	AAATTGAAGAGCTTAGGGCTTTTGGGCTGCAAGTCCCAAGAATAATGTGGCTGGGC	357
DB	44	GlnMetAlaGluGluGlyLeuThrGlyIleProTrpProGluGluGlyGlyIleGly	63
QY	358	TTCTCCAACACCATGTATC-----TCAAGCATAGGGAGATCATCAGCATGGATGGTCCATC	414
DB	64	AlaAspTyrValSerTyrValIleAlaValGluGluLeuSerArgValCysAlaSerThr	83
QY	415	ACTGTGACCTGCGAGCGCACCGGCTATTGGCTCAAGGGATCATCTTGGCTGGCACT	474
DB	84	GlyValThrLeuSerAlaHisLeuSerLeuAlaSerTrpProValTyrLysPheGlyThr	103
QY	475	GAGGAGCAGAAAGCGCAATACTTGCCTAAACTGGCGTCGGGAGCAGCATTCGAGCCTTC	534
DB	104	GluGluGlnLysGlnPheLeuArgProMetAlaGluGlyLysIleGlyAlaTyr	123
QY	535	TGCTCTACGAGCGCAGCAGTGGGAGCGATGCAGCCTCAATCCGAGCAGAGCCACACTA	594
DB	124	GlyLeuThrGluProGlySerGlySerAspAlaAlaAsnMetLysThrThrAlaValLeu	143
QY	595	AGTGAACAGCAGACACTACATCTCAATGGCTCCAGCTCGGATTAATGAGGA	654
DB	144	GluGlyAsp-----AspTyrIleLeuAsnGlySerLysIlePheIleThrAsnGlyGly	161
QY	655	CTGGCCCAATTTTACTGTGTGTGCAAGACTGAGTCTGATTCGATGATGATGATG	714
DB	162	IleAlaAspIleTyrIleValPheAlaValThrGlu-----	173
QY	715	AAAGCAAAA-----ATCACAGCATTCATAGTAGAAAAGACATTTGGTGGATC	762
DB	174	ProGluLysArgHisLysGlyValSerAlaPheIleValGluAlaAspThrProGlyPhe	193
QY	763	ACTAATGGGAACCCGAGATAATATAGGATTCGGGGCTCCACACTTGTGAATCCAT	822
DB	194	SerValGlyLysLysGluLysLysLeuGlyIleArgSerSerProThrThrGluIleIle	213
QY	823	TTTGAACACCAAGATACCTCTGGAAACATCTTGGAGAGTCGAGATGGGTTTAAG	882
DB	214	PheGluAspCysArgValProLysGluAsnLeuLeuGlyLysGluGlyAspGlyPheLys	233
QY	883	GTGGCCATGAACATCTCAACAGCGCGCTTTCAGCATGGCGAGCGCTCGTGGCTGGCTG	942
DB	234	IleAlaMetMetThrLeuAspGlyGlyArgAsnGlyIleAlaAlaGlnAlaValGlyIle	253
QY	943	CTCAAGAGATTGATGAAATGACTGTGACTGACCTGCACAGGAAACAGTTTACAG	1002
DB	254	AlaGlnGlyAlaLeuAspAlaAlaValAlaTyrAlaAsnGluArgLysGlnPheGlyLys	273

QY	1003	AGGCTCAGTGAATTTGCGATTGATTTCAGGACAAATTTTCACCTGATGGCTCAGAAGCTTAC	1062
DB	274	ProIleGlyGlnGlnGlnGlyIleAlaPheLysLeuAlaAspMetAlaThrLysValGlu	293
QY	1063	GTCAATGAGAGTATGACCTACCTCACAGCAGGAGTGTCTGGACCAACCTGGCTTCCCGAC	1122
DB	294	AlaSerArgLeuLeuThrTyr---GlnAlaAlaTyrArgGluSerGluGlyLeu---Ser	311
QY	1123	TGCTCCATCGAGCAGCAGCCATCGTGAAGGTGTTTCAGCTCCGAGCGCCCTGGCAGTGTGTG	1182
DB	312	TyrGlyLysGluSerAlaMetSerLysLeuPheAlaGlyAspThrAlaMetAspValThr	331
QY	1183	AGTGAGCGCTGCAGATCTCTCGGGCTTGGCTTACACAGGAGGACTATCGTACGAGCGC	1242
DB	332	ValGluAlaValGlnValPheGlyGlyTyrGlyTyrThrLysGluTyrProValGluArg	351
QY	1243	ATATCTCGTGACACCCGATCTCTCTCATCTTCGAGGGACCAATGAGATTCCTCGGATG	1302
DB	352	TyrMetArgAspAlaLysIleThrGlnIleTyrGluGlyThrAsnGluIleGlnArgLeu	371
QY	1303	TACATGCC 1311	
DB	372	ValIleSer 374	

RESULT 15
S55421
acyl-CoA dehydrogenase (EC 1.3.99.3) acdA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S55421; B69581
R;Glaser, P.; Danchin, A.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning and sequencing of the Bacillus subtilis chromosomal region from 3:
A;Reference number: S55414
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <GLA>
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R;Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chof
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabbret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B69581
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-379 <KUN>
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A;Experimental source: strain 168
C;Genetics:
A;Gene: acdA
C;Superfamily: acyl-CoA dehydrogenase
C;Keywords: oxidoreductase

Alignment Scores:	3.1e-35	Length:	379
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Percent Similarity:	58.42%	Conservative:	60
Best Local Similarity:	42.12%	Mismatches:	140
Query Match:	19.06%	Indels:	13

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Db 36 ArgPheAspArgGluLeuPheArgGluMetAlaAsnLeuGlyLeuThrGlyIleProTir 55
QY 334 CCAGAGAATATGCTGCGCTGGCTTCTCCACACCATGTAC-----TCAAGACTAGGGGAG 390
Db 56 ProGluAspTyrGlyIleGlySerAspTyrLeuAlaTyrValIleAlaValGluGlu 75
QY 391 ATCATCAGCATGAGTGGCTCATCTGCTGACCTGGCAGCGACACAGGCTATTGGGCTC 450
Db 76 LeuSerLysValCysAlaSerThrGlyValThrLeuSerAlaHisIleSerLeuCySer 95
QY 451 AAGGGATCATCTTGGCTGGCTAGGAGCAGAAAGCCAAATACTTGCCTAAACTGGCG 510
Db 96 TrpProLeuPheAlaPheGlyThrGluGlnLysThrGluTyrLeuThrGlnLeuAla 115
QY 511 TCCGGGAGCACATTGGCAGCTTCTGCTCAGGAGCCAGCCAGTGGGAGCGATGCAGCC 570
Db 116 LeuGlyGluLysIleGlyAlaPheAlaLeuThrGluAlaGlySerGlySerAspAlaGly 135
QY 571 TCAATCCGAGCAGACACACACTAAGTGAAGACAAGACACTACATCTCAATGGCTCC 630
Db 136 SerMetLysThrAlaGluArgIleGlyAsp-----AspTyrValLeuAsnGlySer 153
QY 631 AAGGTCCTGATTAATGAGGAGCTGGCCAAATATTTTACTGTGTGTTGCAAGACTGAG 690
Db 154 LysValPheIleThrAsnGlyGlyValAlaAspIleTyrIleValPheAlaValThr--- 172
QY 691 GTCGTTGATTCATGATGATCAGTGAAGACAAA---ATCAGCATTCATAGTAGAAGA 747
Db 173 -----AspProGluLysLysLysGlyValThrAlaPheIleValGluLys 188
QY 748 GACTTTGGTGGAGTCACTAATGGGAACCCGAGACATAAATTAGGCATTCGGGGCTCCAAC 807
Db 189 AspPheGluGlyPhePheThrGlyLysGluLysLysLysLeuGlyIleArgSerSerPro 208
QY 808 ACTTGTCAAGTCCATTTTGAACCAACAGATACCTCTGGAACACATCTTGGAGAGGTC 867
Db 209 ThrThrGluIleMetPheGluAspCysValValProAlaSerLysArgLeuGlyGluGlu 228
QY 868 GGAGATCGGTTTAAGTGGCCATGAACATCTCAACAGCGCGCGTTCAGCATGGGCGAGC 927
Db 229 GlyGluGlyPheLysIleAlaMetLysThrLeuAspGlyGlyArgAsnGlyIleAlaAla 248
QY 928 GTCGTGCTGGCTCTCAAGAGATTGATTGAATGACTGCTGAGTACGCTGCACAAAG 987
Db 249 GlnAlaValGlyIleAlaGlnGlyAlaLeuAspAlaAlaLeuGlnTyrAlaLysGluArg 268
QY 988 AACACAGTTTAAACAGAGCGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCACATG 1047
Db 269 LysGlnPheGlyLysSerIleAlaGluGlnGlnGlyIleAlaPheLysLeuAlaAspMet 288
QY 1048 GCTCAGAAGGCTTACGTATGAGAGATATGACCTACCTCAGCAGCGGATGCTGGACCAA 1107
Db 289 AlaThrMetIleGluAlaSerArgLeuThrTyr---GlnAlaAlaTrpLeuGluSer 307
QY 1108 CTTGGCTTTCCGACTGCTCCATCGAGGCGCCATGGTGAAGGTGTTTCAGCTCCGAGGCC 1167
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QY 1168 GCCTGGCGAGTGTGAGTGGCGCTGCAGATCTCGGGGCTTGGGCTACACAAAGGAC 1227
Db 327 AlaMetLysValThrThrGluAlaValGlnIlePheGlyGlyTyrGlyTyrThrLysAsp 346
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Db 347 TyrProValGluArgTyrMetArgAspAlaLysAlaIleThrGlnIleIleTyrGluGlyThrGln 366
QY 1288 GAGATTCTCCGGATGTACATCGCC 1311
Db 367 GluIleGlnArgLeuValIleSer 374
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Job time : 99.2291 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 2, 2005, 13:13:41 ; Search time 303.736 Seconds
(without alignments)
6281.796 Million cell updates/sec

Title: US-09-945-326-3

Perfect score: 3423

Sequence: 1 acagcggtggtgggtctt.....accctctgacaggaatgc 1863

Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=uniprot_QPWT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09945326 @CGN 1 1 861 @runat 02052005 135410 22353 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2704	79.0	625	ACD9 MOUSE	Q9h2n5 mus musculus
3	2526	73.8	498	Q9H9W4	Q9h9w4 homo sapien
4	2374.5	69.4	622	Q6DDF2	Q6dddf2 xenopus lae
5	1739	50.8	343	Q9BUK5	Q9bux5 homo sapien
6	1360.5	39.7	659	Q7T2C2	Q7t2c2 brachydanio
7	1360	39.7	656	ACDV MOUSE	P50544 mus musculus
8	1356.5	39.6	655	ACDV RAT	P45953 rattus norv
9	1345	39.3	655	ACDV BOVIN	P48818 bos taurus
10	1318	38.5	655	ACDV MACFA	Q9hxy7 macaca fasc
11	1308	38.2	655	1 ACDV HUMAN	P49748 homo sapien
12	1295.5	37.8	655	2 Q9V8T1	Q9v8t1 drosophila
13	1288	37.6	639	2 Q7Q868	Q7q868 anopheles g
14	1273.5	37.2	604	2 Q7Q870	Q7q870 anopheles g
15	1210.5	35.4	613	2 Q19057	Q19057 caenorhabdi
16	897.5	26.2	408	2 Q6AHQ5	Q6ahq5 caenorhabdi

17	895	26.1	589	2	Q67K07	Q67k07 symbiobacte
18	888.5	26.0	577	2	Q72K21	Q72k21 thermus the
19	845.5	24.7	594	2	Q631W4	Q631w4 bacillus ce
20	845.5	24.7	594	2	Q72Y79	Q72y79 bacillus ce
21	845.5	24.7	594	2	Q81XJ1	Q81xj1 bacillus an
22	845.5	24.7	594	2	Q6HBP9	Q6hbp9 bacillus th
23	845.5	24.7	600	2	Q815X2	Q815x2 bacillus ce
24	842.5	24.6	594	2	Q65F73	Q65f73 bacillus li
25	821	24.0	594	2	Q9K784	Q9k784 bacillus na
26	815.5	23.8	594	2	Q32176	Q32176 bacillus su
27	789.5	23.1	594	2	Q8ENT4	Q8ent4 oceanobacil
28	751.5	22.0	569	2	Q738L4	Q738l4 bacillus ce
29	750.5	21.9	569	2	Q81DR7	Q81dr7 bacillus ce
30	749	21.9	569	2	Q6HJ21	Q6hj21 bacillus th
31	745.5	21.8	569	2	Q63BL2	Q63bl2 bacillus ce
32	742	21.7	569	2	Q81QR7	Q81qr7 bacillus an
33	737.5	21.5	571	2	Q65IW9	Q65iw9 bacillus li
34	734	21.4	169	2	Q9CZC5	Q9czc5 mus musculu
35	728	21.3	642	2	Q742M4	Q742m4 mycobacteri
36	719.5	21.0	382	2	Q8EM49	Q8em49 oceanobacil
37	713	20.8	386	2	Q7PSM8	Q7psm8 fusobacteri
38	711	20.8	650	1	Y873 MYCTU	P63429 mycobacteri
39	711	20.8	650	1	Y897 MYCBO	P63430 mycobacteri
40	710	20.7	376	2	Q81JV7	Q81jv7 bacillus an
41	709.5	20.7	381	2	Q8R674	Q8r674 fusobacteri
42	709	20.7	158	2	Q7TSP3	Q7tsp3 rattus norv
43	705	20.6	376	2	Q72XA5	Q72xa5 bacillus ce
44	705	20.6	381	2	Q814S8	Q814s8 bacillus ce
45	704	20.6	376	2	Q6HAU1	Q6haul bacillus th

ALIGNMENTS

RESULT 1
ID ACD9 HUMAN STANDARD; PRT; 621 AA.
AC Q9H845; Q8WXX3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acyl-CoA dehydrogenase family member 9, mitochondrial precursor
DE (SC 1.3.99.-) (ACAD-9).
GN Name=ACAD9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY.
RC TISSUE=Dendritic cell;
RX MEDLINE=2246103; PubMed=12359260; DOI=10.1016/S0006-291X(02)02336-7;
RA Zhang J., Zhang W., Zou D., Chen G., Wan T., Zhang M., Cao X.;
RT "Cloning and functional characterization of ACAD-9, a novel member of
RT human acyl-CoA dehydrogenase family."
RL Biochem. Biophys. Res. Commun. 297:1033-1042(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuna M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Konai F., Hara R., Takeuchi K., Arita M.,
RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aoeuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,

781 GATAAATTAGCATTCGGGCTCCACACTTGAGTGTGAGTCCATTTTGAACACCCAGATA 840
Db AsplysLeuGlyIleArgGlySerAsnThrCysGluValHisPheGluAsnThrLysIle 280
841 CCTGTGAAAAACATCCCTTCGAGAGTCGAGATGGGTTTAAGGTGGCCATGAACATCCTC 900
Db ProValGluAsnIleLeuGlyValGlyAspGlyPheLysValAlaMetAsnIleLeu 300
901 AACAGCGCGCGTTCAGCATGGGCGGTCGTGGCTGGCTGCTCAAGAGATTGATTGAA 960
Db AsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeuIleGlu 320
961 ATGACTGCTAGTACGCTCCACAGAAACAGTTTAAACAGAGCTCAGTGAATTGGA 1020
Db MetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGluPheGly 340
1021 TTGATTTCAGAGAAATTTGCACTGATGGCTCAGAGGCTTACGTCATGGAGAGTATGACC 1080
Db LeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSerMetThr 360
1081 TACCTCACAGCAGGATGCTGGACCAACCTGGCTTTCCGACTGCTCCATCGAGGCGACC 1140
Db TyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGluAlaAla 380
1141 ATGCTGAGCTGTTACGCTCCGAGGCGCTGGCAGTGTGTGAGTGGCGCTGCAGATC 1200
Db MetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeuGlnIle 400
1201 CTCGGGGCTTGGCTACACAGGAGCTATCCGTACGAGCGCATCTGCTGCACACCCGC 1260
Db LeuGlyGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAspThrArg 420
1261 ATCCTCCTCATCTTCGAGGGAACCAATGAGATTCTCGGATGTACATCGCCCTGACGGGT 1320
Db IleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeuThrGly 440
1321 CTCAGATCCCGCGCATCTGACTACAGATCCATGATGATTAACAGGCGCAAGTG 1380
Db LeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAlaLysVal 460
1381 AGCACAGTCATGATACCGTTGCGGAGCTTCGGGACTCCCTGGGCGCAACTGTGGAC 1440
Db SerThrValMetAspThrValGlyArgGluArgAspSerLeuGlyArgThrValAsp 480
1441 CTGGGCTGACAGGCAACCATGAGTTGTGCACCCAGCTTCGGGACAGTGCACCAAG 1500
Db LeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAlaAsnLys 500
1501 TTTGAGGAGAACCTTACTGCTTCGGCGGACCGTGGAGACATGCTGCTCCGCTTGGC 1560
Db PheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuLeuArgPheGly 520
1561 AACACCATCATGAGGAGCAGCTGTACTCAAGCGGTGGCCAACTCCTCATCAACCTG 1620
Db LysThrIleMetGluGlnLeuValLeuLysArgValAlaAsnIleLeuIleAsnLeu 540
1621 TATGGCATGACGCGCTGCTGTCGCGGCGCAGCGCTCCATCCGCAATGGGCTCCGCAAC 1680
Db TyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeuArgAsn 560
1681 CAGACACAGAGTTCTTCTGGCCCAACACTTCTGGTGTGAAGCTTACTTGCAGATCTC 1740
Db HisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGlnAsnLeu 580
1741 TTCAGCTCTCTCAGCTGGCAGATGCTCCAGAAAACCTAGATGAGCAGATTAGAAA 1800
Db PheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIleLysLys 600
1801 GTGTCCAGCAGATCTCTTGAAGACGAGCGCTATATCTGTCCCAACCTCTGGACAGGACA 1860
Db ValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAspArgThr 620
1861 TGC 1863

Db 621 Cys 621

RESULT 2

ACD9_MOUSE STANDARD; PRT; 625 AA.
AC Q8JZK5; Q8BK76; Q8C0B5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acyl-CoA dehydrogenase family member 9, mitochondrial precursor
(EC 1.3.99.-) (ACAD-9).
GN Name:Acad9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Vagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanpin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bratt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayate N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Villalon D.K., Morzy D.M., Soder

QY 1309 GCCTGACGGTCTGCAGCATGCCGCCGCGCTGCTGACTACCGAGTCCATGAGCTTAAA 1368
 Db 441 AlaleuThrrGlyLeuGlnHisAlaGlyArgileLeuThrSerArgilLeuGlyLeuLys 460
 QY 1369 CAGCCAAAGTGCAGCAGTCATGATACCGTGGCCGGAGGCTTGGGACTCCCTGGGC 1428
 Db 461 SerGlyasnValThrrValMetGluThrIleGlyArgLysLeuArgSerLeuGly 480
 QY 1429 CGAAGTGTGGACCTGGGGCTGCAGAGCAACATGGAGTGTGTGCACCCAGCTTGGGAC 1488
 Db 481 ArgThrValAspLeuGlyLeuThrGlyAspLeuGlyValValHisProSerLeuGlyAsp 500
 QY 1489 AGTCCCAAGTTGAGGAGAACACCTACTGCTTGGCCGGACCGTGGAGACACTGCTG 1548
 Db 501 SerAlaAsnLysLeuGluGluAsnValHisTyPheGlyArgThrValGluThrLeu 520
 QY 1549 CTCGCTTTCGCAAGACCATCATGAGGAGCAGCTGTGTGAGCGGGTGGCCCAACATC 1608
 Db 521 LeuArgPheGlyLysAsnIleValGluGluGlnLeuValLeuLysArgValAlaAsnIle 540
 QY 1609 CTCATCAACCTGTATGTCATGACGGCGTCTGTGCGGGCCAGCCGCTCCATCCGCATT 1668
 Db 541 LeuIleasnLeuTyrglyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIle 560
 QY 1669 GGGCTCCGCAACCAACGACGAGGAGTCTTCTTGGCCCAACCTTCTGCGTGGAGCTTAC 1728
 Db 561 GlyLeuArgAsnHisAspHisGluValLeuLeuAlaAsnMetPheCysValGluAlaTy 580
 QY 1729 TTCGAGATCTTTCAGCTCTCTCAGCTGCAGACAGTATCTCCAGAAACCTAGATGAG 1788
 Db 581 PheGlnAsnLeuPheSerLeuSerGlnLeuAspLysAsnAlaProGluAsnLeuAspGlu 600
 QY 1789 CAGATTAAAGAAAGTGTCACAGATCTTTCAGAGAGCGAGCTATATCTTGCCACCCCT 1848
 Db 601 GlnIleLysLysValSerArgGlnIleLeuGluLysArgAlaTyrlleCysAlaHisPro 620
 QY 1849 CTGACGAGG 1857
 Db 621 LeuAspArg 623
 RESULT 3
 Q9H9W4
 ID Q9H9W4 PRELIMINARY; PRT; 498 AA.
 AC Q9H9W4
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ12506.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14702039; DOI=10.1038/ng1285;
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 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 CC -/- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
 EMBL; AK022568; BAB14104.1; -;
 DR HSSP; Q06319; 1BUC.
 DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006089; Acyl-CoA dh.
 DR InterPro; IPR006090; Acyl-CoA dh C.
 DR InterPro; IPR006091; Acyl-CoA dh M.
 DR InterPro; IPR006092; Acyl-CoA dh N.
 DR InterPro; IPR009075; AcylCoADH_C-like.
 DR InterPro; IPR009100; AcylCoA dehyd_NM.
 DR InterPro; IPR005829; Sug transporter.
 DR Pfam; PF00441; Acyl-CoA dh; 1.
 DR Pfam; PF02770; Acyl-CoA dh M; 1.
 DR Pfam; PF02771; Acyl-CoA dh N; 1.
 DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
 DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 KW FAD; Flavoprotein; Oxidoreductase.
 SQ SEQUENCE 498 AA; 55083 MW; A57B7121B8PB1310 CRC64;
 Alignment Scores:
 Pred. No.: 4,64e-162 Length: 498
 Score: 2526.00 Matches: 498
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 73.79% Indels: 0
 DB: 2 Gaps: 0
 US-09-945-326-3 (1-1863) x Q9H9W4 (1-498)
 QY 370 ATGTACTCAAGACTAGGAGAGATCATCAGCATGGTGGTCCATCATCTGACCCCTGGCA 429
 Db 1 MetTySerArgLeuGlyGluIleIleSerMetAspGlySerIleThrValThrLeuAla 20
 QY 430 GGCACACAGCTATTGGCTCAAGGGGATCATCTTGGCTGGCAGCTGAGGAGCAAGGCC 489
 Db 21 AlaHisGlnAlaIleGlyLeuLysGlyIleIleLeuAlaGlyThrGluGluLysAla 40
 QY 490 AANTACTTGCCTAACTGGTCCGGGAGCACCATTGCGAGCTTCTGCTCCAGGAGCCA 549
 Db 41 LysTyLeuProLysLeuAlaSerGlyGluHisIleAlaAlaPheCysLeuThrGluPro 60
 QY 550 GCCAGTGGGAGCGATGCAGCTCAATCCGAGCAGAGCCACACTAAGTGAAGCAACAAG 609
 Db 61 AlaSerGlySerAspAlaAlaSerIleIleArgSerArgAlaThrLeuSerGluAspLys 80
 QY 610 CACTACATCTCAATGGCTCCAAAGGTCTGGATTACTTAATGAGGAGCTGGCCAATATTTT 669
 Db 81 HisTyIleLeuAsnGlySerLysValTrpIleThrAsnGlyGlyLeuAlaAsnIlePhe 100
 QY 670 ACTGTGTTTGCAGAGTACGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 729
 Db 101 ThrValPheAlaLysThrGluValValAspSerAspGlySerValLysAspLysIleThr 120
 QY 730 GCATTCATAGTAGAAGAGACTTTTGGTGGAGTCACTAATGGGAAACCCGAGAGATAATTA 789
 Db 121 AlaPheIleValGluArgAspPheGlyGlyValThrAsnGlyLysProGluAspLysLeu 140

Percent Similarity: 85.41% Conservative: 74
 Best Local Similarity: 73.42% Mismatches: 87
 Query Match: 69.37% Indels: 3
 DB: 2 Gaps: 1

US-09-945-326-3 (1-1863) x Q6DDF2 (1-622)

QY 10 TGCGGGCTCTTCCTGCGCACACCGCTGCGGCTCGTGCCTGCCGGGTCTGTCTCT 69
 DB 8 CysGly-----ArgAlaAspLeuThrArgValTrpAlaGlyProAlaGlyPro 24
 QY 70 ACCCGAACCGCGCTACTCGCGCACACCGCTGTACGAGCTTCGCCAAGAGCTT 129
 DB 25 GluLeuPheProArgSerPheThrCysSerProHisArgLeuAlaLysGluLeu 44
 QY 130 TTCCTAGCGAAATCAAGAGAAAGAGTTTCCCATTTCCAGAAAGTTAGCCAGATGAA 189
 DB 45 PheLeuGlySerIleArgLysAspGluValPheProTyrProGluIleSerLysGluGlu 64
 QY 190 CTTAATGAATCAATCAGTTCTTGGGACCCGTGGAATAATTTCTCACTGAAGAGTGGAC 249
 DB 65 LeuGluGluIleAenGlnPheValAlaProValGluLysPhePheAenGluGluValAsp 84
 QY 250 TCCGAAATTTGACAGGAAGGAAATCCAGATCAATCTTGGAGAAATTCAGAGC 309
 DB 85 SerLysLeuIleAspGlnThrAlaLysIleProProGluThrLeuAspGlyLeuLysAen 104
 QY 310 CTAGGGCTTTTGGGCTCAAGTCCAGAGAAATATGTCGCTCGGCTCTTCCCAACACC 369
 DB 105 LeuGlyLeuPheGlyMetGlnIleProGluGluTyrGlyGlyLeuGlyLeuSerAenThr 124
 QY 370 ATGTACTCAAGACTAGGGAGATCATCAGCATGGATGGTCCATCACTGTGACCTGGCA 429
 DB 125 MetTyrAlaArgLeuGlyGluIleSerLeuAspGlyAlaIleAlaValThrLeuAla 144
 QY 430 GCGCACAGGCTATTGCGCTCAAGGGATCATCTTGGCTGCGACTGAGGAGCAGAGCC 489
 DB 145 AlaHisGlnAlaIleGlyLeuLysGlyIleLeuIleAlaGlyAenAspGluGlnLysAla 164
 QY 490 AATATCTTGTCTAACTGGCTCGGGGAGCACATTCAGCTTCTGCTCCCTCACGAGCCA 549
 DB 165 LysTyrLeuProLysLeuAlaSerGlyGlyIleAlaAlaPheCysLeuThrGluPro 184
 QY 550 GCCAGTGGGAGCGATGAGCTCAATCCGAGCAGAGCCACACTAAGTGAAGACAAGAAG 609
 DB 185 GlySerGlySerAspAlaAlaSerIleGlnSerArgAlaThrLeuThrProAspGlyLys 204
 QY 610 CACTACATCTCAATGCTCAAGTCTGAGTCTGAGTACTAATGAGGACTGGCCATATTTT 669
 DB 205 HisPheLeuLeuAenGlySerLysIleTrpIleSerAsnGlyGlyLeuAlaAspIlePhe 224
 QY 670 ACTGTGTTTCAAGACTGAGGCTGTTGATTCTGATCGATCAGTGAAGACAAATCACA 729
 DB 225 ThrValPheAlaArgThrGluValAlaLysAspGlyValThrLysAspLysIleSer 244
 QY 730 GCATTCATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGAAACCCGAGATTAATTA 789
 DB 245 AlaPheIleValGluArgAlaPheGlyGlyValThrHisGlyLysProGluAspLysLeu 264
 QY 790 GGCATTCGGGGCTCCACACTTGTGAAGTCAATTTGAAAACACCAAGATACCTGTGAA 849
 DB 265 GlyIleArgGlySerAenThrCysGluLeuHisPheGluAenThrLysValProValGlu 284
 QY 850 AACATCTCTGAGAGGTCGAGATGGGTGTTAAGTGGCCCATGAACATCTTCAACAGCGGC 909
 DB 285 AsnValIleGlyGluValGlyGlyGlyPheLysValAlaMetAenIleLeuAenSerGly 304
 QY 910 CGGTTACAGCATGGCAGCGCTGCTGGCTGGGCTGCTCAAGAGATTGATTGAATGACTGCT 969
 DB 305 ArgPheSerMetGlySerAlaSerAlaGlyIleIleLysLysLeuIleGluMetThrAla 324
 QY 970 GAGTACCGCTGCACAGGAAACAGTTTAAACAGAGGCTCAGTGAATTTGATTGATTTCAG 1029

Db 325 GluTyrAlaCysThrArgLysGlnPheAenLysLysLeuSerAspPheGlnLeuIleGln 344
 QY 1030 GAGAAATTTGCACCTGATGGCTCAGAAAGCTTACGTCTATGAGAGATATGACCTACCTCACA 1089
 Db 345 GluLysPheAlaLeuMetAlaGlnLysAlaPheValMetGluSerMetAlaTyrLeuThr 364
 QY 1090 GCAGGATGCTGACACCACTGCTTCCGACTGCTCCATCGAGGCGAGCATGCTGTAAG 1149
 Db 365 AlaGlyMetMetAspArgProGlyLeuProAspCysSerValGluAlaAlaMetValLys 384
 QY 1150 GTGTTCAAGTCCGAGCGCGCTGCGAGTGTGAGTGGAGCGCTGACAGATCTCTCGGGGC 1209
 Db 385 ValPheSerSerGluGlyAlaTrpLeuCysValSerGluAlaLeuGlnIleLeuGlyGly 404
 QY 1210 TTGGGCTACACAAGGAGCTATCCGTACGAGCGCATCTATCGCTGACACCCGCTCTCTCTC 1269
 Db 405 LeuGlyTyrMetLysAspTyrProTyrGluArgTyrLeuArgAspSerArgIleLeuLeu 424
 QY 1270 ATCTTCAGGGAACCAATGAGATCTCCGATGTACATCCGCTGACGGGTCTGCAGCAT 1329
 Db 425 IlePheGluGlyThrAenGluIleLeuArgMetTyrIleAlaLeuThrGlyMetGlnHis 444
 QY 1330 GCGCGCGCATCTGACTACAGCATCCATGAGCTTAAACAGGCCAAAGTGAGCACAGTC 1389
 Db 445 AlaGlyLysIleLeuThrGlyLysIleLysGluMetLysLysGlyAenValGlyValAla 464
 QY 1390 ATGATACCTTGGCGGAGGCTTCGGGACTCCCTGGGCGCAACTGTGGACCTGGGGCTG 1449
 Db 465 MetGluLeuPhePheLysLysLeuArgAspSerMetGlyArgAenValAenLeuGlyLeu 484
 QY 1450 ACAGGCACCATCGAGTTGTGACCCCGAGTCTTGGCGGACAGTGCACCAACAGTTTGAGAG 1509
 Db 485 ThrGlyAenGluGlyValValHisProSerLeuGluGluSerAlaLysLysLeuGluGlu 504
 QY 1510 AACACTTACTGCTTCGCGCGGACCGTGGAGACACTGCTGCTCGCTTGGCAAGACCATC 1569
 Db 505 AsnValTyrTyrPheGlyThrThrValGluSerLeuLeuTyrArgPheGlyLysIleThr 524
 QY 1570 ATGAGGAGCAGCTGGTACTGAAGCGGCTGGCCCAACATCTCATCACTGTATGGCATG 1629
 Db 525 ValGluGluGlnLeuAlaLeuLysArgValAlaAspValIleIleAenLeuTyrAlaMet 544
 QY 1630 ACGGCGTGTGTCGCGGCGGACCGCTCATCGCATTCGGCTTGGCTCCGACACCGACAC 1689
 Db 545 ThrAlaValIleSerArgAlaSerArgSerIleSerValGlyLeuProAenHisAspHis 564
 QY 1690 GAGTCTCTTGGCCCAACACCTTCTCGTGGAGCTTACTTGCAGATCTCTTCAGCCTC 1749
 Db 565 AspValLeuLeuAlaAenMetPheCysSerGluValTyrPheLysAenAenTyrThrLeu 584
 QY 1750 TCTCAGCTGGACAAGTATGCTCCAGAAACCTAGATGAGCAGAGATTAAAGAAAGTGTCCCAG 1809
 Db 585 AlaGlnLeuGlyLysHisSerProGluAenGlnAenAspSerIleArgLysIleAlaGly 604
 QY 1810 CAGATCTTGGAGGCGGAGCTTATCTGTGCCACCGCTCTGACAGGACACA 1860
 Db 605 HisIleLeuGluLysArgGlyTyrThrCysSerHisProLeuAenAspArgThr 621

RESULT 5
 Q9BUX5 PRELIMINARY; PRT; 343 AA.
 ID Q9BUX5; AC Q9BUX5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ACAD9 protein (Fragment).
 GN Name=ACAD9;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N. A.

RC TISSUE=Muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krywinski M.I., Skalska U., Smalish D.E., Schnrnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC001817; AAH01817.2; -;
 DR HSSP; P15651; 1UQ1.
 DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006089; Acyl-CoA dh.
 DR InterPro; IPR006090; Acyl-CoA dh C.
 DR InterPro; IPR009075; AcylCoA_DH_C-like.
 DR InterPro; IPR005829; Sug_transporter.
 DR Pfam; PF00441; Acyl-CoA dh; 1.
 DR PROSITE; PS00073; ACYL COA DH 2; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 FT NON TER 1 1
 SQ SEQUENCE 343 AA; 38569 MW; 10E1781937745C00 CRC64;
 Alignment Scores:
 Pred. No.: 6.39e-109 Length: 343
 Score: 1739.00 Matches: 343
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.80% Indels: 0
 DB: 2 Gaps: 0
 US-09-945-326-3 (1-1863) x Q9BUX5 (1-343)
 QY 835 AAGTACCTCTGGAACACATCTTGGAGAGTGGAGTGGTAAAGTGGCCATGAC 894
 DB 1 LysileProValGluAsnIleLeuGlyGluValGlyAspGlyPheLysValAlaMetAsn 20
 QY 895 ATCTCTCAACAGCGCGGTTTCAGCATGGGCGAGGCTGCTGGCTGGCTCAAGAGATTG 954
 DB 21 IleLeuAsnSerGlyArgPheSerMetGlySerValValAlaGlyLeuLeuLysArgLeu 40
 QY 955 ATTGAATGACTGCTGAGTACGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1014
 DB 41 IleGluMetThrAlaGluTyrAlaCysThrArgLysGlnPheAsnLysArgLeuSerGlu 60
 QY 1015 TTTGGATTGATTTCAGAGAAATTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
 DB 61 PheGlyLeuIleGlnGluLysPheAlaLeuMetAlaGlnLysAlaTyrValMetGluSer 80
 QY 1075 ATGACCTACCTCAGCAGGAGGAGTGGACCAACCTGGCTTTCCCGAGCTCTCCATCGAG 1134
 DB 81 MetThrTyrLeuThrAlaGlyMetLeuAspGlnProGlyPheProAspCysSerIleGlu 100
 QY 1135 GCAGCCATGGTGAAGGTGTTCAGCTCGGAGCGCGCTGGCAGTGTGTGAGTGAAGCGCTG 1194

DB 101 AlaAlaMetValLysValPheSerSerGluAlaAlaTrpGlnCysValSerGluAlaLeu 120
 QY 1195 CAGATCTCTGGGGCTTGGGCTACACAGGAGTATCCGTTACGAGCGCATCTCGGTGAC 1254
 DB 121 GlnIleLeuGlyLeuGlyTyrThrArgAspTyrProTyrGluArgIleLeuArgAsp 140
 QY 1255 ACCCGATCTCTCTCATCTTCAGAGGAGCAATAGATATCTCCGGATGTACATCGCCCTG 1314
 DB 141 ThrArgIleLeuLeuIlePheGluGlyThrAsnGluIleLeuArgMetTyrIleAlaLeu 160
 QY 1315 ACCGGCTCTGAGCATGCCCGCGCATCTCTGACTTACAGAGTATCCATGAGCTTAAACAGGCC 1374
 DB 161 ThrGlyLeuGlnHisAlaGlyArgIleLeuThrThrArgIleHisGluLeuLysGlnAla 180
 QY 1375 AAGTGAAGCAGTCTATGATACCTGGTGGCGGAGCTTCGGGACTCCCTGGCGCGCAACT 1434
 DB 181 LysValSerThrValMetAspThrValGlyArgLeuArgAspSerLeuGlyArgThr 200
 QY 1435 GTGACCTCGGGCTGACAGGCAACCATGAGTGTGCACCCAGTCTTCGGGACAGTGCC 1494
 DB 201 ValAspLeuGlyLeuThrGlyAsnHisGlyValValHisProSerLeuAlaAspSerAla 220
 QY 1495 AACAGCTTTGAGGAGAACACCTACTCTTCGGCGGAGCGCTGGAGACACTGTGCTCCCGC 1554
 DB 221 AsnLysPheGluGluAsnThrTyrCysPheGlyArgThrValGluThrLeuLeuArg 240
 QY 1555 TTTGGCAAGACCATCATGAGGAGGAGCTGTGACTGAAGCGGTGGCCACATCTCTCATC 1614
 DB 241 PheGlyLysThrIleMetGluGlnLeuValLeuLysArgValAlaAsnIleLeuIle 260
 QY 1615 AACCTATTGGATGACGCGCTGTCTCGCGGCGAGCGCTCCATCCGATTCGGCTCGGCTC 1674
 DB 261 AsnLeuTyrGlyMetThrAlaValLeuSerArgAlaSerArgSerIleArgIleGlyLeu 280
 QY 1675 CGAACACGACGACGAGGTTCTTTGGCCAAACACTCTCTGCTGGTGAAGCTTACTTGCAG 1734
 DB 281 ArgAsnHisAspHisGluValLeuLeuAlaAsnThrPheCysValGluAlaTyrLeuGln 300
 QY 1735 AATCTCTTCAGCTCTCTCAGCTGGACAGTATGCTCCAGAAACCTAGATGAGCAGATT 1794
 DB 301 AsnLeuPheSerLeuSerGlnLeuAspLysTyrAlaProGluAsnLeuAspGluGlnIle 320
 QY 1795 AAGAAAGTCTCCAGCAGATCTTTCAGAGCGAGCTATATCTGTGCCACCTCTCGGAC 1854
 DB 321 LysLysValSerGlnGlnIleLeuGluLysArgAlaTyrIleCysAlaHisProLeuAsp 340
 QY 1855 AGGACATGC 1863
 DB 341 ArgThrCys 343
 RESULT 6
 QY72C2 ID QY72C2 PRELIMINARY; PRT; 659 AA.
 AC QY72C2;
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Acyl-Coenzyme A dehydrogenase, very long chain.
 GN ORFNames=zgc:64067;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krywinski M.I., Skalska U., Smalish D.E., Schnrnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
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 DR ENBL; BC001817; AAH01817.2; -;
 DR HSSP; P15651; 1UQ1.
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 DR InterPro; IPR006090; Acyl-CoA dh C.
 DR InterPro; IPR009075; AcylCoA_DH_C-like.
 DR InterPro; IPR005829; Sug_transporter.
 DR Pfam; PF00441; Acyl-CoA dh; 1.
 DR PROSITE; PS00073; ACYL COA DH 2; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 FT NON TER 1 1
 SQ SEQUENCE 343 AA; 38569 MW; 10E1781937745C00 CRC64;

FT CONFLICT 567 567 Q -> K (in Ref. 5).
 FT CONFLICT 571 571 AD -> OG (in Ref. 5).
 FT CONFLICT 573 573 A -> P (in Ref. 5).
 FT CONFLICT 593 593 G -> A (in Ref. 5).
 FT CONFLICT 596 596 T -> A (in Ref. 5).
 FT CONFLICT 612 612 A -> P (in Ref. 5).
 FT CONFLICT 628 628 H -> Q (in Ref. 4).
 SQ SEQUENCE 656 AA; 70875 MW; A0110CA5C6CF4F89 CRC64;

Alignment Scores:
 Pred. No.: 3.41e-83 Length: 656
 Score: 1360.00 Matches: 287
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 Best Local Similarity: 48.24% Mismatches: 184
 Query Match: 39.73% Indels: 18
 DB: 1 Gaps: 9

US-09-945-326-3 (1-1863) x ACDV_MOUSE (1-656)

QY	103	CTGTGACGAGCT-----TTGCCAAAGAGCTTTTCTTAGGCAAAATCAAGAAG	150
DB	66	ProAlaArgAlaGluSerLysSerPheAlaValGlyMetPheLysGlyGlnLeuThrIle	85
QY	151	AAAGAAGTTTCCATTCCAGAGTT---AGCCAAGATGAACCTTAATGAATCAATCAG	207
DB	86	AspGlnValPheProTyrProSerValLeuSerGluGlnAlaGlnPheLeuLysGlu	105
QY	208	TTCTTGGGACCCGGGAAATTTCTTCACTGAAGAGGTGGAGTCCCGAAATAATTGACCAG	267
DB	106	LeuValGlyProValAlaArgPhePheGluGluValAsnAspProAlaLysAsnAspAla	125
QY	268	GAAGGAAATCCAGATGAATTTGGAGAAATTTGAAGACCTTAGGCTTTTGGCTG	327
DB	126	LeuGluLysValGluAspAspThrLeuGlnGlyLeuLysGluLeuGlyAlaPheGlyLeu	145
QY	328	CAAGTCCAGAAATATGTGGCTGGCTTCTCCAAACCATGTACTCAAGACTAGGG	387
DB	146	GlnValProSerGluLeuGlyGlyLeuGlyLeuSerAsnThrGlnTyrAlaArgLeuAla	165
QY	388	GAGATCATCAGCATG---GATGGTTCATCATCTGTGACCTTGGCAGCGCACCGCTATT	444
DB	166	GluLeuValGlyMetHisLeuPheLeuGlyValSerValThrLeuGlyAlaHisGlnSerIle	185
QY	445	GGCCTCAAGGGGATCATCTTGGCTGGCAGCTGAGGAGCAGAAAGCAATACTTCCCTAAA	504
DB	186	GlyPheLysGlyIleLeuLeuTyrGlyThrLysAlaGlnArgGluLysTyrLeuProArg	205
QY	505	CTGGCTCCGGGAGCAGATCTGAGCTTCTGCTCCAGGAGCCAGCCAGTGGAGCGAT	564
DB	206	ValAlaSerGlyGlnAlaLeuAlaPheCysLeuThrGluProSerSerGlySerAsp	225
QY	565	GCACCTCAATCCGGAGCAGACCCACACTAAGTCAAGACAAGACGACTACATCCTCAAT	624
DB	226	ValAlaSerIleArgSerAlaIleProSerProCysGlyLysTyrThrLeuAsn	245
QY	625	GGCTCCAGGTCTGGATTACTTAATGAGGAGCTGGCCCAATATTTTACTGTGTTCGAAAG	684
DB	246	GlySerLysIleTrpIleSerAsnGlyLeuAlaAspIlePheThrValPheAlaLys	265
QY	685	ACTGAGTCTGTGAT---TCTGATGATCAGTGAAGACAACAAATACAGCATTCATAGTA	741
DB	266	ThrProIleLysAspAlaAlaThrGlyAlaValLysGluLysGluIleThrAlaPheValVal	285
QY	742	GAAGAAGACTTTGTGGAGTCACTAATGGGAAACCCGAAAGATAAATTAGGCATTTCGGGGC	801
DB	286	GluArgSerPheGlyGlyValThrHisGlyLeuProGluLysLysMetGlyIleLysAla	305
QY	802	TCCAACACTTGTGAAGTCCATTTTGAACACACCAAGATACCTGTGGAAACATCTCTTGA	861
DB	306	SerAsnThrSerGluValTyrPheAspGlyValLysValProSerGluAsnValLeuGly	325
QY	862	GAGTCCGAGATGGGTTTAAAGTGGCCATGACATCTCTCAACAGCGCGGCTTCAGCATG	921

DB	326	GluValGlyAspGlyPheLysValAlaValAsnIleLeuAsnAsnGlyArgPheGlyMet	345
QY	922	GGCAGCTCGTGGCTGGGCTGCTCAAGAGATTTGATTGAAATGACTGCTGACTACGCTGC	981
DB	346	AlaAlaThrLeuAlaGlyThrMetLysSerLeuIleAlaLysAlaValAspHisAlaThr	365
QY	982	ACAAGGAACAGTTTAAACAAGAGCTCAGTGAATTTGGATTGATTCAGGAGAAATTTGCA	1041
DB	366	AsnArgThrGlnPheGlyAspLysIleHisAsnPheGlyValIleGlnGluLysLeuAla	385
QY	1042	CTGATGGCTCAGAAGGCTTACGTCATGAGAGATGATGACCTACCTCAGACAGGAGTGTG	1101
DB	386	ArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaTyrMetLeuSerAlaAsnMet	405
QY	1102	GACCAACTGGCTTTCCCGACTGCTCCATCGAGCAGCCATCGTGAAGGTGTTTCACTCC	1161
DB	406	AspGln---GlyPheLysAspPheGlnIleGluAlaAlaIleSerLysIlePheCysSer	424
QY	1162	GAGCCGCTGGCAGGTGTGTGAGTGAGGCGCTGCAGATCTCTCGGGGCTTGGGTACACA	1221
DB	425	GluAlaAlaTrpLysValAlaAspGluCysIleGlnIleMetGlyGlyMetGlyPheMet	444
QY	1222	AGGACTATCCGTACGAGCGCATCTCGCTGACACCCGCTCTCTCTCTCTCTCTCTCTCT	1281
DB	445	LysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePheGluGly	464
QY	1282	ACCAATGAGATTTCTCCGATGTATCGCTCTGACGGGTCTGACAGCATCGCGCCGATC	1341
DB	465	AlaAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysGlyLysGlu	484
QY	1342	CTGACTACAGGATCCATGAGCTTAAACAG-----GCCAAGTGAGCAGCAGTATGAT	1395
DB	485	LeuThrGlyLeuGlyAsnAlaLeuLysAsnProPheGlyAsnValGlyLeuLeuMetGly	504
QY	1396	ACGTTTGGCGGAGGCTTGGGAGCTCCCTGGCGCGAAGCTGTGGACCTGGGGCTCACAGG	1455
DB	505	GluAlaGlySerGlnLeuArgArgThrGlyIleGlySerGlyLeuSerLeuSer---	523
QY	1456	AACCATGAGATTGTGCACCCCGAGCTTTGGCGGAGCTGCCAACCAAGTTTGGAGGAGAAC	1515
DB	524	-----GlyIleValHisProGluLeuSerArgSerGlyGluLeuAlaValGlnAlaLeu	541
QY	1516	TACTGTTCCGGCGGACCGTGGAGACACTGCTGCTCGCTTGGCAAGACCATCATGGAG	1575
DB	542	AspGlnPheAlaThrValValGluAlaLysLeuValLysHisLysLysGlyIleValAsn	561
QY	1576	GAGCAGCTGTACTGAAGCGGTGGCCAACTCTCATCACTCACTGATGGATGGATGATGAT	1635
DB	562	GluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeuLysAlaMetValVal	581
QY	1636	GTGCTGTGCGGGCGGACCGCTCCATCCGATTTGGGCTCCGCAACACGACCGAGGTT	1695
DB	582	ValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHisGluLys	601
QY	1696	CTCTTGCCCAACACTTCTCGTGGAGCT-----TACTTGCAGATCTCTTACG	1746
DB	602	MetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMetAlaSer	621
QY	1747	CTCTCTCAGCTGGCAGATGATGCTCCAGAAAACCTAGATGAGCAGATTAAAGAAATGTCC	1806
DB	622	GlnSerSerProGlnHis-----GlnGluLeuPheArgAsnPheArgSerIleSer	639
QY	1807	CAGCAGATCTCTGAGAGCGAGCGCTATATCTGTGCCCCACCTCTG	1851
DB	640	LysAlaMetValGluAsnGlyGlyLeuValThrGlyAsnProLeu	654

RESULT 8

ACDV RAT

ID ACDV RAT

PRT; 655 AA.

AC P45953;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)


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Db      384 AlaArgMetAlaIleLeuGlnTyrValThrGluSerMetAlaIleValThrGluSerAlaAsn 403
Qy      1099 CTGACCAACCTGGCTTTCCGAGTGTGAGTGAGCGCGTGCAGATCTCTCGGGGCTGGGTAC 1218
Db      404 MetAspGln---GlyPheLysAspPheGlnIleGluAlaIleSerLysIlePheGly 422
Qy      1159 TCCAGAGCCCGCTGGCAGTGTGAGTGAGCGCGTGCAGATCTCTCGGGGCTGGGTAC 1218
Db      423 SerGluAlaIleTrpLysValThrAspGluCysIleGlnIleMetGlyGlyMetGlyPhe 442
Qy      1219 ACAAGGACTATCGTACGAGCGCATCTCGTGACACCGCGCATCTCTCTCATCTTCGAG 1278
Db      443 MetLysGluProGlyValGluArgValLeuArgAspIleArgIlePheArgIlePheGlu 462
Qy      1279 GGAACCAATGAGATCTCCGAGTGTATACATCGCTCGAGCGGTCTGACGATCGCGCGCGC 1338
Db      463 GlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMetAspLysGlyLys 482
Qy      1339 ATCTGACTACAGGATCCATGAGCTTAAACAG-----GCCAAGTGAGACACAGTCATG 1392
Db      483 GluLeuThrGlyLeuGlyAsnAlaLeuLysAsnProLeuGlyAsnValGlyLeuLeuIle 502
Qy      1393 GATACCGTTGGCGGAGCGCTTCGGAGTCTCCGTGGCGGAACCTGGACCTGGCGGCTGACA 1452
Db      503 GlyGluAlaSerLysGlnLeuArgArgThrGlyIleGlySerGlyLeuSerLeuSer 522
Qy      1453 GGCAACCATCGAGTGTGACCCCGAGTCTTGGGACAGTGCCACAAAGTTTGAGGAGAAC 1512
Db      523 -----GlyIleValHisProGluLeuSerArgSerGlyGluLeuAlaValGlnAla 539
Qy      1513 ACCTACTGCTTGGCGCGGACCGTGGAGACACTGTCTGCTCGCGCTTTGGCAAGACCATCATG 1572
Db      540 LeuGluGlnPheAlaThrValValGluAlaLysLeuMetLysHisLysLysGlyIleVal 559
Qy      1573 GAGGACAGCTGTGACTGAAGCGGTGGCAACATCTCTCATCACTGTATGATGATGATGATG 1632
Db      560 AsnGluGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeuTyAlaMetVal 579
Qy      1633 CGCGTGTCTGCGGGGCGGACCGCTCCATCGCATCGGCTCGCGTCCGCAACACGACACGAG 1692
Db      580 ValValLeuSerArgAlaSerArgSerLeuSerGluGlyTyrProThrAlaGlnHisGlu 599
Qy      1693 GTTCTCTTGCCCAACACTCTCTGCTGGTGAAGCT-----TACTTGCAGATCTCTCTTC 1743
Db      600 LysMetLeuCysAspSerTrpCysIleGluAlaAlaThrArgIleArgGluAsnMetAla 619
Qy      1744 AGCTCTCTCAGCTGGGACAAAGTATGTCTCCAGAAACCTAGATGACGAGATTAGAAAGTG 1803
Db      620 SerLeuGlnSerAsnProGln-----GlnGlnGluLeuPheArgAsnPheArgSerIle 637
Qy      1804 TCCAGCAGATCTTGGAGAGCGAGCTATATCTGTGCCACCTCTG 1851
Db      638 SerLysAlaMetValGluAsnGlyLeuValThrSerAsnProLeu 653

RESULT 9
ACDV_BOVIN
ID ACDV_BOVIN STANDARD; PRT; 655 AA.
AC P48818;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE precursor (EC 1.3.99.-) (VLCAD).
GN Name=ACADVL; Synonyms=VLCAD;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;

```

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RA Zhang X., Liu W., Zhu H., Sun X.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Active toward esters of long-chain and very-long chain
CC fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC ETF.
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC of different substrate specificities are present in mammalian
CC tissues.
CC -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC
CC -----
CC EMBL; U30817; AAA74051.1; --
CC HSSP; Q06319; IBUC.
CC InterPro; IPR006089; Acyl-CoA dh.
CC InterPro; IPR006090; Acyl-CoA dh C.
CC InterPro; IPR006091; Acyl-CoA dh M.
CC InterPro; IPR006092; Acyl-CoA dh N.
CC InterPro; IPR009100; AcylCoA dehyd_NM.
CC InterPro; IPR009075; AcylCoADH_C_like.
CC Pfam; PF00441; Acyl-CoA dh; 1.
CC Pfam; PF02770; Acyl-CoA dh N; 1.
CC Pfam; PF02771; Acyl-CoA dh N; 1.
CC PROSITE; PS00072; ACYL_COA_DH_1; 1.
CC PROSITE; PS00073; ACYL_COA_DH_2; 1.
CC FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
CC Oxidoreductase; Transit peptide.
CC FT TRANSIT 1 40 Mitochondrion (By similarity).
CC CHAIN 41 655 Acyl-CoA dehydrogenase, very-long-chain
CC specific.
CC FT DOMAIN 41 482 Catalytic.
CC SQ SEQUENCE 655 AA; 70520 MW; F9DC06285023CFC0 CRC64;
Alignment Scores:
Pred. No.: 3 52e-82 Length: 655
Score: 1345.00 Matches: 285
Percent Similarity: 65.51% Conservative: 110
Best Local Similarity: 47.26% Mismatches: 194
Query Match: 39.29% Indels: 14
DB: 1 Gaps: 9
US-09-945-326-3 (1-1863) x ACDV_BOVIN (1-655)
Qy 67 TCTACCGCGAAGCGCGCTACTCGCACCGACGCGCGCTGTACGAGCTTCCGCAAGAG 126
Db 57 SerGluAlaSerThrArgGluLysArgAlaAsnSerValSerLysSerPheAlaValGly 76
Qy 127 CTTTCTCTAGGCAAAATCAAGAGAAGAAGTTTCCATTTCCAGAGTT--AGCCAA 183
Db 77 ThrPheLysGlyGlnLeuThrThrAspGlnValPheProTyrProSerValLeuAsnGlu 96
Qy 184 GATGAATTAATGAATCAATCATAGTTCTTGGGACCGCTGGGAAATTTCTTCACTGAAGAG 243
Db 97 AspGlnThrGlnPheLeuLysGluLeuValGlyProValThrArgPheGluGluVal 116
Qy 244 GTGACTCCCGAAAAATTGACAGGAGGAGAAATCCAGATGAAATTTGGAGAAATG 303
Db 117 AsnAspAlaAlaLysAsnAspMetLeuGluArgValGluGluThrThrMetGlnGlyLeu 136
Qy 304 AAGAGCCTAGGCGCTTTTGGGCTGCAAGTCCGAGAGAATATGTCGCTGGGCTTCTCC 363

```

Db 137 LysGluLeuGlyAlaPheGlyLeuGlnValProAsnGluLeuGlyValGlyLeuCys 156
Qy 364 AACACATGTAAGTCAAGACTAGGGAGATCATCAGCATG--GATGGTCCATCACTGTG 420
Db 157 AsnThrGlnTyrAlaArgLeuValGluValGlyMetTyrAspLeuGlyValGlyLeu 176
Qy 421 ACCCTGGCAGCGACCAAGGCTATTGGCTCAAGGGGATCATCTTGGCTGCACCTGAGGAG 480
Db 177 ValLeuGlyAlaHisGlnSerIleGlyPheLysGlyLeuLeuPheGlyThrLysAla 196
Qy 481 CAGAAAGCCAAATCTTGGCTAACTGGCTCGGGAGACACATTCAGAGCTTCTGCCTC 540
Db 197 GlnLysGluLysTyrLeuProLysLeuAlaSerGlyGluThrIleAlaAlaPheCysLeu 216
Qy 541 ACGGAGCCAGCGAGCGAGTGCAGCTCAATCCGAGGAGAGCCACACTAAGTGAA 600
Db 217 ThrGluProSerGlySerAspAlaAlaSerIleArgSerSerAlaValProSerPro 236
Qy 601 GACAAGAACATCATCTCAATGGCTCAAGGCTCTGGATTACTAATGAGGAGCTGGCC 660
Db 237 CysGlyLysTyrThrLeuAsnGlySerLysIleTyrIleSerAsnGlyGlyLeuAla 256
Qy 661 AATATTTTACTGTGTTGCAAGACTGAGCTCGTTGAT---TCTGATGGATCAGTGAA 717
Db 257 AspIlePheThrValPheAlaLysThrProValThrAspThrAlaThrGlyAlaValLys 276
Qy 718 GACAAATACAGCATTCATAGTAGAAGAGACTTTGGTGGAGTCACTAATGGAAACCC 777
Db 277 GluLysIleThrAlaPheValGluArgSerPheGlyValThrHisGlyProPro 296
Qy 778 GAAGATAAATTAGGCATTCGGGGCTCAACACTTGTGAAGTCCATTTTGAACACCAAG 837
Db 297 GluLysLysMetGlyIleLysAlaSerAsnThrAlaGluValTyrPheAspGlyValArg 316
Qy 838 ATACCTGTGAAGAACATCTTGGAGAGCTGGAGATGGGTTAAGTGGCCATGAACATC 897
Db 317 ValProAlaGluAsnValLeuGlyGluValGlyGlyPheLysValAlaMetHisIle 336
Qy 898 CTCACAGCGCGCGGTTCAGCATGGGAGCGGTCTGGCTGGGTCTCAAGAGATGATT 957
Db 337 LeuAsnGlnArgPheGlyMetAlaAlaLeuAlaGlyThrMetLysGlyIleIle 356
Qy 958 GAAATGACTGCTGAGTAGCGCTGCACAGGAACAGTTTAAACAGAGGCTCAGTGAATTT 1017
Db 357 AlaLysAlaValAspHisAlaAlaAsnArgThrGlnPheGlyGluLysIleHisAsnPhe 376
Qy 1018 GCATTGATTCAGGAAATTTGCACTGATCGCTCAGAGGCTTACGTCATGGAGAGCTATG 1077
Db 377 GlyLeuIleGlnGluLysLeuAlaArgMetAlaMetLeuGlnTyrValThrGluSerMet 396
Qy 1078 ACCTACCTCAGCAGGAGTCTGGACCAACCTGGCTTTCCGACTGCTCCATCGAGGCA 1137
Db 397 AlaTyrMetValSerAlaAsnMetAspGln---GlySerThrAspPheGlnIleGluAla 415
Qy 1138 GCCATGTGAAGGTGTTTCACTCCGAGCGCGCTGGCAGTGTGTGAGTAGGCGCTGCAG 1197
Db 416 AlaIleSerLysIlePheGlySerGluAlaAlaTyrLysValThrAspGluCysIleGln 435
Qy 1198 ATCTCTGGGGCTGGGCTACACAGGAGCTATCCGTACGAGCGCATCTCGCTGACACC 1257
Db 436 IleMetGlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeu 455
Qy 1258 CGCATCTCTCATCTTCGAGGGAACCAATGAGATTCTCCGGATGTACATCGCCCTCAGC 1317
Db 456 ArgIlePheArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGln 475
Qy 1318 GGTCTGACAGTCCGCGCGCATCTCTGACTACAGGATCCATGAGCTTAACAG----- 1371
Db 476 GlyCysMetAspLysGlyLysGluLeuSerGlyLeuGlyAsnAlaLeuLysAsnProPhe 495
Qy 1372 GCCAAAGTGACACATCATCGTTGGCGGAGGCTTGGGACTCCCTGGGCGGA 1431
Db 496 GlyAsnAlaGlyLeuLeuGlyGluAlaGlyLysGlnLeuArgArgAlaGlyLeu 515

Qy 1432 ACTGTGGACCTGGGCTGACAGGCAACCATGAGTGTGCACCCAGTCTTGGGACAGT 1491
Db 516 GlySerGlyLeuSerLeuSer-----GlyIleValHisGlnGluLeuSerArgSer 532
Qy 1492 GCCAACAGTTTGGAGAGAACACCTACTCTTGGCGCGGACCGTGGAGACACTGCTGCTC 1551
Db 533 GlyGluLeuAlaValGlnAlaLeuGluGlnPheAlaThrValValGluAlaLysLeuIle 552
Qy 1552 CGCTTTGGCAAGACCATCATGAGGAGCAGCTGTACTGAAGCGGTGGCCACATCCTC 1611
Db 553 LysHisLysLysAspIleIleAsnGluGlnPheLeuLeuGlnArgLeuAlaAspSerAla 572
Qy 1612 ATCAACCTGTATGGCAGCGCGCTGTCTCGCGGCGCAGCGCTCCATCCGCACTGGG 1671
Db 573 IleAspLeuTyrAlaMetValValLeuSerArgAlaSerArgSerLeuSerGluGly 592
Qy 1672 CTCGCGAACACGACGACGAGGTCTCTTGGCCACACACTTCTGCTGGAGCT----- 1725
Db 593 HisProThrAlaGlnHisGluLysMetLeuCysAspSerTyrCysIleGluAlaAla 612
Qy 1726 ---TACTTCAGAACTCTCTCAGCTCTCTCAGCTGGCAAGTATGCTCCAGAAAACCTA 1782
Db 613 ArgIleArgGluAsnMetThrAlaLeu---GlnSerAspProGlnGlnGlnGlu---Leu 630
Qy 1783 GATGACGACATTAAAGTAAGTCTCCAGCAGATCTTTGAGAGCGAGCCTATATCTGTGCC 1842
Db 631 PheArgAsnPhelySerIleSerLysAlaLeuValGluArgGlyGlyValValThrSer 650
Qy 1843 CACCCTCTG 1851
Db 651 AsnProLeu 653
RESULT 10
ACDV_MACFA STANDARD; PRT; 655 AA.
ID Q8HX17;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE precursor (EC 1.3.99.-) (VLCAD) (QcCE-11706).
DE Name=ACADVL; Synonyms=VLCAD;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex.
RA Kusuda J., Osada N., Hida M., Sugano S., Hashimoto K.;
RT "Isolation and characterization of cDNA for macaque neurological
RT disease genes";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Active toward esters of long-chain and very-long chain
CC fatty acids such as palmitoyl-CoA and stearoyl-CoA (By
CC similarity).
CC -! CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
CC ETF
CC -! COFACTOR: FAD.
CC -! PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC step.
CC -! SUBUNIT: Homodimer (By similarity).
CC -! SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -! MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC of different substrate specificities are present in mammalian
CC tissues.
CC -! SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC
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CC EMBL; AB083302; BAC20581.1; --
 DR HSSP; Q06319; 18UC.
 DR InterPro; IPR006089; Acyl-CoA dh.
 DR InterPro; IPR006090; Acyl-CoA dh. C.
 DR InterPro; IPR006091; Acyl-CoA dh. M.
 DR InterPro; IPR006092; Acyl-CoA dh. N.
 DR InterPro; IPR009100; Acyl-CoA dehyd. NM.
 DR InterPro; IPR009075; AcylCoADH_C-like.
 DR Pfam; PF00441; Acyl-CoA dh; 1.
 DR Pfam; PF02770; Acyl-CoA dh M; 1.
 DR Pfam; PF02771; Acyl-CoA dh N; 1.
 DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
 DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
 KW FAD; Fatty acid metabolism; Flavoprotein; Mitochondrion;
 KW Oxidoreductase; Transist peptide.
 FT TRANSIT 1 40 Mitochondrion (By similarity).
 FT CHAIN 41 655 Acyl-CoA dehydrogenase, very-long-chain
 specific.
 FT DOMAIN 41 482 Catalytic.
 SQ SEQUENCE 655 AA; 70443 MW; DCC7AA898EFCB333 CRC64;
 Alignment Scores:
 Pred. No.: 2.35e-80 Length: 655
 Score: 1318.00 Matches: 280
 Percent Similarity: 64.72% Conservative: 107
 Best Local Similarity: 46.82% Mismatches: 197
 Query Match: 38.50% Indels: 14
 DB: 1 Gaps: 8
 US-09-945-326-3 (1-1863) x ACVD_MACFA (1-655)
 QY 88 CTGGCCACGACCGCGCTGTACGAGCT-----TTGCGCAAGAGCTTTTCCTA 135
 Db LeuAsnLysAlaLysProAlaLysAlaGluSerLysSerPheAlaValAlaMetPheLys 79
 QY 136 GGCNAATCAAGAAGAAGAGTTTCCATTTCACAGTT---AGCCAGATGAACCT 192
 Db GlyGlnLeuThrAspGlnValPheProTyrProSerValLeuAsnGlnGluThr 99
 QY 193 AATCAATCAATGATCTTGGGACCGTGGCAAAATTTCTTCACTGAAGAGGTGGACTCC 252
 Db GluPheLeuLysGluLeuValGluProValSerArgPheGluValAlaAsnAspPro 119
 QY 253 CGAAATATTCACGAGGAGGAAATCCAGATGAAATTTGGAGAAATTTGAAGAGCTTA 312
 Db AlaLysAsnAspThrLeuGluMetValGluThrThrLeuGlnGlyLeuLysGluLeu 139
 QY 313 GGGCTTTTGGCTGAAGTCCCGAAGAATATGTTGGCTGGCTCTCTCCACACCATG 372
 Db GlyAlaPheGlyLeuGlnValProSerGlyLeuGlyValGlyLeuGlyAsnThrGln 159
 QY 373 TACTCAAGATAGGGAGATCATCAGCATG---GATGGTCCATCATCTGACCTGGCA 429
 Db TyrAlaArgLeuValGluLeuValGlyMetHisAspLeuAlaValGlyIleThrLeuGly 179
 QY 430 GCGCACGAGCTATTGGCTCAAGGGGATCATCTTGGCTGGCATGAGGAGCAGAAAGCC 489
 Db AlaHisGlnSerIleGlyPheLysGlyIleLeuLeuPheGlyThrLysAlaGlnLysGlu 199
 QY 490 AATATCTTGCCTAACTGGGCTCGGGGAGCACAATTGACGCTTCTGCTCAGCGAGCCA 549
 Db LysTyrLeuProLysLeuAlaSerGlyGluThrLeuAlaAlaPheCysLeuThrGluPro 219
 QY 550 GCAGTGGGAGCGATGAGCTCAATCCGAGGAGGAGCCACACTAGTGAAGACAGAAG 609
 Db SerSerGlySerAspAlaAlaSerIleArgThrSerAlaValProSerProCysGlyLys 239
 QY 610 CACTACATCTCAATGGCTCCAAGGTCTGGATTACTAATGAGGAGCTGGCCATATTTT 659

Db TyrTyrThrLeuAsnGlySerLysLeuThrPheSerAsnGlyGlyLeuAlaAspPhe 259
 QY 670 ACTGTGTTTCCAAAGACTGAGGTCTGTGAT---TCTGATGCTCAGTGAAGACAAAATC 726
 Db ThrValPheAlaLysThrProValThrAspProAlaThrGlyAlaValLysGluLys 279
 QY 727 ACAGCATTCATAGTAAAGAGACTTTGGTGGAGTCACTAATGGGAACCCGAAGATAAA 786
 Db ThrAlaPheValValGluAlaGlyPheGlyGlyValThrHisGlyProGluLysLys 299
 QY 787 TTAGGCATTCGGGCTCCACACTTGTGAAGTCCATTTCGAAACACCAAGATACCTGTG 846
 Db MetGlyLysLysAlaSerAsnThrAlaGluValLeuPheAspGlyValArgValProSer 319
 QY 847 GAAACATCTTCGAGAGGTCCGAGATGGGTTAAAGTGGCCATGAACATCTCTCAACAG 906
 Db GluAsnValLeuGlyGluValGlySerGlyPheLysValAlaMetHisLysLeuAsn 339
 QY 907 GCGCGTTTACGATGGGACGCGTGGTGGCTGCTCAAGAGATTGATTGAAATGACT 966
 Db GlyArgPheGlyMetAlaAlaLeuAlaGlyThrMetArgGlyIleIleThrLysAla 359
 QY 967 GCTGAGTACGCTGCACAGGAAACAGTTTAAACAGAGGCTCAGTGAATTTGATTGATT 1026
 Db ValAspTyrAlaThrAsnArgIleGlnPheGlyGluLysIleHisAsnPheGlyLeu 379
 QY 1027 CAGGAGAAATTTGCACTGATGGCTCAGAGGCTTACGTCTCAGAGAGTATGACTTCTC 1086
 Db GlnGluLysLeuAlaArgMetValMetLeuGlnTyrValThrGluSerMetAlaTyrMet 399
 QY 1087 ACAGCAGGATGCTGGACCAACCTGGCTTTCCGACTGTCTCCAGCTCAGGAGGAGGAT 1146
 Db ValSerAlaAsnMetAspGln---GlySerThrAspPheGlnIleGluAlaAlaSer 418
 QY 1147 AGGTGTTTACGCTCCAGGCGCGCTGCGAGTGTGTGAGTGAGGCGGTGAGAGTCTCTGG 1206
 Db LysIlePheGlySerGluAlaAlaThrLysValThrAspGluCysIleGlnIleMetGly 438
 QY 1207 GCGTTCGGCTACACAGGAGCTATCCGTACGAGCGCTACTCGTGACACCCCATCCTC 1266
 Db GlyMetGlyPheMetLysGluProGlyValGluArgValLeuArgAspLeuArgLys 458
 QY 1267 CTCTATCTTCAGGAGAACCAATGAGATTCTCCGATGTATCATCCGCTCAGCGGTCTGCG 1326
 Db ArgIlePheGluGlyThrAsnAspIleLeuArgLeuPheValAlaLeuGlnGlyCysMet 478
 QY 1327 CATGCCGCGCATCTGACTACAGGATCCATGAGCTTAAACAG-----GCCAAGTG 1380
 Db AspLysGlyLysGluLeuSerGlyLeuGlySerAlaLeuLysAsnProPheGlyAsnAla 498
 QY 1381 AGCACAGTATGATACCTTGGCGGAGGCTTGGGAGCTCCCTGGGCGGCACTGTGGAC 1440
 Db GlyLeuLeuGlyGlyGluAlaGlyLysGlnLeuArgArgAlaGlyLeuGlySerGly 518
 QY 1441 CTGGGCTCAGCAGGCAACCATGAGTTGTGCACCCAGTCTTCGCGACAGTGCACCAAG 1500
 Db LeuSerLeuSer-----GlyIleValHisProGluLeuSerArgSerGlyGluLeu 535
 QY 1501 TTGAGGAGAACACCTTACTGCTTCCGCGGAGCGTGTGAGACACTGTGCTCCGCTTGGC 1560
 Db AlaValGlnAlaLeuGlnPheAlaThrValValGluAlaLysLeuLysHisLys 555
 QY 1561 AGACCATCATGGAGGAGGAGTGTGACTGAAGCGGTGGCCAACTCTCATCAACCTG 1620
 Db LysGlyIleValAsnGlnPheLeuLeuGlnArgLeuAlaAspGlyAlaIleAspLeu 575
 QY 1621 TATGGCATCAGCGCTGTGCGGGGCGAGCCGCTCCATCCGATTCGCTGGCTCCGCAAC 1680
 Db TyrAlaMetValValLeuSerArgAlaSerArgSerLeuSerGluGlyHisHisThr 595
 QY 1681 CAGCACGAGGTTCTCTTGGCCCAACACTTCTGCTGCTGGAAGCTTACTTGCAGAACTCT 1740

Db 596 AlaGlnHisGluLysMetLeuCyAspThrTyrCysIleGluAlaAlaAlaArgIleArg 615
Qy 1741 TTCAGCTCTCTCAGCTGGGCAAGTAGTGTCTCCAGAAAC---CTAGTAGGACAGATAAG 1797
Db 616 GluGlyMetAlaAlaLeuGlnSerAspProArgGlnHisGluLeuTyrArgAenPheLys 635
Qy 1798 AAAGTGTCCAGCAGATCTCTTGAGAGCGAGCTATATCTGTGCCACCTCTCG 1851
Db 636 SerIleSerLysAlaLeuValGluArgGlyGlyValThrAsnAenProLeu 653
RESULT 11
ACDV HUMAN STANDARD; PRT; 655 AA.
ID ACDV HUMAN STANDARD; PRT; 655 AA.
AC P49748; O76056; Q8WU0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial
DE precursor (EC 1.3.99.-) (VLCAD).
GN Name=ACADVL; Synonyms=VLCAD;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95397809; PubMed=7668252;
RA Aoyama T., Souiri M., Ueno I., Kamiyo T., Yamaguchi S., Rhead W.J.,
Tanaka K., Hashimoto T.;
RT "Cloning of human very-long-chain acyl-coenzyme A dehydrogenase and
molecular characterization of its deficiency in two patients.";
RL Am. J. Hum. Genet. 57:273-283(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND VARIANTS.
RC TISSUE=Placenta;
RX MEDLINE=96254975; PubMed=8845838; DOI=10.1093/hmg/5.4.461;
RA Andresen B.S., Bross P., Vianey-Saban C., Divry P., Zabot M.-T.,
Roe C.R., Nada M.A., Byskov A., Kruse T.A., Neve S., Kristiansen K.,
Knudsen I., Corydon M.J., Gregersen N.;
RT "Cloning and characterization of human very-long-chain acyl-CoA
dehydrogenase cDNA, chromosomal assignment of the gene and
RT identification in four patients of nine different mutations within the
RT VLCAD gene.";
RL Hum. Mol. Genet. 5:461-472(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Peripheral blood;
RX MEDLINE=96125338; PubMed=8554625;
RA Orii K.O., Aoyama T., Souiri M., Orii K.E., Kondo N., Orii T.,
Hashimoto T.;
RT "Genomic DNA organization of human mitochondrial very-long-chain acyl-
RT CoA dehydrogenase and mutation analysis.";
RL Biochem. Biophys. Res. Commun. 217:987-992(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Liver, Lung, and Pancreas;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN CHARACTERIZATION.
RP MEDLINE=95286809; PubMed=7769092;
RA Aoyama T., Souiri M., Ushikubo S., Kamiyo T., Yamaguchi S.,
Kelley R.I., Rhead W.J., Uetake K., Tanaka K., Hashimoto T.;
RT "Purification of human very-long-chain acyl-coenzyme A dehydrogenase
and characterization of its deficiency in seven patients.";
J. Clin. Invest. 95:2465-2473(1995).
RN [6]
RP REVIEW ON VARIANTS.
RX MEDLINE=99138660; PubMed=9973285;
RA Andresen B.S., Olpin S., Poorthuis B.J.H.M., Scholte H.R.,
Vianey-Saban C., Wanders R., Ijlst L., Morris A., Pourfarzam M.,
Bartlett K., Baumgartner E.R., de Klerk J.B.C., Schroeder L.D.,
Corydon T.J., Lund H., Winter V., Bross P., Bolund L., Gregersen N.;
RT "Clear correlation of genotype with disease phenotype in very-long-
chain acyl-CoA dehydrogenase deficiency.";
Am. J. Hum. Genet. 64:479-494(1999).
RN [7]
RP VARIANTS VLCAD DEFICIENCY GLU-130 DEL; LYS-299 DEL; GLN-382 AND
TRP-613.
RX MEDLINE=96108970; PubMed=8554073;
RA Souiri M., Aoyama T., Orii K., Yamaguchi S., Hashimoto T.;
RT "Mutation analysis of very-long-chain acyl-coenzyme A dehydrogenase
(VLCAD) deficiency: identification and characterization of mutant
RT VLCAD cDNAs from four patients.";
RL Am. J. Hum. Genet. 58:97-106(1996).
RN [8]
RP VARIANT VLCAD DEFICIENCY HIS-450.
RX MEDLINE=98206416; PubMed=9546340;
RA Smelt A.H., Poorthuis B.J.H.M., Onkenhout W., Scholte H.R.,
Andresen B.S., van Duinen S.G., Gregersen N., Wintzen A.R.;
RT "Very long chain acyl-coenzyme A dehydrogenase deficiency with adult
onset.";
RL Ann. Neurol. 43:540-544(1998).
RN [9]
RP VARIANTS VLCAD DEFICIENCY.
RX MEDLINE=99177129; PubMed=10077518;
RA Mathur A., Sims H.F., Gopalakrishnan D., Gibson B., Rinaldo P.,
Vockley J., Hug G., Strauss A.W.;
RT "Molecular heterogeneity in very-long-chain acyl-CoA dehydrogenase
deficiency causing pediatric cardiomyopathy and sudden death.";
Circulation 99:1337-1343(1999).
RL [10]
CC -1- FUNCTION: Active toward esters of long-chain and very-long chain
fatty acids such as palmitoyl-CoA and stearoyl-CoA.
CC -1- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
ETF.
CC -1- COFACTOR: FAD.
CC -1- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
step.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P49748-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P49748-2; Sequence=VSP_007734;
CC Note=No experimental confirmation available;
CC -1- DISBASE: Defects in ACADVL are the cause of very long chain acyl-
CoA dehydrogenase deficiency (VLCAD deficiency) [MIM:201475].
CC VLCAD deficiency is an autosomal recessive disease which leads to
impaired long-chain fatty acid beta-oxidation. It is clinically
heterogenous, with three major phenotypes: a severe childhood
form, with early onset, high mortality, and high incidence of
cardiomyopathy; a milder childhood form, with later onset, usually
with hypoketotic hypoglycemia as the main presenting feature, low
mortality, and rare cardiomyopathy; and an adult form, with
isolated skeletal muscle involvement, rhabdomyolysis, and

CC myoglobinuria, usually triggered by exercise or fasting.
CC -|- MISCELLANEOUS: A number of straight-chain acyl-CoA dehydrogenases
CC of different substrate specificities are present in mammalian
CC tissues.
CC -|- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D43682; BAA07781.1; -
CC EMBL; L46590; AAA79002.1; -
CC EMBL; X86556; CAA60253.1; -
CC EMBL; D78298; BAA23057.1; -
CC EMBL; D78279; BAA23057.1; JOINED.
CC EMBL; D78280; BAA23057.1; JOINED.
CC EMBL; D78281; BAA23057.1; JOINED.
CC EMBL; D78282; BAA23057.1; JOINED.
CC EMBL; D78283; BAA23057.1; JOINED.
CC EMBL; D78284; BAA23057.1; JOINED.
CC EMBL; D78285; BAA23057.1; JOINED.
CC EMBL; D78286; BAA23057.1; JOINED.
CC EMBL; D78287; BAA23057.1; JOINED.
CC EMBL; D78288; BAA23057.1; JOINED.
CC EMBL; D78289; BAA23057.1; JOINED.
CC EMBL; D78290; BAA23057.1; JOINED.
CC EMBL; D78291; BAA23057.1; JOINED.
CC EMBL; D78292; BAA23057.1; JOINED.
CC EMBL; D78293; BAA23057.1; JOINED.
CC EMBL; D78294; BAA23057.1; JOINED.
CC EMBL; D78295; BAA23057.1; JOINED.
CC EMBL; D78296; BAA23057.1; JOINED.
CC EMBL; D78297; BAA23057.1; JOINED.
CC EMBL; BC000399; AAH00399.1; -
CC EMBL; BC012912; AAH12912.1; -
CC EMBL; BC020218; AAH20218.1; -
CC PIR; S54183; S54183.
CC HSP; Q06319; IBCU.
CC Genew; HGNC:92; ACADVL.
CC H-InvdB; HIX0013488; -
CC Reactome; P49748; -
CC MIM; 201475; -
CC GO; GO:0005739; C:mitochondrion; TAS.
CC GO; GO:0004466; F:long-chain-acyl-CoA dehydrogenase activity; TAS.
CC GO; GO:0015980; P:energy derivation by oxidation of organic c.; TAS.
CC GO; GO:0006635; P:fatty acid beta-oxidation; TAS.
CC InterPro; IPR006089; Acyl-CoA dh.
CC InterPro; IPR006090; Acyl-CoA dh C.
CC InterPro; IPR006091; Acyl-CoA dh M.
CC InterPro; IPR006092; Acyl-CoA dh N.
CC InterPro; IPR009100; AcylCoA dehyd NM.
CC Pfam; PF00441; Acyl-CoA dh; 1.
CC Pfam; PF02770; Acyl-CoA dh M; 1.
CC Pfam; PF02771; Acyl-CoA dh N; 1.
CC PROSITE; PS00072; ACYL_COA_DH_1; 1.
CC PROSITE; PS00073; ACYL_COA_DH_2; 1.
CC KW Alternative splicing; Cardiomyopathy; Disease mutation; FAD;
CC Fatty acid metabolism; Flavoprotein; Mitochondrion; Oxidoreductase;
CC Polymorphism; Transit peptide.
CC TRANSIT 1 40 Mitochondrion (By similarity).
CC FT CHAIN 41 655 Acyl-CoA dehydrogenase, very-long-chain

Alignment Scores:

Pred. No.: 1.12e-79 Length: 655
Score: 1308.00 Matches: 276
Percent Similarity: 64.97% Conservative: 106
Best Local Similarity: 46.94% Mismatches: 194
Query Match: 38.21% Indels: 12

DB: 1 Gaps: 8
US-09-945-326-3 (1-1863) x ACV_HUMAN (1-655)
QY 109 CGAGCTTTCGCAAGAGCTTTCTAGGCAAAATCAAGAAAGAAAGATTTTCCCATTT 168
Db 71 LysSerPheAlaValGlyMetPheLysGlyGlnLeuThrThrAspGlnValPheProThr 90
QY 169 CCAGAAGTTAGCCAAAGATGAACCTTAATGAA---ATCAATCAGTTCTTTGGGACCGTGAA 225
Db 91 ProSerValLeuAenGluGlnThrGlnPheLeuLysGluValGluProValSer 110
QY 226 AATTTCTCACTCAAGAGGTGGACTCCGAAAATTTGACCAGGAGGAAATCCCATCAT 285
Db 111 ArgPhePheGluGluValAenAspProAlaLeuAenAspAlaLeuGluMetValGluGlu 130
QY 286 GAAACTTTTGAGAAATTTGAAGAGCTTAGGCTTTTGGGCTGCAAGTCCAGAGAAATAT 345
Db 131 ThrThrTrpGlnGlyLeuLysGluLeuGlyAlaPheGlyLeuGlnValProSerGluLeu 150
QY 346 GTGGCTGGCTTCTCCCAACACCATGTACTCAAGACTAGGGGAGATCATCAGCATG--- 402
Db 151 GlyGlyValGlyLeuCysAenThrGlnTyrAlaArgLeuValGluLeuValGlyMetHis 170
QY 403 GATGGTCCATCACTGTGACCTGGCAGCCAGCCAGCATTTGGCCCTCAGGGGATCATC 462
Db 171 AspLeuGlyValGlyIleThrLeuGlyAlaHisGlnSerIleGlyPheLysGlyIleLeu 190
QY 463 TTGGCTGGCACTGAGGAGCAGAAAGCAATACTTGCCTAAACTGGCGTCCGGGAGCAC 522
Db 191 LeuPheGlyThrLysAlaGlnLysGluLysTyrLeuProLysLeuAlaSerGlyGluThr 210
QY 523 ATTGCAGCTTCTGCTCAGCGGAGCCAGCCAGTGGGAGCGATCGAGCTCAATCCGAGC 582
Db 211 ValAlaAlaPheCysLeuThrGluProSerSerGlySerAspAlaAlaSerIleArgThr 230
QY 583 AGAGCCACACTAAGTGAAGCAGACACTACCTCAATGGCTCAGAGTCTGGATT 642
Db 231 SerAlaValProSerProCysGlyLysTyrThrLeuAenGlySerLysLeuTrpIle 250
QY 643 ACTAATGGAGGACTGGCCTAATATTTTACTGTGTGTGCAAGACTGAGGTCTGTAT--- 699
Db 251 SerAsnGlyLeuAlaAlaPheThrValPheAlaLysThrProValThrAspPro 270
QY 700 TCTGATGGATCAGTGAAGCAAAATCACAAGCATTCATAGTAGAAGAGACTTTGGTGA 759
Db 271 AlaThrGlyAlaValLysGluLysIleThrAlaPheValValGluArgGlyPheGly 290
QY 760 GTCCTAATGGGAAACCCGAGATAATTAGGCATTCGGGGCTCCACACTTGTGAATC 819
Db 291 IleThrHisGlyProGluLysLysMetGlyIleLysAlaSerAenThrAlaGluVal 310
QY 820 CATTTTGAACACCAAGATACCTGTGAAAACATCTTCGAGAGGTGCGAGATGGGTTT 879
Db 311 PhePheAspGlyValArgValProSerGluAenValLeuGluValGlySerGlyPhe 330
QY 880 AAGGTGGCCATGAACATCTCTCAACAGCGCGGTTTCAAGTATGGCAGCGTGTGGTGG 939
Db 331 LysValAlaMethIleLeuAenAenGlyArgPheGlyMetAlaAlaLeuAlaGly 350
QY 940 CTGCTCAAGAGATTGATTGAATAGCTGCTGAGTAGCCCTGCACAGGAACAGTTTAA 999
Db 351 ThrMetArgGlyIleAlaLysAlaValAspHisAlaThrAenArgThrGlnPheGly 370
QY 1000 AAGAGCTCAGTGAATTTGGATTGATTTCAGGAGAAATTTTCACCTGATGGCTCAGAAGCT 1059
Db 371 GluLysIleHisAenPheGlyLeuIleGlnGluLysLeuAlaArgMetValMetLeuGln 390
QY 1060 TAGCTCATGGAGAGTATGACTTACCTCACAGCAGGAGTATGCGACCAACCTGTTCCC 1119
Db 391 TyrValThrGluSerMetAlaTyrMetValSerAlaAenMetAspGln---GlyAlaThr 409
QY 1120 GACTGTCCATCAGCAGGAGCCATGTTGTAAGGTGTTTTCAGTCCGAGGCCCTGTCAGTGT 1179

RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
 DR EMBL; AE003796; AA057579.1; -
 DR HSP; Q06319; 18UC.

DR IntAct; Q9V8T1; -
 DR FlyBase; FBgn0034432; CG7461.
 DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006089; Acyl-CoA dh.
 DR InterPro; IPR006090; Acyl-CoA dh.C.
 DR InterPro; IPR006091; Acyl-CoA dh.M.
 DR InterPro; IPR006092; Acyl-CoA dh.N.
 DR InterPro; IPR009075; Acyl-CoADH C like.
 DR InterPro; IPR009100; AcylCoA dehyd_NM.
 DR Pfam; PF02770; Acyl-CoA dh.M; 1.
 DR Pfam; PF02771; Acyl-CoA dh.N; 1.
 DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
 DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
 DR FAD; Flavoprotein; Oxidoreductase.
 SQ SEQUENCE 655 AA; 71326 MW; 00916BD701E127CB CRC64;

Alignment Scores:

Pred. No.:	7.8e-79	Length:	655
Score:	1295.50	Matches:	280
Percent Similarity:	61.84%	Conservative:	104
Best Local Similarity:	45.09%	Mismatches:	212
Query Match:	37.85%	Indels:	25
DB:	2	Gaps:	9

US-09-945-326-3 (1-1863) x Q9V8T1 (1-655)

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DB	44	AlaSerLeuCySerGlnIleAlaThrHisSerProLysLeuGlyAlaGluSerAsnArg	63
QY	82	CGGCTACTGCGCACACCGCCCTGTACGAGCTTTCGCCAAGAGCTTTCTTAGGCAAA	141
DB	64	SerLysGluLysAlaSerGluAsn--GluSerPheMetAlaAsnIlePheArgGlySer	82
QY	142	ATCAGAAGAAAGAGTTTCCCATTTCCAGAGTTTCCAGAGTAACTTAATGAATC	201
DB	83	LeuValSerSerGlnValPheProTyProAspValLeuThrAlaGluGlnLysGluLeu	102
QY	202	---AATCAGTCTTGGGACCGTGGAAATCTTCACTGAAGAGTGGACTCCCGAAA	258
DB	103	ThrAsnSerLeuIleAspProPheGluArgPheSerAspValAsnAspAlaAlaArg	122
QY	259	ATTGACAGGAAGGAAATCCCAAGATGAACTTTGGAGAAATTTGAAGAGCTAGGCGTT	318
DB	123	AsnAspAlaAsnSerLysIleAspAspThrThrAlaLeuTrpGluLeuGlyAla	142
QY	319	TTTGGGCTGCAAGTCCAGAGAATATGTGGCTCGGCTTCTCCACACCATGTACTCA	378
DB	143	PheGlyIleGlnValProSerGluPheGlyGlyLeuGlyLeuAsnThrGlnTyGly	162
QY	379	AGACTAGGGGAGATCATCAGCATG---GATGGGTCCATCATCTGACCCCTGGCAGCCAC	435
DB	163	ArgLeuCyAlaIleValGlyValAsnAspLeuGlyIleThrIleGlyAlaHis	182
QY	436	CAGGCTATTGGCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAGAAGCCAAATAC	495
DB	183	GlnSerIleGlyPheLysGlyIleLeuLeuTyGlyThrProGluGlnLysGluLysTy	202
QY	496	TTGCCTAACTGGGCTCCGGGAGCACAATGACGCTTTCGCTCAGGAGCCAGCCAGT	555
DB	203	LeuProLysValAlaAlaGluGlnValTyAlaAlaPheAlaLeuThrGluProSerSer	222
QY	556	GGGAGCGCATCGCCTCAATCCGAGCAGAGCCACACTAAGTGAAGACAGAGCAGCTAC	615
DB	223	GlySerAspAlaGlySerIleArgCysArgAlaValLysSerAlaAspGlyLysHisTy	242

QY	616	ATCCTCAATCGCTCCAAAGGTCTGGATTACTAATGGAGGACTGGCCAAATATTTTACTGTG	675
DB	243	ValLeuAsnGlySerLysIleTrpIleSerAsnGlyGlyIleAlaGluIleMetThrVal	262
QY	676	TTTGCAAGAGCTGAGTCTGTTGAT---TCTGTGATCAGTGAAGACAAAATCACAGCA	732
DB	263	PheAlaGlnThrGluGlnValAspProLysThrGlyLysLysAspLysValThrAla	282
QY	733	TTTCATAGTGAAGAGACTTTTGGTGGAGTCACTAATGGAAACCCGGAAGATAAATTAGGC	792
DB	283	PheIleValGluArgSerPheGlyGlyValThrAsnGlyProProGluLysLysMetGly	302
QY	793	ATTGGGGCTCCCAACTTGTGAAGTCCATTTTGAATAACACCAAGATACCTGTGGAAAC	852
DB	303	IleLysAlaSerAsnThrAlaGluValTyPheGluAspValLysIleProIleGluAsn	322
QY	853	ATCCTTGGAGAGTCCGAGATGGTGTAAAGTGGCCATGAACATCTTCAACAGCGGCGG	912
DB	323	ValLeuGlyLysGluGlyAspGlyPheLysValAlaMetAsnIleLeuAsnAsnGlyArg	342
QY	913	TTGAGCATGGGACGCTGCTGGCTGCTCAAGAGATTTGATTGAATGACTGCTGAG	972
DB	343	PheGlyMetGlyAlaThrLeuSerGlyThrMetLysLysCysIleGluGlnAlaThrGlu	362
QY	973	TACGCTGCAAGGAAACAGTTTAAACAGAGGCTCAGTGAATTTGATTGATTTCAGAG	1032
DB	363	HisAlaAsnAsnArgValGlnPheGlyGlnLysLeuLysAsnTyGlySerIleGlnGlu	382
QY	1033	AAATTTGCAGTGGCTCAGAGGCTTACGTATGAGAGTATGACCTACCTCACAGCA	1092
DB	383	LysLeuAlaGlnMetAsnIleLeuGlnTyAlaThrGluSerMetAlaPheThrIleSer	402
QY	1093	GGGATGCTGACCAACCTGGCTTTCCCGACTGTCCATCGAGGAGGAGCATGTGAAGGTG	1152
DB	403	GlnAsnMetAsp---AlaGlySerLysAspTyHisLeuGluAlaAlaIleSerLysIle	421
QY	1153	TTGAGTCCGAGCGCTGCGAGTGTGAGTGAGCGCTGCAGATCTCGGGGGCTTG	1212
DB	422	TyrAlaSerGluSerAlaTrpTyValCysAspGluAlaIleGlnIleLeuGlyGlyMet	441
QY	1213	GGCTACACAGGAGCATCTCGTACGAGCATCTGCTGACACCCGCTCTCTCTCATC	1272
DB	442	GlyTyMetValAspAsnGlyLeuGluArgValLeuArgAspLeuArgIlePheArgIle	461
QY	1273	TTGAGGAACCAATGAGATTCTCCGATGTACATCCCTGAGCGGTCTGCAGCATGCC	1332
DB	462	PheGluGlyThrAsnAspIleLeuArgLeuPheIleAlaLeuThrGlyIleGlnTyAla	481
QY	1333	GGCGCATCTGACTACCAAGATCTCATGACTTAAACAG-----GCC	1374
DB	482	Gly-----SerHisLeuLysGluLeuGlnArgAlaPheLysAsnProSerAla	497
QY	1375	AAAGTGACACATCATGTGATCCGTTGGCGGAGGCTTCGGGACTCTCTGGGCGGAACT	1434
DB	498	AsnLeuGlyLeuIlePheLysGluAlaSerArgArg-----AlaAlaSerThr	513
QY	1435	GTGAGCTGGGGCTGACAGCAACCACTGGAGTGTGCACCCCACTGTGGGACAGTGC	1494
DB	514	ValGlyLeuGlyGlyThrAspLeuSerGlyHisValValGlyGluLeuLeuProTyAla	533
QY	1495	AACAAGTTTGAGAGAACACTTACTGCTTCGGCGGAGCCCTGGAGACACTGCTGCTCCG	1554
DB	534	LysLysThrAlaHisCysIleAspLeuPheGlyGlnSerValGluGluLeuLeuLeuArg	553
QY	1555	TTTGGCAAGACCATCATGGAGGAGCAGCTGGTACTGAAGGGGTGGCCACATCTCTCATC	1614
DB	554	TyrAsnLeuAsnIleValAsnGluGlnIleLeuLeuThrArgLeuAlaAsnAlaIle	573
QY	1615	AACTGTATGGCATACGCGCGTGTGCGGGCCAGCCGCTCCATCCCATTTGGGCTC	1674
DB	574	AspIleTyAlaMetValValThrGlnSerArgSerSerArgAlaValAsnLeuAsnLeu	593

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QY 1675 CGCAACACGACGACGAGGTTCTCTTGGCCAAACACACCTTCTGCTGGGAAGCTTACTTGCAG 1734
Db 594 ProThrAlaGlnHisGluLeuAsnMetThrLysAlaLeuThrIleGlnAlaSerAspArg 613
QY 1735 AATCTCTTCAGCCTCTCTCAGCTGGACAAAGTATGCTCCAGAAAACCTTAGATGACAGATT 1794
Db 614 ValIleLysAsnLeuGlnAlaAlaThrSerSerHisArgSerLeuAsnGluLysIle 633
QY 1795 AAGAACTGCTCCAGCAGATCTCTGAGACGGAGCCTATATCTGTGCCCCACCTCTGGAC 1854
Db 634 SerThrIleAlaLysThrThrLeuGluAsnGlyGlyValThrThrThrGlyIleLeuAsp 653
QY 1855 AGG 1857
Db 654 Gln 654

RESULT 13
QY Q7Q868 PRELIMINARY; PRT; 639 AA.
AC Q7Q868 ID
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE AGCP15352 (Fragment).
GN Name=agCG50940; ORFNames=ENSGG00000009991;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008944; EAA10216.1; -.
DR HSP; Q06319; IBCU.
DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006089; Acyl-CoA dh.
DR InterPro; IPR006090; Acyl-CoA dh. C.
DR InterPro; IPR006091; Acyl-CoA dh. M.
DR InterPro; IPR009075; AcylCoADH_C like.
DR InterPro; IPR009100; AcylCoA_dh; 1.
DR Pfam; PF00441; Acyl-CoA dh; 1.
DR Pfam; PF02770; Acyl-CoA dh M; 1.
DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW FAD; Flavoprotein; Oxidoreductase.
FT NON TER 1
FT SEQUENCE 639 AA; 70246 MW; 45790371A4D12CB5 CRC64;

Alignment Scores:
Pred. No.: 2.48e-78 Length: 639
Score: 1288.00 Matches: 282
Percent Similarity: 62.66% Conservative: 109
Best Local Similarity: 45.19% Mismatches: 187
Query Match: 37.63% Indels: 46
DB: 2 Gaps: 11

US-09-945-326-3 (1-1863) x Q7Q868 (1-639)
QY 79 CGGCGGTACTGCGCCAGCAGCCCG----- 102
Db 28 ArgArgCysLeuSerAlaAlaProGlnAlaLysGlnAlaGlnAlaThrPro 47
QY 103 -----CCTGTACGAGCTTTCGCCAAGAGCTTTCCTAGGCAAAATC 144
Db 48 SerGluAlaGluLysArgProAsnMetSerPheLeuThrAsnIlePheArgGlyGlnVal 67

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QY 145 AAGAAGAAAGAAAGTTTCCCAATTTCCAGAAGTTAGCCAAAGATGAACCTTAATGAA---ATC 201
Db 68 GlnProAlaGlnValPheProTyrProGluAlaLeuAspAlaGluGlnLysGluTyrIle 87
QY 202 AATAGTTCTTGGGACCCGTCGTAATAATTCCTTCACTGAAGAGGTGGACTCCCGCAAAATTT 261
Db 88 AlaSerPheValAspProValThrLysPhePheGluGluValAsnAspProValLysAsn 107
QY 262 GACCCAGGAAGGAATATCCAGATGAACTTTGGAGAAATTCGAAGAGCCTAGGCTTTT 321
Db 108 AspValAsnAlaSerIleAspGluLysThrCysGluAlaLeuTrpAspLeuGlyAlaPhe 127
QY 322 GGGCTGCAAGTCCCAAGAATATGTGGCTGGGCTTCTCCAAACACCACTGACTCAAGA 381
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QY 382 CTAGGGGAGATCATC---AGCATGGATGGTCCATCATCTGTGACCTCGCAGGCGCACCG 438
Db 148 MetCysAspIleGlyGlyGlnAspLeuGlyLeuGlyIlePheIleGlyAlaHisGln 167
QY 439 GCTATTGGCCTCAAGGGGATCATCTTGGCTGGCACTGAGGAGCAGAAAGCCAAATACTTG 498
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QY 499 CCTAAACTGGCTCCGGGAGCACATTCTGCTCAGGCTTCTGCTCAGGAGCCAGCCAGTGG 558
Db 188 ProMetValSerThrGlyLysValTyrAlaAlaPheAlaLeuThrGluProSerSerGly 207
QY 559 AGCGATGACGCTCAATCCGAGCAGACGACCACTAAGTGAAGACAAAGAGCACTACATC 618
Db 208 SerAspAlaGlySerIleArgCysArgAlaValLysSerAlaAspGlyLysIstYrVal 227
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Db 328 GlyMetAlaAlaThrLeuSerGlyThrMetArgAlaCysIleGlnLysAlaAlaGluHis 347
QY 976 GCCTGCACAGAAACAGTTTAAACAGAGCTCAGTGAATTTGGATTGATTCAAGGAGAAA 1035
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QY 1036 TTTGCACTAGTGGCTCAGAAGGCTTACGTCATGAGAGATGATGACCTCAACAGCAGGG 1095
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QY 1096 ATGCTGACCAACCTGGCTTTCCCGACTGCTCCATCGAGCAGCCATGTTGAGGTGTTTC 1155
Db 388 AsnMetAsp---ThrGlySerLeuAspTyrHisIleGluAlaIleSerLysValPhe 406
QY 1156 AGCTCCGAGCGCCCTGGCAGTGTGTGAGTGAGCGCTCGAGATCTCGGGGCTTGGGC 1215
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[illegible]

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